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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE
EXPRESSION IN HUMAN ADULT LIVER

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene
expression in a sample derived from human adult liver is described. Also described are single exon nucleic acid probes expressed in
the adult liver and their use in methods for detecting gene expression.



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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S. patent application serial nos. 09/632,366, filed August 3, 2000 and 09/608,408, filed June 30, 2000; claims the benefit under 35 U.S.C. s 119(e) of U.S. provisional patent application serial nos. 60/236,359, filed September 27, 2000, 60/234,687, filed September 21, 2000, 60/207,456, filed May 26, 2000, and 60/180,312, filed February 4, 2000; and further claims the benefit under 35 U.S.C. s 119(a) of UK patent application no. 0024263.6, filed October 4, 2000, the disclosures of which are incorporated herein by reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20

The present application includes a Sequence Listing in electronic format, filed pursuant to PCT Administrative Instructions 801 - 806 on a single CD-R disc, in triplicate, containing a file named pto_ADULT_LIVER.txt, created 24 January 2001, having 26,335,065 bytes. The Sequence Listing contained in said file on said disc is incorporated herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In particular, the present invention relates to unique genome-derived single exon nucleic acid probes expressed in human

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adult liver and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of mRNA - are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches - and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species - there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

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While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of
5 a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium,
10 *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the
15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many
20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that
25 function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting
30 coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et
35 al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

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Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al., *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature* 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas

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et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the liver are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition,
20 onset, and/or aggressiveness of most, if not all, of these diseases; although causative mutations in single genes have been identified for some, these disorders are believed for the most part to have polygenic etiologies. There is a need for methods and apparatus that permit prediction, diagnosis
25 and prognosis of diseases of the liver particularly those diseases with polygenic etiologies.

Summary of the Invention

30 The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the
35 expression of putative genes identified within genomic

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sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human adult liver, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 13,109 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid

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probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 25,995 or a complimentary sequence, or a portion of such a sequence.

5 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

10 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said
15 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most
20 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single
25 exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The
30 nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride,
35 polytetrafluoroethylene, polystyrene, polycarbonate,

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polyacetal, polysulfone, celluloseacetate,
cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable
5 set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or
10 more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-
15 derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of
20 SEQ ID Nos. 13,110 - 25,995, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 13,109.

Accordingly, in a third aspect of the invention,
25 there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human adult liver which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 13,109 or a complementary sequence or a
30 fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human adult liver.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a
35 nucleotide sequence as set out in any of SEQ ID NOS.:

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13,110 - 25,995 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring
5 human gene expression in a sample derived from human adult liver which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 25,996 - 38,578 or a complementary sequence or a fragment thereof wherein said probe
10 hybridizes at high stringency to a nucleic acid expressed in the human adult liver.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous
15 nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon
20 nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb,
25 preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or
30 PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first
35 member of a specific binding pair. Suitable fluorescent

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labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single
5 exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks
10 homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance
15 with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is
20 provided a method of measuring gene expression in a sample derived from human adult liver, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said
25 first collection of nucleic acids derived from mRNA of human adult liver; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is
30 provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably
35 labeled nucleic acids to a single exon probe,

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wherein said detectably labeled nucleic acids are derived from mRNA from the adult liver of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 25,995 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 13,110 - 25,995, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 - 13,109.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ

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ID NOS.: 25,996 - 38,578.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOs: 25,996 - 38,578, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

15 Detailed Description of the Invention

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary

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planar substrate, as is described, *inter alia*, in Brenner
et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000);
in such case, the term "microarray" and phrase "nucleic
acid microarray" refer to the plurality of beads in
5 aggregate.

As used herein with respect to a nucleic acid
microarray, the term "probe" refers to the nucleic acid
that is, or is intended to be, bound to the substrate; in
such context, the term "target" thus refers to nucleic acid
10 intended to be bound thereto by Watson-Crick
complementarity. As used herein with respect to solution
phase hybridization, the term "probe" refers to the nucleic
acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising
15 SEQ ID NO.", and variants thereof, intends a nucleic acid
probe, at least a portion of which probe has either (i) the
sequence directly as given in the referenced SEQ ID NO., or
(ii) a sequence complementary to the sequence as given in
the referenced SEQ ID NO., the choice as between sequence
20 directly as given and complement thereof dictated by the
requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and
the equivalent acronym "ORF" refer to that portion of an
exon that can be translated in its entirety into a sequence
25 of contiguous amino acids i.e. a nucleic acid sequence
that, in at least one reading frame, does not possess stop
codons; the term does not require that the ORF encode the
entirety of a natural protein.

As used herein, the term "amplicon" refers to a
30 PCR product amplified from human genomic DNA, containing
the predicted exon.

As used herein the term "exon" refers to the
consensus prediction of the various exon and gene
predicting algorithms i.e. a nucleic acid sequence
35 bioinformatically predicted to encode a portion of a

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natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.: The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual

object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional
5 information.

Brief Description of the Drawings

10 The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the
15 functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the
20 process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

25 FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution,
30 among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or
35 more but not all tested tissues ("1" - "9"), or expressed

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in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained

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in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100
5 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger
10 contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was
15 erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession,
20 species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will
25 be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100
30 in the present invention include GenBank, and particularly include several divisions thereof, including the
htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the
35 National Institutes of Health and is maintained by the

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National Center for Biotechnology Information (NCBI).
Databases of genomic sequence from species other than
human, such as mouse, rat, *Arabidopsis*, *C. elegans*, *C.*
briggsii, *Drosophila*, zebra fish, and other higher
5 eukaryotic organisms will also prove useful as genomic
sequence database 100.

Genomic sequence obtained by query of genomic
sequence database 100 is then input into one or more
processes 200 for identification of regions therein that
10 are predicted to have a biological function as specified by
the user. Such functions include, but are not limited to,
encoding protein, regulating transcription, regulating
message transport after transcription into mRNA, regulating
message splicing after transcription into mRNA, of
15 regulating message degradation after transcription into
mRNA, and the like. Other functions include directing
somatic recombination events, contributing to chromosomal
stability or movement, contributing to allelic exclusion or
X chromosome inactivation, and the like.

20 The particular genomic sequence to be input into
process 200 will depend upon the function for which
relevant sequence is to be identified as well as upon the
approach chosen for such identification. Process step 200
can be iterated to identify different functions within a
25 given genomic region. In such case, the input often will
be different for the several iterations.

Sequences predicted to have the requisite
function by process 200 are then input into process 300,
where a subset of the input sequences suitable for
30 experimental confirmation is identified. Experimental
confirmation can involve physical and/or bioinformatic
assay. Where the subsequent experimental assay is
bioinformatic, rather than physical, there are fewer
constraints on the sequences that can be tested, and in
35 this latter case therefore process 300 can output the

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entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in
5 process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can
10 be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a
15 combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation
20 can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magneto-optical disk, flash memory, or the
25 like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an
30 experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly
35 to the succeeding process, or stored in permanent or

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interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

5 FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

10 The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene
15 prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding
20 regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences
25 and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be
30 determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements
35 of the subsequent analytical method. Alternatively, or in

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addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate
5 criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

10 Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any
15 given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

20 Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given
25 BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated
30 into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are
35 typically updated on a frequent, even hourly, basis. Thus,

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as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query

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criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

5 Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

 Preprocessing 24 suitable for most approaches and
10 methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like.
15 Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

 Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence,
20 vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

25 Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies
30 a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

35 Once identified, undesired sequence can be

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removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X".

- 5 Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of
10 highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can
15 also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25.
20 Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion
25 from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the
30 informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include,
35 but are not limited to, encoding protein, regulating

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transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%;

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and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used

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approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative
5 sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

10 Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and
15 approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be
20 identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into
25 putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-
30 specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative
35 exon length, sequence GC content, existence of possible

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secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using
5 amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance
10 of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested
15 experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for
20 experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred
25 embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention
30 provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of
35 nucleic acid microarray, the genome-derived single exon

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nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it

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has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for

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amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see

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above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include

5 polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can

10 also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as

15 described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by

20 presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version

25 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using

30 ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of

35 the present invention, a plurality of *E. coli* genes can

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readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high

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throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon *et al.*, or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas *et al.*, *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure

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expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse

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transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector

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sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence.

With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without

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such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham *et al.*, *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

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In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and

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thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely
5 constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be
10 performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered
15 (i.e., mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the
20 genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the
25 microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed
30 on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the
35 melting temperature of probes hybridized to their

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complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the
5 microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ*
10 synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

15 The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

20 Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome
25 has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

30 Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as
35 *Saccharomyces cerevisiae*, particularly in genomic sequence

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drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of

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nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluoer; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically
5 fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to
10 standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage,
15 to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it
20 is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally
25 as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially
30 identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well
35 of a microtiter dish. Although a 96 well microtiter plate

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can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions
5 (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of
10 individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first
15 common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the
20 amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of
25 agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of
30 probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable
35 media that provide probe identification and addressing

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information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

5 If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not
10 required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

15 Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

20 Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be
25 identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases,
30 such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any
35 sequence query algorithm, such as BLAST ("basic local

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alignment search tool"). The results of such query – including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence – can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given

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the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity

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or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.

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For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

5 Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

10 Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction.

15 Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be
20 made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

 As earlier described, increased predictive reliability can be achieved by requiring consensus among
25 methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

 Although FIG. 3 shows three series of
30 horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

35 Furthermore, field 81 can be used to show

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predictions of a plurality of different functions.

However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as
5 a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including
10 interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right
15 borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of
20 annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing
25 an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using
30 genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during
35 amplification and designed to permit reamplification of the

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probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity

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has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to

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indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

5 Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized
10 mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*.
15 BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by
20 DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates
25 unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of
30 such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present
35 invention rapidly produce functional information from

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genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 13,109 of these ORFs in adult liver.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in adult liver is currently available for use in measuring the level of its ORF's expression in adult liver.

Diseases of the liver are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases; although causative mutations in single genes have been identified for some, these disorders are believed for the most part to have polygenic etiologies.

For example, cirrhosis is a major public health problem. In the industrialized world, it is among the top

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ten causes of death; among patients aged 45 to 65, it is the third leading cause of death. The high prevalence is largely the result of alcohol abuse, but other major contributors include chronic hepatitis, biliary disease and iron overload. Approximately 10-15% are cryptogenic.

Cirrhosis is a broad description encompassing the common end stage of many forms of liver injury. Many patients with cirrhosis will remain asymptomatic for years, while others show generalized weakness, anorexia, malaise, and weight loss or, occasionally, more severe symptoms.

The progression from fibrosis, an early consequence of liver disease, to cirrhosis, and the specific histologic morphology that characterizes cirrhosis depend on the extent of injury, the presence of continuing damage, and the response of the liver to damage. The liver may be injured acutely and severely (e.g. necrosis with hepatitis), moderately over months or years (e.g. biliary tract obstruction and chronic active hepatitis), or modestly but continuously (e.g. alcohol abuse).

During the repair process, new vessels connecting the hepatic artery and portal vein to the hepatic venules form within the fibrous sheath that surrounds the surviving nodules of liver cells. These vessels restore the intrahepatic circulatory pathway, but provide relatively low-volume, high-pressure drainage that is less efficient than normal and results in increased portal vein pressure (portal hypertension). Thus, cirrhosis is not static and its features depend on the disease activity and stage.

As cirrhosis is the end stage of many forms of liver disease, many genes have been identified that can contribute to the development of cirrhosis. These include, e.g., the genes responsible for Wilson disease (Online Mendelian Inheritance of Man ("OMIM") 277900), type IV glycogen storage disease (OMIM 232500), galactosemia (OMIM

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230400), and a deficiency of alpha-1-antitrypsin (OMIM 107400). There is substantial evidence, however, for as yet uncharacterized loci which cause cirrhosis.

- For example, Iber and Maddrey, *Prog. Liver Dis.* 2: 290-302 (1965), reviewed 13 previously reported families and 8 new to this study, each with 2 or more affected members. They pointed out that, with a single exception, the multiple cases were in the same generation. Within a given family, the age of onset, clinical course, and biopsy findings were very similar, but there were wide differences between families.

- Kalra et al., *Hum. Hered.* 32:170-175 (1982) studied the families of 220 cases of Indian childhood cirrhosis and 70 families of age-matched controls. The hypotheses of autosomal recessive, partial sex-linkage, and doubly recessive inheritance were found untenable and the authors concluded that multifactorial inheritance was most plausible. Lefkowitz et al., *New Eng. J. Med.* 307:271-277 (1982) described 4 white American sibs who died between ages 4.5 and 6 years of cirrhosis that closely resembled that of the childhood cirrhosis of Asiatic Indians.

Another example of uncharacterized loci which cause cirrhosis are those related to the risk of alcoholism.

- Cloninger, *Science* 236:410-416 (1987), defined two separate types of alcoholism. According to these definitions, type 1 alcohol abuse has its usual onset after the age of 25 years and is characterized by severe psychological dependence and guilt. Type 1 occurs in both men and women and requires both genetic and environmental factors to become manifest. By contrast, type 2 alcohol abuse has its onset before the age of 25; persons with this type of alcoholism are characterized by their inability to abstain from alcohol and by frequent aggressive and antisocial behavior. Type 2 alcoholism is rarely found in

women and is much more heritable.

Despite considerable effort to identify genes related to the risk of alcoholism, relatively few genes have been identified. Some of this work has suggested a relationship between the metabolism of dopamine and alcoholism. Blum et al., J.A.M.A. 263:2055-2060 (1990) and Bolos et al., J.A.M.A. 264:3156-3160 (1990) investigated the relationship of the dopamine D2 receptor (DRD2; OMIM 126450) to alcoholism, but the sample size was small and their results were inconclusive. However, Tiihonen et al., Molec. Psychiat. 4, 286-289 (1999), found a markedly higher frequency in a population of type 1 alcoholics of the low activity allele of the enzyme catechol-O-methyltransferase (COMT, OMIM 116790), which has a crucial role in the metabolism of dopamine, suggesting a role for dopamine metabolism in increased risk of alcoholism. For a brief review of recent progress toward the identification of genes related to risk for alcoholism see Buck, Genome 9:927-928 (1998).

As another example, multiple genes have been shown to predispose to hyperlipoproteinemia or hyperlipidemia. Much attention has been focused on these disorders because there is a strong association of hyperlipidemia, especially hypercholesterolemia, with development of coronary artery disease. Coronary artery disease accounts for at least 25% of all deaths in the United States. Coronary artery disease results when the arteries supplying the heart muscle become occluded by plaques composed of lipids like cholesterol, blood clotting components and blood cells.

The major plasma lipids circulate bound to proteins as macromolecular complexes called lipoproteins. Although closely interrelated, the major lipoprotein classes - chylomicron, very-low-density lipoprotein (VLDL), low-density lipoprotein (LDL), and high-density lipoprotein

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(HDL) - are usually classified in terms of physicochemical properties (e.g., density after centrifugation). Chylomicrons, the largest lipoproteins, carry exogenous triglyceride from the intestine via the thoracic duct to the venous system and into peripheral sites. VLDL carries endogenous triglyceride primarily from the liver to the same peripheral sites for storage or use. Lipases quickly degrade the triglyceride in VLDL to produce intermediate density lipoproteins (IDL) and within 2 to 6 h, IDL is degraded further to generate LDL, which has a plasma half-life of 2 to 3 days. While the overall fate of LDL is unclear, the liver is responsible for removing approximately 70% and active receptor sites have been found on the surfaces of hepatocytes.

Several monogenic conditions that lead to elevated levels of one or more serum lipoproteins have been defined and the responsible gene identified, including, e.g., hyperlipoproteinemia type I (OMIM 238600), familial hypercholesterolemia (OMIM 143890), and familial defective apolipoprotein B (OMIM 107730). However, in many cases the etiology is unknown and there is strong evidence for additional uncharacterized loci.

For example, Zuliani et al., *Arterioscler. Thromb. Vasc. Biol.* 19:802-809 (1999) identified a Sardinian family with a recessive form of hypercholesterolemia with the clinical features of familial hypercholesterolemia (OMIM 603813), and found that previously identified genes were not responsible for this disorder. They proposed that in this new lipid disorder, a recessive defect causes a selective impairment of the LDL receptor function in the liver. Ciccarese et al., *Am. J. Hum. Genet.* 66:453-460 (2000) recently mapped this novel disease locus.

Another example is designated familial combined hyperlipidemia (OMIM 144250) which affects approximately 1-

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2% of the population in the Western world. This disorder can have its basis in mutation in several novel genes, two of which have been mapped to chromosome 1 (Pajukanta et al., *Nature Genet.* 18:369-373 (1998)) and chromosome 11 (Aouizerat et al., *Am. J. Hum. Genet.* 65, 397-412 (1999)). The high frequency of this disorder suggests that most, if not all, hyperlipidemias are of multifactorial genetic etiology.

As yet a further example, primary sclerosing cholangitis (PSC) is a disorder characterized by a patchy obliterative inflammatory fibrosis of the large bile ducts. Chronic inflammation leads to extensive bile duct strictures, cholestasis, and gradual progression to biliary cirrhosis. PSC occurs most often in young men and is commonly associated with inflammatory bowel disease, especially ulcerative colitis. The onset is usually insidious, with gradual, progressive fatigue, pruritus, and jaundice. There is no specific therapy for sclerosing cholangitis, and liver transplantation is the only apparent cure.

The etiology of PSC is not known, but both genetic and immunologic abnormalities have been implicated. However, the frequency of HLA-B8 and HLA-DT2, which are associated with a number of autoimmune diseases, is higher in PSC than normal individuals. Prochazka et al., *New Eng. J. Med.* 322:1842-1844 (1990) found that 100% of 29 patients with primary sclerosing cholangitis carried the HLA-DRW52a antigen, which is normally present in 35% of the population.

As a still further example, sarcoidosis is a disease of unknown cause characterized by non-caseating granulomas in one or more organ systems. These granulomas may resolve completely or proceed to fibrosis. The disorder is systemic, but the liver is affected in approximately 75% of cases. Sarcoidosis occurs mainly in persons aged 20 to

40 yr and is most common in Northern Europeans and American blacks. The lifetime risk of developing sarcoidosis is particularly high among Swedish men (1.15%), Swedish women (1.6%), and African Americans (2.4%).

5 The much greater frequency in African Americans relative to the United States population overall suggests a genetic contribution to etiology. Early research studying familial aggregation indicated that the disease may have a nongenetic basis because the family pattern did not conform
10 to a simple Mendelian mode of inheritance (Allison, Sth. Med. J. 57: 27-32 (1964)). However, Headings et al., Ann. N.Y. Acad. Sci. 278:377-385 (1976) favored multifactorial genetic inheritance of susceptibility. Nowack et al., Arch. Intern. Med. 147:481-483 (1987), found an unusually
15 high frequency of HLA-DR5 in a study of 440 patients with sarcoidosis in Marburg, Germany. They also concluded that the role of an environmental or infectious agent triggering sarcoidosis cannot be envisaged without considering genetically linked cofactors.

20 Other significant diseases of liver are also believed to have a genetic, typically polygenic, etiologic component. These diseases include, e.g., primary biliary cirrhosis, Zellweger syndrome, cholestasis-lymphedema syndrome, Alstrom syndrome, primary pulmonary
25 hypertension, Berardinelli-Seip congenital lipodystrophy, iron overload in Africa, neonatal cholestatic hepatitis, autosomal recessive KID syndrome, familial hypotransferrinemia, type I congenital dyserythropoietic anemia, porphyria variegata, Finnish lactic acidosis with
30 hepatic hemosiderosis, Rotor syndrome, essential hypertension, ARC syndrome, type II conjugated hyperbilirubinemia, Lambert syndrome, ichthyosis congenita with biliary atresia, Kabuki make-up syndrome, Meckel syndrome, cerebral aneurysm-cirrhosis syndrome, glycogen
35 storage diseases, polycystic kidney and hepatic disease,

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isolated Caroli disease, trisomy 18-like syndrome, Osler-Rendu-Weber syndrome 3, fatal intrahepatic cholestasis, Coach syndrome, type C Niemann-Pick disease, and hepatocellular cancer.

- 5 Altered responses to a variety of infectious agents that target the liver, especially acute viral hepatitis, have also been shown or are suspected to have genetic bases or contributions. In addition to differential susceptibility to primary infectious agents,
- 10 these altered responses include predisposition to complicating conditions following contact with particular infectious agents. These include, e.g., development of hepatocellular carcinoma 2 correlated with Hepatitis B infection, and severe hepatic fibrosis following
- 15 *Schistosoma mansoni* infection.

- The central role of the liver in drug metabolism results in exposure of this organ to a large variety of potentially toxic chemical agents and metabolites. These include naturally occurring plant alkaloids and mycotoxins,
- 20 industrial chemicals, and, additionally, pharmacologic agents used in treating disease. The range of manifestations of toxin- and drug-induced liver disease are virtually as broad as the range of acute and chronic disorders and have also been shown or suspected to have
- 25 genetic bases or contributions.

- Such interactions between drugs and genotype have been shown in the response, e.g., to the anticonvulsant phenytoin, which can cause severe hepatitis-like disease in individuals who are impaired in the ability to detoxify a
- 30 metabolite of phenytoin in the liver, and in the response to the drug sodium valproate, which can produce severe hepatotoxicity in certain individuals. The abnormal responses to both of these drugs are believed to be influenced by underlying genetic factors.

- 35 The human genome-derived single exon nucleic acid

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probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human liver, particularly those diseases with polygenic etiology. With each of the single
5 exon probes described herein shown to be expressed at detectable levels in human liver, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

10 For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders, such as cirrhosis), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression
15 profiles known to be characteristic of a given liver disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the
20 patient's liver to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly, using nucleic acids obtained directly or indirectly from transcripts expressed by liver of individuals with known liver disease. Methods for
25 quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single
30 exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of liver disease to be assessed through the massively parallel determination of
35 altered copy number, deletion, or mutation in the patient's

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genome of exons known to be expressed in human liver. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

5 The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art — see Ausubel et al. and Maniatis et al. — each probe reports the level of expression of message specifically containing that ORF.

10 It should be appreciated, however, that the probes of the present invention, for which expression in the adult liver has been demonstrated are useful for both measurement in the adult liver and for survey of expression in other tissues:

15 Significant among such advantages is the presence of probes for novel genes.

 As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be
20 identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were
25 represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence
30 databases.

 Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes
35 that are currently available for achieving these utilities.

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The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and
5 for surveying gene expression in the human.

Gene expression analysis using microarrays - conventionally using microarrays having probes derived from expressed message - is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405,
10 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct
15 Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for
20 example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of
25 Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl.
35 Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al.,

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- "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part. Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead compound derivatives - the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile

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and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in adult liver. The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known amplification technique. One such technique additional to

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PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are
5 to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form
10 suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific
20 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3'
25 primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present
30 invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived
35 single exon microarray of the present invention, the

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genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however - that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) - length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message - a subset of target sequence that is much reduced in complexity as compared to genomic sequence - even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 13,110 - 25,995, respectively, for probe SEQ ID NOS. 1 - 13,109. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 13,110 - 25,995 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c₀t1 DNA, and 0.5 % SDS, in a

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humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in

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both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have
5 sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or
10 both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution
15 hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

20 Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or
25 enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for
30 hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

35 When provided as a collection of plural

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individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human adult liver.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a

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plurality of probes known to be expressed in human adult liver. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group
5 consisting of SEQ ID NOS.: 1 - 13,109.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of
10 probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the
15 same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with
20 a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to
25 their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 13,109 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 13,110 - 25,995, that encodes
30 a protein domain. Thus, each of SEQ ID NOS. 1 - 13,109 can be used, or that portion thereof in SEQ ID NOS. 13,110 - 25,995 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

35 Additionally, kits are available commercially

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- that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X[™] Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL[™]) System, New England Biolabs, Beverly, MA)

- Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

- It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 13,110 - 25,995. Such amino acid sequences are set out in SEQ ID NOS: 25,996 - 38,578. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

- Preparation of Single Exon Microarrays from ORFs Predicted

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in Human Genomic Sequence

Bioinformatics Results

5 All human BAC sequences in fewer than 10 pieces
that had been accessioned in a five month period
immediately preceding this study were downloaded from
GenBank. This corresponds to ~2200 clones, totaling ~350
MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the
10 program CROSS_MATCH, the sequence was analyzed for open
reading frames using three separate gene finding programs.
The three programs predict genes using independent
algorithmic methods developed on independent training sets:
GRAIL uses a neural network, GENEFINDER uses a hidden
15 Markoff model, and DICTION, a program proprietary to
Genetics Institute, operates according to a different
heuristic. The results of all three programs were used to
create a prediction matrix across the segment of genomic
DNA.

20 The three gene finding programs yielded a range
of results. GRAIL identified the greatest percentage of
genomic sequence as putative coding region, 2% of the data
analyzed. GENEFINDER was second, calling 1%, and DICTION
yielded the least putative coding region, with 0.8% of
25 genomic sequence called as coding region.

The consensus data were as follows. GRAIL and
GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and
DICTION agreed on 0.5% of genomic sequence, and the three
programs together agreed on 0.25% of the data analyzed.

30 That is, 0.25% of the genomic sequence was identified by
all three of the programs as containing putative coding
region.

ORFs predicted by any two of the three programs
("consensus ORFs") were assorted into "gene bins" using two
35 criteria: (1) any 7 consecutive exons within a 25 kb window

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were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon

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to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR® green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular

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Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than 1 e^{-100}) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from 1 e^{-5} to 1 e^{-99}). The remaining 45% of

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the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

- All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish *et al.*, *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

10

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

- As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single

5 Exon Microarrays

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message
15 pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial
20 sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to
25 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II
30 enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5.
35 Probe was eluted using 10 mM Tris pH 8.5.

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Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 μ l hybridization solution containing 50% formamide, 5X SSC, 0.2 μ g/ μ l poly(dA), 0.2 μ g/ μ l human c₆t1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

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FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-

05 to $1e-99$; black: E values $> 1e-05$).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective
5 tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

10 It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested
15 tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence
20 databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

25 Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The
30 data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and
35 shows in blue the normalized Cy3 signal intensity for all

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sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

5 As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

10 However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes
15 will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is *not* a prerequisite for incorporation into a genome-derived microarray, and
20 further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach
25 described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis
30 of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene
35 expression panel 24 human cDNAs) (OriGene Technologies,

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Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

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Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normal Expressed Signal	Expression Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin

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AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be
5 important in the central nervous system or brain. The exon

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giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
5 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
10 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed
15 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless
20 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to
25 tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often
30 used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et
35 al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result

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duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1 α (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai *et al.*, *Genomics* 49(2):283-89 (1998)) (AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes *et al.*, *Mol. Genet.* 4(10):1935-44 (1995)).

- As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 \pm 0.11	-1.85 \pm 0.08
Brain	-1.41 \pm 0.11	-1.17 \pm 0.05
BT474	1.85 \pm 0.09	1.66 \pm 0.12
Fetal Liver	-1.62 \pm 0.07	-1.41 \pm 0.05
HBL100	1.32 \pm 0.05	2.64 \pm 0.12
Heart	1.16 \pm 0.09	1.56 \pm 0.10
HeLa	1.11 \pm 0.06	1.30 \pm 0.15
Liver	-1.62 \pm 0.22	-2.07 \pm

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Lung	-4.95 \pm 0.93	-3.75 \pm 0.21
Placenta	-3.56 \pm 0.25	-3.52 \pm 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known

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exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION 5 identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene 10 (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the 15 reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease 20 inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, 25 upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):

30 red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

35

EXAMPLE 4Genome-Derived Single Exon Probes Useful For Measuring
Human Gene Expression

5

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in liver tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 13,109 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

The structures of the 13,109 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 13,109. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 13,110 - 25,995, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

As detailed in Example 2, expression was

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demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are

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presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human adult liver and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human adult liver tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 13,110 - 25,995 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe: "EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.

corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.: The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as the boundary when only two classes were to be defined for analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8).

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Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ - which is probative evidence that the query sequence has previously been shown to be expressed - the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 13,109) and probe exon (SEQ ID NOs.: 13,110 - 25,995, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring

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Expression of Genes in Human Adult liver

Table 4 (545 pages) presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human adult liver.

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Table 4
Single Exon Probes Expressed In Adult Liver

Probe Seq ID No.	Exon Seq ID No.	ORF Seq ID No.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
472	13543	28465	4.76				
814	13356	28513	10.74				
1071	14118		2.15				
1268	14352	27310	10.34				
1318	14371	27311	1.33				
1819	14650	27512	1.33				
1837	14657	27535	1.35				
1853	14656	27563	3.77				
1746	14752	27763	1.22				
1781	14807	27716	7.27				
1639	14640	27307	1.05				
1694	15012	28002	2.13				
2178	15190	28166	2.41				
2238	15305	28312	2.27				
2608	15900	28595	1.49				
2609	15500	28900	1.48				
3229	16277	29178	2.44				
3510	16549	29448	1.38				
3576	16612	29516	8.4				
3620	16556		0.8				
3125	16757	29845	1.21				
4025	17052		0.99				
4263	17507	30176	1.58				
4361	17375	30226	11.57				
4448	17497		1.85				
4500	17510	30376	0.95				
4650	17945	30807	1.18				
4985	17935		0.72				
5174	18195	31011	5.51				
5188	18190	31025	1.15				
5438	18520	31245	2.5				
5438	18520	31245	2.5				
5607	18983		3.94				
5791	19953		8.49				

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe Seq ID NC.	Exon Seq ID NC.	ORF Seq ID NC.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5676	16683		3.66				
5697	16104	32123	1.15				
5643	18100	32126	3.4				
6255	26645	32471	1.84				
6294	16335	32501	1.77				
6663	16719		1.31				
6630	16662	33074	1.20				
6630	16662	33075	1.28				
7485	20425	33705	1.39				
7485	20425	33706	1.39				
7811	20740	34043	1.28				
7811	20740	34044	1.28				
8330	21235		0.47				
8639	21670	34009	1.51				
8095	21684	35339	1.14				
8416	22347	35711	0.84				
8416	22347	35712	0.84				
10093	22679	36370	6.03				
10298	23178	36568	0.58				
10394	23263	36753	1.42				
10523	23412	36826	1.15				
10601	23657	37116	0.74				
10601	23657	37117	0.74				
10911	23798	37224	0.57				
10911	23798	37225	0.57				
11126	24096		3.48				
11457	24380		1.48				
11632	24462	37802	1.43				
11788	24720	38273	2.14				
11834	24778		2.39				
6297	16338	32505	15.42	9.8E-03	A230203.1	NT	Human caprin 155 gene, partial, clones 15, 16, 17 and 18
8393	21513	34833	3.83	9.8E-03	U32716.1	NT	Human caprin 155 gene, partial, clones 15, 16, 17 and 18
10293	21163	35662	0.31	9.8E-03	Y1850.1	NT	Human caprin 155 gene, partial, clones 15, 16, 17 and 18
10293	21163	35662	0.31	9.8E-03	Y1850.1	NT	Human caprin 155 gene, partial, clones 15, 16, 17 and 18
10293	21163	35662	0.31	9.8E-03	Y1850.1	NT	Human caprin 155 gene, partial, clones 15, 16, 17 and 18

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top HB Database Source	Top Hit Descriptor
7342	20338	33604	0.86	9.6E-000 AF06560.1	NT		Gallus gallus ornithine transcarbamoylase (OTC) gene, exon 1
7342	20338	33605	0.86	9.6E-000 AF06560.1	NT		Gallus gallus ornithine transcarbamoylase (OTC) gene, exon 1
10904	23780	37217	1.00	9.6E-000 AF242432.1	NT		Mus musculus Map3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nai1) and general transcription factor III polypeptide 2 (Ct23a2) genes, complete cds
10904	23789	37218	1.00	9.6E-000 AF242432.1	NT		Mus musculus Map3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nai1) and general transcription factor III polypeptide 2 (Ct23a2) genes, complete cds
2715	15709	28704	1	9.4E-000 LL1433.1	NT		Dengue virus type 3 membrane protein (prM)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2715	15709	28705	1	9.4E-000 LL1433.1	NT		Dengue virus type 3 membrane protein (prM)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2995	19071	28915	1	9.4E-000 AF043785.1	NT		Mus musculus A13 gene, gene for anthrionin, complete cds
6900	19021	33806	0.57	9.4E-000 JF79130	SWISSPROT		HYPOHECTAL PROTEIN MG447 HDV1QLO
8977	21618	34650	1.22	9.3E-000 AF193060.1	NT		Homo sapiens cytochrome-A receptor protein (CDAR) gene, exons 2, 3, and 4
8958	22482	38942	3.44	9.3E-000 JF11210	SWISSPROT		IMMEDIATEEARLY PROTEIN 1 (IE1) (IMMEDIATEEARLY PHOSPHOPROTEIN PP89)
7874	20801	34104	0.44	9.2E-000 Q01767	SWISSPROT		3 BETA-HYDROXYSTEROID DEHYDROGENASE TYPE IV (3BETA-HSD IV) (3-BETA-HYDROXY-DELTA(4)-STEROID DEHYDROGENASE) (3-BETA-HYDROXY-5-ENE STEROID DEHYDROGENASE) (PROGESTERONE REDUCTASE)
5478	18580	31403	2.54	9.1E-000 AF09500.1	NT		Leishmania cephalitis cyclochrome B (c4b) gene, partial cds; mitochondrial gene for mitochondrial product
5478	18580	31404	2.54	9.1E-000 AF09500.1	NT		Leishmania cephalitis cyclochrome B (c4b) gene, partial cds; mitochondrial gene for mitochondrial product
8994	22699	32691	1.21	9.0E-000 F06241	SWISSPROT		NT-PODOPUSIN
6259	19321	32484	5.18	9.0E-000 F06241	EST_HUMAN		30705303R1 NH_MGC_31 Homo sapiens cDNA, clone IMAGE:36145923
6541	16980	33870	2.11	8.7E-000 AF019788.1	NT		Cynops pyrrhogaster Cp125 premature mRNA, partial cds
6541	16980	33871	2.11	8.7E-000 AF019788.1	NT		Cynops pyrrhogaster Cp125 premature mRNA, partial cds
493	33335	32071	1.63	8.4E-000 J03180.1	NT		Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
8987	17345	34650	4.11	8.1E-000 J03197.181	NT		Homo sapiens insulin receptor substrate 1 (IRS1) protein (cDNA)
6900	19021	33806	0.57	9.0E-000 JF79130	SWISSPROT		BREIFELDIA RESISTANCE PROTEIN
7738	20935	37219	1.07	7.9E-000 JF7241.1	NT		BREIFELDIA RESISTANCE PROTEIN
8920	21833	33819	1.58	7.9E-000 JF5441	SWISSPROT		Thrombospondin, complete cds; genome, segment 3/5
8920	21833	33820	1.58	7.9E-000 JF5441	SWISSPROT		Thrombospondin, complete cds; genome, segment 3/5
8011	12074	32200	3.91	7.5E-000 F070817.1	SWISSPROT		THROMBOSPONDIN 1 PRECURSOR
8513	22241	36902	3.81	7.4E-000 J04903	SWISSPROT		THROMBOSPONDIN 1 PRECURSOR
8920	21833	33819	1.58	7.5E-000 JF5441	SWISSPROT		THROMBOSPONDIN 1 PRECURSOR
8920	21833	33820	1.58	7.5E-000 JF5441	SWISSPROT		THROMBOSPONDIN 1 PRECURSOR
8011	12074	32200	3.91	7.4E-000 F070817.1	SWISSPROT		THROMBOSPONDIN 1 PRECURSOR
8513	22241	36902	3.81	7.4E-000 J04903	SWISSPROT		THROMBOSPONDIN 1 PRECURSOR
8920	21833	33819	1.58	7.5E-000 JF5441	SWISSPROT		THROMBOSPONDIN 1 PRECURSOR
8920	21833	33820	1.58	7.5E-000 JF5441	SWISSPROT		THROMBOSPONDIN 1 PRECURSOR
8011	12074	32200	3.91	7.4E-000 F070817.1	SWISSPROT		THROMBOSPONDIN 1 PRECURSOR
8513	22241	36902	3.81	7.4E-000 J04903	SWISSPROT		THROMBOSPONDIN 1 PRECURSOR
8920	21833	33819	1.58	7.5E-000 JF5441	SWISSPROT		THROMBOSPONDIN 1 PRECURSOR
8920	21833	33820	1.58	7.5E-000 JF5441	SWISSPROT		THROMBOSPONDIN 1 PRECURSOR
8011	12074	32200	3.91	7.4E-000 F070817.1	SWISSPROT		THROMBOSPONDIN 1 PRECURSOR
8513	22241	36902	3.81	7.4E-000 J04903	SWISSPROT		THROMBOSPONDIN 1 PRECURSOR
8920	21833	33819	1.58	7.5E-000 JF5441	SWISSPROT		THROMBOSPONDIN 1 PRECURSOR
8920	21833	33820	1.58	7.5E-000 JF5441	SWISSPROT		THROMBOSPONDIN 1 PRECURSOR
8011	12074	32200	3.91	7.4E-000 F070817.1	SWISSPROT		THROM

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Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar (Top) Hit E-Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10727	23813		0.76	4.5E+00	U9128.1	NT	Human heteroduplex isomorphous region, Hicase 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
4147	17108		13.45	4.5E+00	AF18265.1	EST	Enicospina eulalia Hs9a (Hs9) gene, partial cds
9105	20335		5.45	4.5E+00	AF172092.1	EST	PMO-3170547-31101-00-2025-24 ET0547 Homo sapiens cDNA
309	13402	26319	3.37	4.7E+00	AF22062.1	EST	60187656AF1 NIH LM5C 56 Homo sapiens cDNA clone IMAGE:4089716 5'
3318	16395	20319	3.33	4.7E+00	BF22052.1	EST	60187656AF1 NIH LM5C 55 Homo sapiens cDNA clone IMAGE:4089716 5'
3318	16395	20325	1	4.7E+00	AL163260.2	EST	Homo sapiens chromosome 21 segment H521 (CG6)
8287	21102	34485	0.55	4.5E+00	U97559.1	NT	Mollusca trochophore larval section 111 of 150 of the complete genome
9735	22802	30046	1.04	4.5E+00	SE046437.1	EST	768910.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:3322008 3' similar to TR-078140 075140 KIAA0646 PROTEIN, contains element PTNS repetitive element
9738	22852	35047	1.04	4.5E+00	SE816437.1	EST	768910.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:3322008 3' similar to TR-078140 075140 KIAA0646 PROTEIN, contains element PTNS repetitive element
10877	23793		0.73	4.5E+00	AF240786.1	NT	Homo sapiens guanine S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
8239	21144		0.54	4.5E+00	AF129177.1	NT	Isaiahobacteriella orientalis isochlorophosphatase synthase (ISCT) gene, complete cds
12034	24876	38381	2.37	4.5E+00	AE001044.1	NT	Archaeobacteriella fujidensis section 83 of 172 of the complete genome
12175	25011	38515	1.85	4.5E+00	BF098241.1	EST	60212328F1 NIH LM5C 56 Homo sapiens cDNA clone IMAGE:4280276 5'
13107	25777		4.27	4.5E+00	SE008271.1	EST	Q1931038F1 NIH LM5C 56 Homo sapiens cDNA clone IMAGE:4280276 5'
3087	16195	20036	1.02	4.4E+00	BF050953.1	EST	60307258F1 NCI CGAP Bm67 Homo sapiens cDNA clone IMAGE:4210284 5'
3087	16195	20036	1.02	4.4E+00	BF050953.1	EST	60307258F1 NCI CGAP Bm67 Homo sapiens cDNA clone IMAGE:4210284 5'
6443	19499		1.76	4.4E+00	KT3414.1	NT	Mutl1 gene for MHC class IIIA associated invariant chain
6515	19550	32741	0.61	4.4E+00	AF158606.1	NT	Nucleoside tetracycline isochlorophosphatase synthase (ISCT) gene, complete cds
6367	19406		0.7	4.3E+00	AF050670.1	NT	Homo sapiens nucleoside tetracycline isochlorophosphatase synthase (ISCT) gene, complete cds
7842	20766	34072	2.48	4.3E+00	Y13402.1	NT	Homo sapiens nucleoside tetracycline isochlorophosphatase synthase (ISCT) gene, complete cds
8560	20076	31289	0.5	4.3E+00	AE014222.1	NT	Pharmodan falciparum 128141111 gene, exon 1
1298	24215	37666	5.48	4.3E+00	AF240786.1	NT	Homo sapiens guanine S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11371	24295		1.58	4.3E+00	11526311	NT	Homo sapiens guanine S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5707	18780		3.07	4.2E+00	PI6444	SWISSPROT	MICROSMAL DEHYDROGENASE PRECURSOR (MDP) (DEHYDROGENASE-1) (RENAL DEFECT DISEASE)
5788	18800	51968	1.08	4.2E+00	P31630	SWISSPROT	CAF-1 PROTEIN (CAF-1) (NUCLEAR PROTEIN)
9538	19005		0.52	4.2E+00	G27030	SWISSPROT	MUTATING-115-DEPENDENT HELICASE (M1882)
7074	20285	33542	1.53	4.2E+00	P13865	SWISSPROT	EXTENSIN PRECURSOR (CEL WALL HYDROXYPROLINE-RICH GLYCOPOLYMER)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7079	20295	33543	1.63	4.2E-000 P13943	SWISSPROT	EXTENSION PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)	
9513	23340	33905	1.43	4.2E-000 P139013	EST_HUMAN	NUB700.1 5' Utrac. NF1_25C. 51 Homo sapiens cDNA clone IMAGE:260962 3'	
10126	22149	33076	1.12	4.2E-000 P13016	SWISSPROT	WIFIN PROTEIN (TWIN TANTIN PROTEIN) (FOU DOMAIN PROTEIN 1) (PDM-1) (DPCU-19) (DCC11)	
8161	26642	32351	0.65	4.1E-000 009185	SWISSPROT	CELLULAR TUMOR ANTIGEN P53	
8161	26642	32351	0.55	4.1E-000 009185	SWISSPROT	CELLULAR TUMOR ANTIGEN P53	
7571	23411	33598	0.74	4.1E-000 B25398.1	EST_HUMAN	BT011072F11 NH_00C_18 Homo sapiens cDNA clone IMAGE:3371634 5'	
7571	23411	33598	0.74	4.1E-000 B25398.1	EST_HUMAN	BT011072F11 NH_00C_38 Homo sapiens cDNA clone IMAGE:4009768 5'	
8111	21023	34340	7.95	4.1E-000 0033010	NT	TYT1 PROTEIN PRECURSOR	
8255	21160	34498	0.68	4.1E-000 0041123.1	SWISSPROT	Human gamma globulin mRNA for caldesmon A, complete cds	
8255	21160	34498	0.68	4.1E-000 0041123.1	SWISSPROT	Human gamma globulin mRNA for caldesmon A, complete cds	
9359	21160	34497	4.76	4.1E-000 003663	SWISSPROT	GENE 68 PROTEIN	
8405	21426	34797	1.14	4.1E-000 U07603.1	NT	GENE 68 PROTEIN	
10059	22594	36378	0.53	4.1E-000 B0462123.1	SWISSPROT	Pan trophoblast pooled sequencing data LTR element in the RNU12 locus	
10197	22594	36380	1.63	4.1E-000 B0462123.1	EST_HUMAN	R0322-7638F1 NH_00C_62 Homo sapiens cDNA clone IMAGE:4333209 5'	
10903	22649		0.65	4.1E-000 A236273.1	NT	Radicalized proviralized strain Madrif 6. Complete genome, segment 4/4	
10790	23602		0.54	4.1E-000 P46414	SWISSPROT	CYCLOIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27) (P27KIP1)	
11322	24241		3.69	4.1E-000 T06716	SWISSPROT	HYPOHECTICAL PROTEIN HWLF1	
11490	24265		14.72	4.1E-000 B365840.1	EST_HUMAN	BT016075F11 NH_00C_71 Homo sapiens cDNA clone IMAGE:3900001 5'	
3604	18641		0.72	4.0E-000 P13828	SWISSPROT	GLC7-INTERACTING PROTEIN 1	
5944	20178	33417	0.90	4.0E-000 005293	SWISSPROT	SUCRASE-ISOMALTAZE, INTESTINAL CONTAINS: SUCRASE, ISOMALTAZE	
5944	20178	33418	0.90	4.0E-000 005293	SWISSPROT	SUCRASE-ISOMALTAZE, INTESTINAL CONTAINS: SUCRASE, ISOMALTAZE	
7287	20178	33417	0.86	4.0E-000 005293	SWISSPROT	SUCRASE-ISOMALTAZE, INTESTINAL CONTAINS: SUCRASE, ISOMALTAZE	
7287	20178	33418	0.86	4.0E-000 005293	SWISSPROT	SUCRASE-ISOMALTAZE, INTESTINAL CONTAINS: SUCRASE, ISOMALTAZE	
7693	20400	33779	1.16	4.0E-000 0033010	SWISSPROT	CELL DIVISION PROTEIN F1001406	
7431	22599	35722	0.81	4.0E-000 C114157	SWISSPROT	HYPOHECTICAL PROTEIN K04404	
10432	23341	35758	0.54	4.0E-000 0010030	SWISSPROT	NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (NMON) (NMON)	
10631	23341	35867	0.97	4.0E-000 A04002.32.1	NT	Human complete genome	
1185	24059	37446	1.77	4.0E-000 P13460	SWISSPROT	CYTOCHROME C OXIDASE SUBUNIT II	
11322	24241		2.81	4.0E-000 P07954	SWISSPROT	GENOME POLYPROTEIN CONTAINS CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE, GLYCOPROTEIN M1), MAJOR ENVELOPE PROTEIN 6, NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)	

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Probe SEQ ID NC:	Exon SEQ ID NC:	ORF BEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
5749	18816	31612	1.43	2.7E+00	U14003.1	NT	Homo sapiens apolipoprotein lipase IV gene, exons 1 and 2
8724	21654		0.77	2.7E+00	U18947.1	NT	Genome browser: chondrocyte (CHSE) gene including complete 5'UTR and complete cds
9520	22447		2.43	2.7E+00	AL111418.1	NT	Genome browser: K1. cDNA library under conditions of mitogenic stimulation
5606	21324	34937	0.64	2.7E+00	AF308199.1	EST_HUMAN	CH22G2.1 NC1, COX2, Pim1, Hemo sapiens, cDNA clone IMAGE2391314 5' similar to gp117733
10678	23862		1.71	2.7E+00	BC026571.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN)
4766	17701	30568	5.9	2.6E+00	AF308148.1	NT	CH22G2.1 NC1, COX2, Pim1, Hemo sapiens, cDNA clone IMAGE2391314 5' similar to gp117733
8738	18812	31507	1.75	2.6E+00	U18947.1	NT	Genome browser: chondrocyte (CHSE) gene including complete 5'UTR and complete cds
6738	18812	31507	1.75	2.6E+00	U18947.1	NT	Genome browser: chondrocyte (CHSE) gene including complete 5'UTR and complete cds
6038	19100		1.85	2.6E+00	Y17962.1	NT	Mus musculus SRY locus containing gene 13 (Sact13), mRNA
7696	25594		0.79	2.6E+00	AJ224639.1	NT	Microbacterium fortium tRNA Ile gene
8196	21093		8.96	2.6E+00	AF235502.1	NT	Homo sapiens Surf-5 and Surf-6 genes
8537	21698	34005	1.33	2.6E+00	AJ132180.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (SHIP) gene, exons 18 through 27, and complete cds
8537	21698	34005	1.33	2.6E+00	AJ132180.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (SHIP) gene, exons 18 through 27, and complete cds
10162	23073	35473	1.97	2.6E+00	AJ161540.2	NT	Faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EY1-49
10841	23727		1.87	2.6E+00	AF308153.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
11498	24381	37828	2.17	2.6E+00	AF143675.1	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
12899	29599		2.17	2.6E+00	U1419220	NT	Hemivirus Z10 segment M1 G162 glycoprotein (Z10) gene, complete cds
1483	14514	27474	2.65	2.6E+00	AJ271844.1	NT	Homo sapiens ATR-binding cassette, sub-family 2 (MDR1/TP), member 4 (ABCB4), mRNA
1483	14514	27475	2.68	2.6E+00	AJ271844.1	NT	Homo sapiens ATR-binding cassette, sub-family 2 (MDR1/TP), member 4 (ABCB4), mRNA
6024	10086	32210	1.99	2.6E+00	P13465	SWISSPROT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
6024	10086	32210	1.99	2.6E+00	P13465	SWISSPROT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
6730	10086	32210	1.54	2.6E+00	P13465	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6730	10086	32210	1.54	2.6E+00	P13465	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
7032	20398	33391	0.98	2.6E+00	D00032.1	NT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
8277	21132	34462	1.26	2.6E+00	AF1946158.1	EST_HUMAN	Vibrio cholerae chol gene and cdb gene for cholera toxin, complete cds
8302	21206	34541	0.49	2.6E+00	AF1946158.1	EST_HUMAN	Vibrio cholerae chol gene and cdb gene for cholera toxin, complete cds
8348	22074	35840	1.54	2.6E+00	D00032.1	NT	Homo sapiens diaphy, heavy polypeptide-1 (DCTCL1) mRNA
10350	20255	36075	0.85	2.6E+00	BC207168.1	EST_HUMAN	Protein DNA for alkaline C-1, complete cds
11871	24616		2.02	2.6E+00	AF173663.1	SWISSPROT	G117197767 NM_1003_17 Homo sapiens cDNA clone IMAGE355190 5'
1330	42108	28915	2.31	2.6E+00	AF173663.1	SWISSPROT	DNAJ PROTEIN
1330	42108	28915	2.31	2.6E+00	AF173663.1	SWISSPROT	DNAJ PROTEIN
1330	42108	28915	2.31	2.6E+00	AF173663.1	SWISSPROT	DNAJ PROTEIN
5075	10151	30072	5.93	2.4E+00	AF004302.1	NT	Mus musculus EF1A1 gene, partial cds; L1NK1 gene, complete cds; and E1N gene, partial cds
5075	10151	30072	5.93	2.4E+00	AF004302.1	NT	Mus musculus EF1A1 gene, partial cds; L1NK1 gene, complete cds; and E1N gene, partial cds
5075	10151	30072	5.93	2.4E+00	AF004302.1	NT	Mus musculus EF1A1 gene, partial cds; L1NK1 gene, complete cds; and E1N gene, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6243	10297	32466	4.27	2.4E+00	P20843	SWISSPROT	VITELLOGENIN PRECURSOR (YOLK PROTEIN 1)
7773	20703	34002	0.63	2.4E+00	B666752.1	EST_HUMAN	LOC238687 N1H1_MGC_59 Homo sapiens cDNA clone IMAGE:4278052 8'
7773	20703	34003	0.63	2.4E+00	B666752.1	EST_HUMAN	LOC238687 N1H1_MGC_59 Homo sapiens cDNA clone IMAGE:4278052 8'
7796	20718	34021	0.43	2.4E+00	P20126	SWISSPROT	RNA REPLICASE POLYPROTEIN
7796	20718	34022	0.43	2.4E+00	P20126	SWISSPROT	RNA REPLICASE POLYPROTEIN
8718	21649	34694	2.25	2.4E+00	P20842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8718	21649	34695	2.25	2.4E+00	P20842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8700	21720		3.32	2.4E+00	A001486.1	NT	Helicobacter pylori strain J99 section 47 of 132 of the complete genome
9210	22138		8.12	2.4E+00	A001486.1	NT	Helicobacter pylori strain J99 section 47 of 132 of the complete genome
6307	22315	35677	8.12	2.4E+00	P24091	EST_HUMAN	LOC238687 N1H1_MGC_59 Homo sapiens cDNA clone IMAGE:4278052 8'
10541	22427	35846	2.85	2.4E+00	P13673	SWISSPROT	ENDOCYTINASE B PRECURSOR (CHN-B)
10541	22427	35847	2.85	2.4E+00	P13673	SWISSPROT	ENDOCYTINASE B PRECURSOR (CHN-B)
10541	22427	35848	2.85	2.4E+00	P13673	SWISSPROT	ENDOCYTINASE B PRECURSOR (CHN-B)
10008	22464	36924	2.82	2.4E+00	X02511.1	NT	SKIN GRANULE PROTEIN PRECURSOR
10737	22623		7.42	2.4E+00	P00059	SWISSPROT	XYLOSE KINASE (XYLOXINASE)
10811	22667	37128	1.95	2.4E+00	BE326702.1	EST_HUMAN	XYLOSE KINASE (XYLOXINASE)
10811	22667	37129	1.95	2.4E+00	BE326702.1	EST_HUMAN	XYLOSE KINASE (XYLOXINASE)
11003	22947	37385	1.41	2.4E+00	Q81481	SWISSPROT	DEHYDRATASE REGULATORY PROTEIN N1RQ
11797	24710	38212	2.5	2.4E+00	AF169552.2	NT	Fraxinus x americana cytochrome oxidase peroxidase (ApoC) gene, ApoC-c allele, complete cds
1281	14314	27253	6.93	2.8E+00	Z46724.1	NT	G. domesticus artificial single chain antibody gene (L3)
4217	17323		1.93	2.8E+00	AJ40081.1	NT	Bos laurus partial cfo gene for cytochrome b
5048	18110		0.81	2.8E+00	N86245.1	EST_HUMAN	J7340F Human testis heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to
7658	20785	34086	2.43	2.8E+00	P07189	SWISSPROT	PROLYL CARBOXYPEPTIDASE
8038	22665	34491	3.16	2.8E+00	P07189	SWISSPROT	PROLYL CARBOXYPEPTIDASE
8233	21168	34491	1.18	2.8E+00	X00765.1	NT	Retinoblastoma protein, C-terminal region
9534	22260	33952	0.56	2.8E+00	95337.1	NT	Myosin IIa, chicken, complete genome
5712	20307	33916	1.73	2.8E+00	Q11127	SWISSPROT	ALPHA-1,3-HYDROXYLTRANSFERASE (GALACTOSIDE 3,4-EPIMERASE)
11271	24197	38113	2.39	2.8E+00	Q07076	SWISSPROT	ALPHA-1,3-HYDROXYLTRANSFERASE (GALACTOSIDE 3,4-EPIMERASE)
11717	24616	38926	1.98	2.8E+00	P28339	SWISSPROT	ANGIOTENSIN II (ANGII) RECEPTOR
12100	20203	38926	2.58	2.8E+00	P28339	SWISSPROT	ANGIOTENSIN II (ANGII) RECEPTOR
12100	20203	38927	2.58	2.8E+00	P28339	SWISSPROT	ANGIOTENSIN II (ANGII) RECEPTOR
12100	20203	38927	2.58	2.8E+00	P28339	SWISSPROT	ANGIOTENSIN II (ANGII) RECEPTOR
12456	22238	31862	5.44	2.8E+00	BE363237.1	EST_HUMAN	LOC238687 N1H1_MGC_59 Homo sapiens cDNA clone IMAGE:4278052 8'

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Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Emission Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4103	17139	30093	0.61	2.2E+00	AF020358.1	NT	Major vault protein class IV cylin. gylphous (clv4) gene, complete cds
4418	17429	30291	5.4	2.2E+00	D07071.1	NT	Rd gene for rapsudin, cont1 (non-coding exon)
4418	17429	30292	5.4	2.2E+00	D07071.1	NT	Rd gene for rapsudin, cont1 (non-coding exon)
5526	18605	31483	11.77	2.2E+00	O68307	SWISSPROT	SORTIN-LIKE RECEPTOR PRECURSOR (SORTIN) CONTAINING LDLR CLASS A REPEATS (NSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN BINDING REPEATS) (LDLR) RELATIVE WITH 11 LIGAND-BINDING REPEATS (LDLR1) >
5526	18605	31484	11.77	2.2E+00	O68307	SWISSPROT	SORTIN-LIKE RECEPTOR PRECURSOR (SORTIN) CONTAINING LDLR CLASS A REPEATS (NSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN BINDING REPEATS) (LDLR) RELATIVE WITH 11 LIGAND-BINDING REPEATS (LDLR1) >
6037	19128	32259	1.04	2.2E+00	BE527220.1	EST_HUMAN	RC3-CT10254-300800-022-468 CT0254 Homo sapiens cDNA
6037	19128	32260	1.04	2.2E+00	BE527220.1	EST_HUMAN	RC3-CT10254-300800-022-468 CT0254 Homo sapiens cDNA
6297	16348	32516	7.48	2.2E+00	BE280383.1	EST_HUMAN	60063340T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:286977 3'
6912	16653	32837	3.09	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN NL2
6982	18912	33126	2.79	2.2E+00	P31459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
7293	18402		3.6	2.2E+00	A459457.1	EST_HUMAN	H9502.11 NC-GWAP_David Homo sapiens cDNA clone IMAGE:1093379 3'
7701	20053	33930	0.87	2.2E+00	AA137027.1	EST_HUMAN	Z9704.1 Staphylococcus aureus 597202 Homo sapiens cDNA clone IMAGE:585743 5'
8051	20944	34280	20.17	2.2E+00	AA448072.1	EST_HUMAN	Z05670.11 Soares, Isid. Nucleo_N23H-F6_3w Homo sapiens cDNA clone IMAGE:765934 5'
8142	21051	34363	0.95	2.2E+00	P4618	SWISSPROT	ALANINE RACEMASE
8142	21051	34368	0.41	2.2E+00	O07089	SWISSPROT	THYMIDYLATE KINASE (TMP KINASE)
8681	21612	34953	0.71	2.2E+00	BE301580.1	EST_HUMAN	b67H12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2663207 3' similar to p5.D45838 Mouse mRNA for nuclear pore-targeting complex component of (MOUSE);
8681	21612	34954	0.71	2.2E+00	BE301580.1	EST_HUMAN	b67H12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2663207 3' similar to p5.D45838 Mouse mRNA for nuclear pore-targeting complex component of (MOUSE);
9890	22795		13.99	2.2E+00	BE741678.1	EST_HUMAN	PT1584759T1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:344891 5'
10097	25691		2.64	2.2E+00	Q04706	SWISSPROT	TRANSFERRIN TYROSINE KINASE
10586	26442	36862	1.93	2.2E+00	A282373.1	EST_HUMAN	GNR303.x1 Soares, placenta, 3004weeks, 2N4H4P83x1 Homo sapiens cDNA clone IMAGE:185695 3' similar to de.T00435 GLUTATHIONE PEROXIDASE (HUMAN);
10586	26442	36863	1.93	2.2E+00	A282373.1	EST_HUMAN	GNR303.x1 Soares, placenta, 3004weeks, 2N4H4P83x1 Homo sapiens cDNA clone IMAGE:185695 3' similar to de.T00435 GLUTATHIONE PEROXIDASE (HUMAN);
10586	26444	36813	2.2	2.2E+00	BE741678.1	EST_HUMAN	PT1584759T1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:344891 5'
10455	23520	37247	2.49	2.2E+00	A182416.1	NT	Homo sapiens ovarian granulosa cell 13.0 kDa protein MORT41 homolog mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Excretion Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession	Top Hit Database Source	Top Hit Descriptor
12615	25707		6.13	1.8E+000/F313454.1	NT	NT	Glyoxalase 1 reductase alternative oxidase 1 (AOX1) gene, nuclear genome encoding mitochondrial protein
12632	29345		4.6	1.8E+000	9900400	NT	Rat liver neuropilin-1-related protein complex 1b (APIC1b), mRNA
1135	14177	27114	2.24	1.7E+000/Q60114	SWISSPROT	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCCROSE 6-FRUCTOSYL TRANSFERASE)
2220	16298	28305	12.28	4.2E+000/A11280.2	EST	EST	Homo sapiens chromosome 21 segment H8202080
2336	18401	28495	2.03	1.7E+000/A11067.1	EST	EST	zshb2.61, Gene: NHNP10_31 Homo sapiens cDNA clone IMAGE:1978137
4670	17578	30440	1.62	1.7E+000/Q60114	SWISSPROT	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCCROSE 6-FRUCTOSYL TRANSFERASE)
5687	18875	31668	1.96	1.7E+000/B063546.1	EST	EST	CUP-812652.171299-127-405 BT2823 Homo sapiens cDNA
5907	18876	31669	1.96	1.7E+000/B063546.1	EST	EST	CUP-812652.171299-127-405 BT2823 Homo sapiens cDNA
6099	18130	32263	0.99	1.7E+000/G97448.1	EST	EST	G946F Fetal liver: Homo sapiens cDNA clone G9463.9 5' end.
6290	16503	32464	3.4	1.7E+000/U09778.6	SWISSPROT	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF1)
6632	16464	33078	0.93	1.7E+000/P65816	SWISSPROT	SWISSPROT	IPROVATE DEHYDROGENASE (IPROVAMIDE)PHOSPHATASE, MITOCHONDRIAL PRECURSOR
7587	26523	33811	1.19	1.7E+000/Q30703	SWISSPROT	SWISSPROT	HYPOHECTIN 38.0KD PROTEIN IN CAT 32A001 INTERGENE REGION
7697	26523	33812	1.19	1.7E+000/Q30703	SWISSPROT	SWISSPROT	HYPOHECTIN 38.0KD PROTEIN IN CAT 32A001 INTERGENE REGION
8518	21223		0.44	1.7E+000/P36186	SWISSPROT	SWISSPROT	HISTONE-BINDING PROTEIN H1N2
8519	21223		0.44	1.7E+000/P36186.1	NT	NT	Mus musculus cDNA receptor gamma locus, OR gamma 2 and gamma 4 gene clusters
8520	21223		0.44	1.7E+000/P36186.1	NT	NT	Mus musculus cDNA receptor gamma locus, OR gamma 2 and gamma 4 gene clusters
8640	21647	34864	1.33	1.7E+000/P503030.1	EST	EST	Mus musculus cDNA acute lymphocytic leukemia T1 (all), mRNA
8640	21647	34870	1.33	1.7E+000/P503030.1	EST	EST	Mus musculus cDNA acute lymphocytic leukemia T1 (all), mRNA
9103	22015	35398	0.26	1.7E+000/P503030.1	EST	EST	Phylogenetic phylogenetic intertrans inducible lip protein (M2) mRNA, complete cds
9107	22015	35398	0.26	1.7E+000/P503030.1	EST	EST	Phylogenetic phylogenetic intertrans inducible lip protein (M2) mRNA, complete cds
9326	22101	35647	0.73	1.7E+000/P50303.1	NT	NT	Phylogenetic phylogenetic intertrans inducible lip protein (M2) mRNA, complete cds
9326	22101	35648	0.68	1.7E+000/P50303.1	NT	NT	Phylogenetic phylogenetic intertrans inducible lip protein (M2) mRNA, complete cds
9372	22309	35959	0.22	1.7E+000/P50303.1	NT	NT	Mus musculus cDNA acute lymphocytic leukemia T1 (all), mRNA
9592	26920	35959	1.76	1.7E+000/Q00478	SWISSPROT	SWISSPROT	Palmitic acyl-CoA synthetase 3A, cytosolic isoform
9592	26920	35964	1.76	1.7E+000/Q00478	SWISSPROT	SWISSPROT	Palmitic acyl-CoA synthetase 3A, cytosolic isoform
10133	23024		1.20	1.7E+000/AF11580.1	EST	EST	HOMEOBOX PROTEIN DLX3
10948	23454		0.63	1.7E+000/AF11580.1	EST	EST	Homo sapiens HSPC282 cDNA, partial cds
12076	24698	38370	1.83	1.7E+000/V23424.1	EST	EST	Homo sapiens MAGC neuropeptide, MAGC Homo sapiens cDNA
2647	26005	1079	1.83	1.6E+000/AF06939.1	NT	NT	O687 Homo sapiens cDNA, Tgfbeta1 antisense/Homo sapiens cDNA, not directional
2657	18076	28076	1.51	1.6E+000/AF07374.1	NT	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2657	18076	28076	1.51	1.6E+000/AF07374.1	NT	NT	Homo sapiens small proline-rich protein (SP-PR3) gene, exons 1, 2, and 3 and complete cds
2663	18076	28076	1.51	1.6E+000/V1344.1	NT	NT	Mus musculus ST6GALNAcII gene, exon 2

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2303	15311		1.36	1.0E+00	X98373.1	NT	B-lymphocyte gamma globulin gene
3002	15354	28598	1.25	1.0E+00	V58423.1	EST_HUMAN	Human gamma globulin gene
3325	16255		1.09	1.0E+00	AB209889.1	NT	Human gamma globulin gene
4115	17198		0.97	1.0E+00	BF570072.1	EST_HUMAN	Human gamma globulin gene
4442	17473	30329	0.97	1.0E+00	AF155827.1	NT	Human gamma globulin gene
4442	17473	30330	0.97	1.0E+00	AF155827.1	NT	Human gamma globulin gene
5207	18168	31041	1.06	1.0E+00	AF127897.1	NT	Human gamma globulin gene
5218	18208	31053	3.05	1.0E+00	Y11344.1	NT	Human gamma globulin gene
6039	19101	32229	2.33	1.0E+00	L04808.1	NT	Human gamma globulin gene
6135	19164	32331	0.86	1.0E+00	AF004951.1	NT	Human gamma globulin gene
6198	19264	32359	0.48	1.0E+00	BE571873.1	EST_HUMAN	Human gamma globulin gene
6198	19264	32400	0.48	1.0E+00	BE571873.1	EST_HUMAN	Human gamma globulin gene
6743	19777	32960	0.85	1.0E+00	BF360703.1	EST_HUMAN	Human gamma globulin gene
7007	20034	33267	1.16	1.0E+00	AW294881.1	EST_HUMAN	Human gamma globulin gene
7615	20500	33842	2.24	1.0E+00	BE57267.1	EST_HUMAN	Human gamma globulin gene
8008	21539		1.82	1.0E+00	Q4078	SWISSPROT	Human gamma globulin gene
8450	21680	35240	3.13	1.0E+00	AJ237191.1	NT	Human gamma globulin gene
8457	22095	35747	1.05	1.0E+00	11437222	NT	Human gamma globulin gene
8457	22095	35748	1.05	1.0E+00	11437222	NT	Human gamma globulin gene
8902	22698	34684	1.44	1.0E+00	X52048.1	NT	Human gamma globulin gene
9002	22698	34686	1.44	1.0E+00	X52048.1	NT	Human gamma globulin gene
10115	23008		0.67	1.0E+00	AF004951.1	NT	Human gamma globulin gene
10254	23144	36553	1.67	1.0E+00	T41290.1	EST_HUMAN	Human gamma globulin gene
10045	23531		0.64	1.0E+00	AF121361.1	NT	Human gamma globulin gene
10062	23598	35867	1.18	1.0E+00	AF183044.1	EST_HUMAN	Human gamma globulin gene
10062	23598	35868	1.18	1.0E+00	AF183044.1	EST_HUMAN	Human gamma globulin gene
10259	24155	37364	2.31	1.0E+00	P4817	SWISSPROT	Human gamma globulin gene
11240	24170	37517	2.47	1.0E+00	P4817	SWISSPROT	Human gamma globulin gene
11265	24169	37537	1.52	1.0E+00	A4210387.1	EST_HUMAN	Human gamma globulin gene

Table 4
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Single Exon Probes Expressed in Adult Liver

Probe NO.	Enon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10195	23060	36467	1.87	1.3E+00/0.00754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE	LYSOSOMAL ALPHA-MANNOSIDASE (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID
10271	23161	36571	1.53	1.3E+00/0.0276201	EST_HUMAN	ALPHA-MANNOSIDASE (LAMAN)	wb560771 NC_024671.H11 Homo sapiens cDNA clone IMAGE:2482106 3'
10341	23261	36847	0.89	1.3E+00/0.1226621	NT	Lectinucoside beta; dendrotoxin NCD0-1n71	Lectinucoside beta; dendrotoxin NCD0-1n71 chromosomal insertion, junction DNA
10341	23260	36848	0.89	1.3E+00/0.1226621	NT	Lectinucoside beta; dendrotoxin NCD0-1n71	Lectinucoside beta; dendrotoxin NCD0-1n71 chromosomal insertion, junction DNA
10378	23268	36950	3.8	1.3E+00/0.EE93379.2	EST_HUMAN	BO1671.GRI.NH_MGC_67	BO1671.GRI.NH_MGC_67 Homo sapiens cDNA clone IMAGE:3686106 3'
10378	23265	37023	1.37	1.3E+00/0.AEO04392.1	NT	Vilro chromosome II	Vilro chromosome II, section 49 of 63 of the complete chromosome
10378	23261	37040	1.93	1.3E+00/0.AE29955.1	NT	Campylactatyl; karameyn phosphatidesterase (apha-7) gene, complete cds	Campylactatyl; karameyn phosphatidesterase (apha-7) gene, complete cds
10725	23811		1.83	1.3E+00/0.AL163302.2	NT	Homo sapiens chromosome 21	Homo sapiens chromosome 21, segment H621H102
11135	24068		4.55	1.3E+00/0.014117	SWISSPROT	DHAPYRIMIDINASE (DHAPSE)	DHAPYRIMIDINASE (DHAPSE) (HYDANTOINASE) (DHP)
11344	24263	37703	2.47	1.3E+00/0.P52369	SWISSPROT	MRNA 3' END PROCESSING PROTEIN RNAT16	MRNA 3' END PROCESSING PROTEIN RNAT16
11392	24294	37728	2.01	1.3E+00/0.18862.2	NT	Mus musculus dentin gene	Mus musculus dentin gene
11970	24413	38308	3.48	1.3E+00/0.04042.1	NT	Bacillus subtilis genomic DNA, 23.945 fragment	Bacillus subtilis genomic DNA, 23.945 fragment
12049	24480	38394	5.09	1.3E+00/0.268982.1	NT	Apple mosaic virus RNA 2	Apple mosaic virus RNA 2, putative polymerase gene, complete cds
12204	26068		1.93	1.3E+00/0.F174885.1	NT	Coats protein (mRNA) coding for polyoma virus	Coats protein (mRNA) coding for polyoma virus, complete cds
12259	26370		3.14	1.3E+00/0.5168743.1	NT	ELF1 GLOVOTRIN PRECURSOR (WATER GLOVOTRIN) (MERGENSE GLYCOPROTEIN)	ELF1 GLOVOTRIN PRECURSOR (WATER GLOVOTRIN) (MERGENSE GLYCOPROTEIN)
12752	28259	37800	3.77	1.3E+00/0.F33464.1	EST_HUMAN	SWISSPROT	SWISSPROT
12814	28454		1.48	1.3E+00/0.017055.1	NT	Naphthalene/benzo(a)-pyrene	Naphthalene/benzo(a)-pyrene, complete cds, microsatellite gene for microsatellite
13028	29716		1.54	1.3E+00/0.089278.1	NT	220R68.AT1	220R68.AT1 S. aureus, field, New Zealand, 1981
13213	29847		1.79	1.3E+00/0.AG76248.1	EST_HUMAN	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)
13409	29843		1.31	1.3E+00/0.P00228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)
13409	29844		1.31	1.3E+00/0.P00228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)
13409	29845		1.31	1.3E+00/0.P00228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)
13409	29846		1.31	1.3E+00/0.P00228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)
13409	29847		1.31	1.3E+00/0.P00228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)
13409	29848		1.31	1.3E+00/0.P00228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)
13409	29849		1.31	1.3E+00/0.P00228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)
13409	29850		1.31	1.3E+00/0.P00228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)
13409	29851		1.31	1.3E+00/0.P00228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)
13409	29852		1.31	1.3E+00/0.P00228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)
13409	29853		1.31	1.3E+00/0.P00228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)
13409	29854		1.31	1.3E+00/0.P00228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)
13409	29855		1.31	1.3E+00/0.P00228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)
13409	29856		1.31	1.3E+00/0.P00228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)
13409	29857		1.31	1.3E+00/0.P00228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFRP-IL1)
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10356	20839	37307	2176	1.0E-09	AJ004982.1	EST HUMAN	384022.11 Sordal liver, spleen, INFLS, ST Homo sapiens cDNA clone IMAGE:438008 5'
10388	28712	37320	1.11	1.0E-09	U11970.1	NT	Human MPO-oligonucleotide specificity group 127, complete cds
11528	24438	37896	1.59	1.0E-09	AJ271494.1	EST HUMAN	358811.11 Sordal_liver, spleen, INFLS, ST Homo sapiens cDNA clone IMAGE:435463 3' similar to
12462	19645	37346	1.37	1.0E-09	ZJ7022.1	EST HUMAN	Human ALDOSE 1,6-BISPHOSPHATASE, complete cds
12509	29172	37346	3.26	1.0E-09	AF15308	SWISSPROT	Hsodm, aldolase gene encoding cytosolic polypeptide
12703	29358	37346	2.04	1.0E-09	AF070784.1	EST HUMAN	T-RIBONUCLEOTIDYL PRE-2' RIBOSYL (RFTOMODULIN) (TM)
2084	19578	28877	1.27	9.9E-07	AF103322.2	EST HUMAN	EST388295 IMAGE, sequences, MAGE Homo sapiens cDNA
3467	19701		0.96	9.9E-07	AF174685.1	NT	Homo sapiens chromosome 21, segment HS21G102
5500	18601	32016	1174	9.9E-07	AJ49457.1	SWISSPROT	Alpha-maleic acid dehydrogenase, complete cds
6084	19148	32280	0.92	9.9E-07	Q98657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
8503	22709		1.76	9.9E-07	U62697.1	NT	PROBABILE OXIDOREDUCTASE ZK1260.TIN CHROMOSOME 11
10084	22677		2.07	9.9E-07	U23842.1	SWISSPROT	Lycopodium secundatum putative Mt copy1 nonalcohol resistance gene
11157	24038	37533	2.46	9.9E-07	AJ005029.1	NT	B2 BRADYKININ RECEPTOR (BK2 RECEPTOR)
646	13015	29523	1.13	9.9E-07	F72967	SWISSPROT	Danio rerio mRNA for Eph-like receptor tyrosine kinase nr8
2316	13324		1.1	9.9E-07	AJ003108.1	NT	Callithrix jacchus UBE1 gene derived retroposon on the Y chromosome
7964	20501	33789	4.81	9.9E-07	AJ302188.1	NT	Enticodactylase sp. JM693 partial gGrES gene for GGrES-like protein and partial gGrEL gene for GGrEL-like protein, isolate JM693
7964	20501	33789	4.81	9.9E-07	AJ302188.1	NT	Enticodactylase sp. JM693 partial gGrES gene for GGrES-like protein and partial gGrEL gene for GGrEL-like protein, isolate JM693
8094	21000	34330	1.20	9.9E-07	BF074015.1	EST HUMAN	601403337F1 NH, MGC, 90 Homo sapiens cDNA clone IMAGE:3900049 5'
8094	21000	34331	1.21	9.9E-07	BF074015.1	EST HUMAN	601403337F1 NH, MGC, 90 Homo sapiens cDNA clone IMAGE:3900049 5'
9278	22000	35503	0.98	9.9E-07	U98662	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10918	23903		0.71	9.9E-07	AJ435595.1	EST HUMAN	405604.11 NO, CGAP, OGBT Homo sapiens cDNA clone IMAGE:1371647 3'
11432	24348	37763	2.02	9.9E-07	BE389705.1	EST HUMAN	601110258F1 NH, MGC, 10 Homo sapiens cDNA clone IMAGE:3300760 5'
11432	24348	37764	2.02	9.9E-07	BE389705.1	EST HUMAN	601110258F1 NH, MGC, 10 Homo sapiens cDNA clone IMAGE:3300760 5'
12598	25294		1.84	9.9E-07	U2111.2	NT	Homo sapiens X28 region near ALO locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Guanine/Calcium-dependent protein kinase 1 (CAMK1), creatine transporter (CRTX), C-M protein (C-M), adenocarcinoma protein 5
7526	20489	33745	2.22	9.7E-07	U26716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9, 10, 11, 12 and optional segments b, c, d and e, partial cds
8070	21989	35353	1.89	9.7E-07	AF146112.1	NT	Thalassemia erythroid alpha and resistance protein Y10 (Y10) gene, complete cds
8075	22001	35359	1.46	9.7E-07	U00344.1	NT	Schistosoma japonicum esterase-methyltransferase (met) and restriction endonuclease (met)
8597	22326	35668	0.82	9.7E-07	BF706622.1	EST HUMAN	601032102F1 NH, MGC, 7 Homo sapiens cDNA clone IMAGE:394504 5'

Table 4
Single Exon Probes Expressed in Adult Liver

Probe Seq ID NC:	Exon Seq ID NC:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5122	18125		3.52	8.7E-01	AF21970.1	NT	Pseudomonas aeruginosa lipopolysaccharide (lps), relative transcriptional regulatory protein. OtsR (otsR), ortho-
5350	18174		0.73	8.7E-01	AF21970.1	NT	transcriptional regulatory protein. OtsR (otsR), ortho-transcriptional regulatory protein. OtsR (otsR), ortho-
5617	21146	31186	0.65	8.7E-01	AF21970.1	NT	transcriptional regulatory protein. OtsR (otsR), ortho-transcriptional regulatory protein. OtsR (otsR), ortho-
5617	21146	31889	0.65	8.7E-01	AF21970.1	NT	transcriptional regulatory protein. OtsR (otsR), ortho-transcriptional regulatory protein. OtsR (otsR), ortho-
5495	22419	35774	0.74	8.7E-01	AF21970.1	NT	transcriptional regulatory protein. OtsR (otsR), ortho-transcriptional regulatory protein. OtsR (otsR), ortho-
5495	22419	35774	0.74	8.7E-01	AF21970.1	NT	transcriptional regulatory protein. OtsR (otsR), ortho-transcriptional regulatory protein. OtsR (otsR), ortho-
10298	22148	36559	1.77	8.7E-01	AF21970.1	NT	transcriptional regulatory protein. OtsR (otsR), ortho-transcriptional regulatory protein. OtsR (otsR), ortho-
10793	22679	37108	0.59	8.7E-01	AF21970.1	NT	transcriptional regulatory protein. OtsR (otsR), ortho-transcriptional regulatory protein. OtsR (otsR), ortho-
10793	22679	37108	0.59	8.7E-01	AF21970.1	NT	transcriptional regulatory protein. OtsR (otsR), ortho-transcriptional regulatory protein. OtsR (otsR), ortho-
11271	24163	37644	6.02	8.7E-01	AF21970.1	NT	transcriptional regulatory protein. OtsR (otsR), ortho-transcriptional regulatory protein. OtsR (otsR), ortho-
12137	24686	36493	4.03	8.7E-01	AF21970.1	NT	transcriptional regulatory protein. OtsR (otsR), ortho-transcriptional regulatory protein. OtsR (otsR), ortho-
12137	24686	36497	4.03	8.7E-01	AF21970.1	NT	transcriptional regulatory protein. OtsR (otsR), ortho-transcriptional regulatory protein. OtsR (otsR), ortho-
12678	25735		2.12	8.7E-01	AF21970.1	NT	transcriptional regulatory protein. OtsR (otsR), ortho-transcriptional regulatory protein. OtsR (otsR), ortho-
497	13637		1.66	8.0E-01	X71012.1	NT	Rat (Rattus norvegicus) gene for insulin-like growth factor II
633	13928	20884	4.44	8.0E-01	W60480.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:343576 5'
2289	15297	28304	1.17	8.0E-01	463210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous
3086	16719	29811	0.9	8.0E-01	AL161865.2	NT	xenotransfected), perlecanin 1 (CYP27A1b) mRNA
3365	18584	29778	1.54	8.0E-01	U46724.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
5413	18584		1.6	8.0E-01	AB014075.1	NT	Drosophila melanogaster mRN (Dros) mRNA, complete cds
8116	19175	32309	8.31	8.0E-01	X90547.1	NT	end 12 ORFs, complete and partial cds
8116	19175	32310	8.31	8.0E-01	X90547.1	NT	end 12 ORFs, complete and partial cds
6539	25551	32668	0.51	8.0E-01	X76772.1	NT	Chicken lipoprotein lipase gene
7008	20033	33295	1.66	8.0E-01	AF161821.1	NT	polyprotein (Coxsackie B4 virus CB4, heat-misc, EZ, originally derived from Edwards CB4 human strain,
7008	20033	33295	1.66	8.0E-01	AF161821.1	NT	Genomic RNA, Complete, 7397 nt
7957	20973		0.53	8.0E-01	AF161821.1	NT	Gus transposon recombinant activating protein 1 (RAC-1) gene, partial cds
8506	27437		1.49	8.0E-01	AF200596.1	NT	Gus transposon recombinant activating protein 1 (RAC-1) gene, partial cds
8506	27437		1.49	8.0E-01	AF200596.1	NT	Helicobacter pylori 26695 (strain 69) of 134 of the complete genome
8502	271551		0.78	8.0E-01	AF201763.1	NT	Helicobacter pylori 26695 (strain 69) of 134 of the complete genome
7027	20053	33286	1.25	8.0E-01	AF163241.1	NT	Drosophila melanogaster collagen response mediator protein (CRMP) mRNA, complete cds
7949	20371	34182	2.54	8.0E-01	BE542612.1	EST_HUMAN	Staphylococcus aureus complete genome
							801071071 NH_MGC_8 Homo sapiens cDNA clone IMAGE:343566 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	QRF SEQ ID NO.	Expression Signal	Mean Sample (Top) Hi ELAST E Value	Top Hi Accession No.	Top Hi Database Source	Top Hi Descriptor
8170	22028	354198	0.99	8.1E-01	AF001571.1	NT	Bacillus thuringiensis genomic DNA, section 11/14
8170	22098	354199	0.99	8.1E-01	AF001571.1	NT	Bacillus thuringiensis genomic DNA, section 11/14
8229	22237	39821	1.24	8.1E-01	AF022677.1	EST_HUMAN	Q04288 CELL GROWTH REGULATING NUCLEOPROTEIN, contains BEX22.1 PPRO repeats
10225	23511	30844	0.96	8.1E-01	P08425	SWISSPROT	PROBABLY F4 PROTEIN
10896	23784	37286	0.95	8.1E-01	N94541.1	EST_HUMAN	K16872F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K16872.5 similar to
11014	23751	38297	3.42	8.1E-01	B5524598.1	EST_HUMAN	EST (CLONE COPE11)
11014	23751	38297	3.42	8.1E-01	B5524598.1	EST_HUMAN	RC3-TN0038-220800-028-410 TN080 Homo sapiens cDNA
11914	24751	38256	3.42	8.1E-01	B5524598.1	EST_HUMAN	RC3-TN0038-220800-028-410 TN080 Homo sapiens cDNA
12077	26157	31871	1.81	8.1E-01	AF007111.1	NT	Thrombospondin section 23 of 136 of the complete genome
1277	13265	31871	2.84	8.0E-01	AJ271810.1	NT	Staphylococcus aureus partial pta gene for phosphatase allele 15
308	13401	20318	6.50	8.0E-01	AJ133722.1	NT	Bovine lactoferrin and HIF genes
2049	18098	20072	1.48	8.0E-01	B5530962.1	EST_HUMAN	602072479P1 NCI COAP Bm67 Homo sapiens cDNA clone IMAGE:4216091.5
3128	18177	20072	1.18	8.0E-01	AF127697.1	NT	Salmonella typhimurium effector receptor (SBO27) gene, partial cds
3358	18422	25003	0.9	8.0E-01	A3006102.1	NT	Mus musculus gene for outcortin glycoprotein, complete cds
3787	18768	30521	0.98	8.0E-01	AL162768.2	NT	Nicotinic acetylcholine receptor (nAChR) beta 3 subunit
4649	17855	30521	7.44	8.0E-01	X63739.2	NT	G. gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
5103	18100	30946	1.18	8.0E-01	7657352	NT	Mus musculus myosin IXa (Myosin)
5245	18328	31177	1.01	8.0E-01	BE27216.1	EST_HUMAN	60117897F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3057068.5
8649	21600	33774	1.09	8.0E-01	AF001480.1	EST_HUMAN	RC0ANN1012-270300-027-H06 NN1012 Homo sapiens cDNA
0090	22018	33774	1.39	8.0E-01	Y11095.1	NT	Rice stripe virus RNA 3
11394	24310	37796	1.94	8.0E-01	Q02793	SWISSPROT	CREG-BINDING PROTEIN
478	13547	25467	1.01	7.9E-01	D11476.1	NT	Lysine-rich nuclear protein
719	13795	25467	0.92	7.9E-01	AF002130.1	NT	Unpublished human section 31 of 99 of the complete genome
1622	14672	25467	18.76	7.9E-01	A040465.1	NT	Homo sapiens mRNA for KIAA1462 protein, partial cds
2290	19269	28267	6.28	7.9E-01	A0004816.1	NT	Oryzopsis cuniculatus mRNA for mitochondrion, complete cds
2291	19269	28268	2.4	7.9E-01	AF130489.1	NT	Danio rerio t-p1-associated protein 1 (t-p1) mRNA, complete cds
3576	18813	29516	3.17	7.9E-01	AF228664.1	NT	Gallus gallus SOX9 transcription factor (SOX9) mRNA, complete cds
4403	17416	30550	0.67	7.9E-01	BE26912.1	EST_HUMAN	U0110203P1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3053785.5
4722	17727	30550	0.82	7.9E-01	6783746	NT	Mus musculus enigma (Enm), mRNA
4722	17727	30550	0.82	7.9E-01	6783746	NT	Mus musculus enigma (Enm), mRNA
5320	18304		0.69	7.9E-01	AF135718.1	NT	Chlamydia trachomatis peptidoglycanase, gene, complete cds

Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) hit BLAST E Value	Top Hit Accession	Top Hit Database Source	Top Hit Descriptor
3042	16956	29562	4.62	7.7E-01	R118035.1	NT	Homo sapiens PRO1075 mRNA, complete cds
4903	17613	30379	2.52	7.7E-01	R159488.1	NT	Colinus catus japonica japonica sub-species japonica beta-actin mRNA, partial cds
4903	17613	30380	2.52	7.7E-01	R159488.1	NT	Colinus catus japonica japonica sub-species japonica beta-actin mRNA, partial cds
5762	18825	31823	1.38	7.7E-01	R16953	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5762	18825	31824	1.38	7.7E-01	R16953	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6181	12238	32385	0.88	7.7E-01	R08902.1	EST_HUMAN	ZNF602.1 Scores final iter splign NFI3 Homo sapiens cDNA, clone IMAGE:127785.3
10398	22348	35958	0.83	7.7E-01	R0241134.1	NT	Daphnia magna hemolymph gene cluster (H83, d8b1 and d8b2 genes), complete cds
12305	25240		5.05	7.7E-01	11467923	NT	Archaeobacillus thauricus, complete genome
8336	19396	32554	3.97	7.6E-01	A1506910.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (VCOB) mRNA, complete cds
6335	19396	32555	3.97	7.6E-01	A1506910.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (VCOB) mRNA, complete cds
6766	18820	30339	0.78	7.6E-01	F03736.1	SWISSPROT	MATING-TYPE PROTEIN ALPHA 24
6766	18820	30339	0.78	7.6E-01	F03736.1	SWISSPROT	seq4b12.1 Stanley Frontal NS pool 2 Homo sapiens cDNA, clone IMAGE:2036979
7170	18442	31345	0.97	7.6E-01	A1293390.1	EST_HUMAN	seq4b12.1 Stanley Frontal NS pool 2 Homo sapiens cDNA, clone IMAGE:2036979
7170	18442	31345	0.97	7.6E-01	A1293390.1	EST_HUMAN	Rattus norvegicus calcium-independent alpha-1a1-oligon receptor mRNA, complete cds
7404	20103	33338	0.83	7.6E-01	U72487.1	NT	
8842	21573	34911	1.44	7.6E-01	A1F46793.1	NT	Miss musculus neuromedin U precursor (NmU) gene, partial cds; PHLIP (Tph) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (PFT27) gene, complete cds; and HBAR (Hbar) gene, complete cds
5703	21524	34680	2.41	7.6E-01	0987532.1	NT	Miss musculus actinin (Actin-binding), mRNA
5703	21524	34680	2.41	7.6E-01	0987532.1	NT	Miss musculus actinin (Actin-binding), mRNA
8300	21890	35183	0.6	7.6E-01	C001098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBT THE 2D)(NCO) (NMDAR2C)
8300	21890	35183	0.6	7.6E-01	C001098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBT THE 2D)(NCO) (NMDAR2C)
8500	21830	35184	0.6	7.6E-01	C001098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBT THE 2D)(NCO) (NMDAR2C)
9819	22725	30109	3.76	7.6E-01	F03932	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR V2
9819	22725	30109	3.76	7.6E-01	F03932	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR V2
8155	24718	39210	2.5	7.6E-01	Z69543.1	NT	H. sapiens mRNA for neurofilament Nf70
8155	24718	39210	2.5	7.6E-01	Z69543.1	NT	H. sapiens mRNA for neurofilament Nf70
11798	24718	39211	3.98	7.6E-01	Z69543.1	NT	H. sapiens mRNA for neurofilament Nf70
12133	21674		3.56	7.6E-01	AL101992.2	NT	Xenopus laevis DNA chromosome 4, contig fragment No. 88
12283	25100		9.4	7.6E-01	A35027002.1	NT	Homo sapiens mRNA for KIAA0695 protein, partial cds
5336	13605		1.29	7.6E-01	AL103301.2	NT	Homo sapiens chromosome 21 segment HS21C101

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	GRF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
605	13671	26574	1.39	7.4E-01	AF026563.1	NT	Homo sapiens FRAB3, compact fragile region, deoxycytidine triphosphate hydrolase (FHT) gene, exon 5
3413	15405	28361	1.22	7.4E-01	C14203.1	EST_HUMAN	C14203, Corin-like human cDNA, 3544 bp, mRNA, (B5972) Homo sapiens cDNA clone BE4267611 5'
4785	17190		1.71	7.4E-01	U45498.1	NT	Homo sapiens skeletal muscle myosin receptor gene (MYR1), exon 92
5338	18415		1.15	7.4E-01	U45498.1	NT	Homo sapiens skeletal muscle myosin receptor gene (MYR1), exon 92
7445	20507	54179	0.95	7.4E-01	AF026563.1	NT	Homo sapiens skeletal muscle myosin receptor protein (MYR1) mRNA, complete cds
12559	25274		4.74	7.4E-01	AF026563.1	NT	Homo sapiens skeletal muscle myosin receptor protein (MYR1) mRNA, complete cds
13071	25553	31757	1.95	7.4E-01	D63697.1	NT	Synuclein, alpha, P250833, complete genome, 927, 1054477-119335
1157	14198	27134	1.1	7.4E-01	A1598146.1	EST_HUMAN	h14608.1 NCL CGAP_Bv646 Homo sapiens cDNA clone IMAGE:2167777 3' similar to canine A1u
2035	18372	25375	1.00	7.4E-01	A001108.1	NT	Homo sapiens mRNA for UAGR34 protein, partial cds
3750	19821	20708	1.38	7.4E-01	AF112533.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
3973	17001	28988	0.99	7.4E-01	AF133310.1	NT	Vibrio cholerae phage CTXphi Calcutta-rfR-a (rfR-a) and Calcutta-rfR-b (rfR-b) genes, complete cds
4416	17427	30289	4.86	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21, segment H82:O45
8425	21368	34697	1.09	7.4E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8425	21368	34698	1.09	7.4E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
5122	22120	35476	0.9	7.4E-01	BF944593.1	EST_HUMAN	0020134591 NCL CGAP_Bv646 Homo sapiens cDNA clone IMAGE:415420 5'
6272	22200		0.9	7.4E-01	U07990.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
6542	22108	35030	7.39	7.4E-01	BE747503.1	EST_HUMAN	0015702031 N11 MGCG 9 Homo sapiens cDNA clone IMAGE:354174 5'
9490	22624	36002	1.31	7.4E-01	AA187695.1	EST_HUMAN	2017001.1 Staphylococcus aureus 157723 Homo sapiens cDNA clone IMAGE:622297 3' similar to
10847	23712	37188	0.82	7.4E-01	11424933	NT	SW-72101, MOUSE P42953 T-COMPLEX PROTEIN 1, THETA SUBUNIT
12000	24621	35436	1.43	7.4E-01	AB021490.2	NT	Homo sapiens NY-REN-46 antigen (L0051183), mRNA
12000	24621	35437	1.43	7.4E-01	AB021490.2	NT	Oryzopsis latipes gene for membrane guanylyl cyclase OGC1, complete cds
12257	26071		5.27	7.4E-01	6733217	NT	Oryzopsis latipes gene for membrane guanylyl cyclase OGC1, complete cds
12363	26190		1.89	7.4E-01	AJ470941.1	EST_HUMAN	Male, muscular complement component 1 inhibitor (C1in), mRNA
4099	17055		0.72	7.4E-01	AF000092.1	EST_HUMAN	h13011.1 NCL CGAP_Bv646 Homo sapiens cDNA clone IMAGE:2043985 3'
4729	17734	30950	0.71	7.3E-01	AJ5001196.1	NT	Angiogenin, human genomic DNA, section 57
4813	17814	30881	4.08	7.3E-01	AJ5001196.1	NT	Drosophila pupal protein (section 52 of 70) of the complete genome
5238	18226	31074	0.95	7.3E-01	AJ5001196.1	NT	Homo sapiens h1017 mRNA, complete cds
5863	19923	33137	5.62	7.3E-01	043103	SWISSPROT	PERCUTANONE, SIDS-COPOLYMER PE-TIDE SYNTHETASE
5863	19923	33137	5.62	7.3E-01	043103	SWISSPROT	Male, muscular complement component 1 inhibitor (C1in), mRNA
5863	19923	33138	5.62	7.3E-01	357121	NT	Male, muscular complement component 1 inhibitor (C1in), mRNA

Express

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID No.	Exon SEQ ID No.	ORF SEQ ID No.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12197	25301		4.27	7.0E-01	A700063.1	NT	Acetylation protein, cytosolic DNA, section 617
716	13774	26994	11.44	7.1E-01	D24070.1	NT	Human cathepsin B mRNA for building skeletal muscle calcium release channels (ryanodine receptor) alpha isoform(SRRT) complete cds
3110	16161	20057	20.14	7.1E-01	A427077.1	NT	Human sapient partial TGF- β 1 gene for T-cell transcription factor-4, exons 1-5-18
4304	17518	30186	5.04	7.1E-01	7203300	NT	Human sapient partial TGF- β 1 gene for T-cell transcription factor-4, exons 1-5-18
4304	17518	30186	5.04	7.1E-01	7203300	NT	Human sapient partial TGF- β 1 gene for T-cell transcription factor-4, exons 1-5-18
8173	18230	32376	1.85	7.1E-01	B758-034.1	EST_HUMAN	Meta maculosa dendritic (Opa) mRNA
8173	18230	32376	1.85	7.1E-01	B758-034.1	EST_HUMAN	Meta maculosa dendritic (Opa) mRNA
7281	20234	33484	6.39	7.1E-01	U62323.1	NT	602165-038F NIH LMG5, 83 Homo sapiens cDNA clone IMAGE426334.9
6205	21600	35044	3.95	7.1E-01	U62444.1	EST_HUMAN	602165-038F NIH LMG5, 83 Homo sapiens cDNA clone IMAGE426334.9
6205	21600	35044	3.95	7.1E-01	U62444.1	EST_HUMAN	602165-038F NIH LMG5, 83 Homo sapiens cDNA clone IMAGE426334.9
9295	22223	35852	0.95	7.1E-01	B507418.1	EST_HUMAN	602165-038F NIH LMG5, 83 Homo sapiens cDNA clone IMAGE426334.9
9295	22223	35852	0.95	7.1E-01	B507418.1	EST_HUMAN	602165-038F NIH LMG5, 83 Homo sapiens cDNA clone IMAGE426334.9
10395	23298	35050	1.95	7.1E-01	B504403.1	EST_HUMAN	602165-038F NIH LMG5, 83 Homo sapiens cDNA clone IMAGE426334.9
10395	23298	35050	1.95	7.1E-01	B504403.1	EST_HUMAN	602165-038F NIH LMG5, 83 Homo sapiens cDNA clone IMAGE426334.9
10854	23779	37206	1.29	7.1E-01	M12981.1	NT	602165-038F NIH LMG5, 83 Homo sapiens cDNA clone IMAGE426334.9
12657	25708		2.16	7.1E-01	A4421492.1	EST_HUMAN	602165-038F NIH LMG5, 83 Homo sapiens cDNA clone IMAGE426334.9
12657	25708		2.16	7.1E-01	A4421492.1	EST_HUMAN	602165-038F NIH LMG5, 83 Homo sapiens cDNA clone IMAGE426334.9
1267	14262	27237	0.85	7.0E-01	A8014574.1	NT	Human T-cell receptor gamma-chain J2 gene
1267	14262	27239	0.85	7.0E-01	A8014574.1	NT	Human T-cell receptor gamma-chain J2 gene
2473	15478	28478	1.54	7.0E-01	N62412.1	EST_HUMAN	Human T-cell receptor gamma-chain J2 gene
2473	15478	28477	1.54	7.0E-01	N62412.1	EST_HUMAN	Human T-cell receptor gamma-chain J2 gene
8186	18181		2.5	7.0E-01	AL163301.2	NT	Human T-cell receptor gamma-chain J2 gene
8177	18234		0.85	7.0E-01	A6021316.1	NT	Human T-cell receptor gamma-chain J2 gene
8949	21879		7.02	7.0E-01	A600253.1	EST_HUMAN	Human T-cell receptor gamma-chain J2 gene
11500	24469	37034	1.92	7.0E-01	AY763942.1	EST_HUMAN	Human T-cell receptor gamma-chain J2 gene
11500	24469	37035	1.92	7.0E-01	AY763942.1	EST_HUMAN	Human T-cell receptor gamma-chain J2 gene
13095	25900	31581	2.36	7.0E-01	U630469	NT	Human T-cell receptor gamma-chain J2 gene
890	14046	20389	66.92	6.9E-01	U68974.1	NT	Human T-cell receptor gamma-chain J2 gene
535	10456	26900	66.92	6.9E-01	U68974.1	NT	Human T-cell receptor gamma-chain J2 gene
1326	13700	27326	2.36	6.9E-01	AA469539.1	EST_HUMAN	Human T-cell receptor gamma-chain J2 gene
3208	18314	29217	1.93	6.9E-01	A602271.2	NT	Human T-cell receptor gamma-chain J2 gene
5552	19047	32184	0.79	6.9E-01	A6039662.1	NT	Human T-cell receptor gamma-chain J2 gene

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6221	16276	33430	0.83	6.0E-01	Y14278.1	NT	Oncofetal retinoblastoma mRNA for A kinase anchor protein DAKAP569, partial
6224	16276	33430	1.52	6.0E-01	BE255618.1	EST_HUMAN	00117355F: NIH, MGC, 17 Homo sapiens cDNA clone IMAGE:353233.5
6230	16276	33430	1.32	6.0E-01	AF240898.1	NT	Strongyloides papillorum species V, complete cds
8559	21450	34524	2.83	6.0E-01	AF240898.1	NT	Strongyloides papillorum species V, complete cds
8559	21450	34524	2.83	6.0E-01	AF101073.2	NT	Arabidopsis thaliana DNA, chromosome 4, contig fragment No. 89
8559	21450	34524	2.83	6.0E-01	AF101073.2	NT	Arabidopsis thaliana DNA, chromosome 4, contig fragment No. 89
8559	21450	34524	2.83	6.0E-01	AF110948.1	NT	Entamoeba histolytica cation translocating ATPase (atpase) gene, partial cds
10217	23108	36508	0.61	6.0E-01	AF200318.1	NT	Musa acuminata isolate Yusa 1 (PL1) mRNA, complete cds
10217	23108	36508	0.61	6.0E-01	AF200318.1	NT	Musa acuminata isolate Yusa 1 (PL1) mRNA, complete cds
10217	23108	36508	0.61	6.0E-01	D80013.1	NT	Musa acuminata isolate Yusa 1 (PL1) mRNA, complete cds
11705	24607	35084	2.1	6.0E-01	D80013.1	NT	Homo sapiens DAN gene, complete cds
12239	25793		1.75	6.0E-01	Q56583	SWISSPROT	FORHEAD BOX PROTEIN C2 (FORHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK-HEAD PROTEIN 1) (MFP-1) (PROTEIN) (TRANSCRIPTION FACTOR FKHL-14)
603	14034	25077	1.36	6.0E-01	AF017784.1	NT	Giantella intestinalis carboxamide kinase gene, complete cds
2723	15718		2.04	6.0E-01	D00071.1	NT	Synchytrium sp. PC25803 complete genome, 2727, 3418862-3975470
2877	14996	27831	1.19	6.0E-01	AA054475.1	EST_HUMAN	gb:U99411.maf ALCOHOL DEHYDROGENASE CLASS I PI CHAIN (HUMAN)
4687	17692	30559	1.56	6.0E-01	J00702.1	NT	Full[partial] prolactin gene: exon 8 and flanks
4688	17694	30822	0.7	6.0E-01	4759521	NT	Homo sapiens mRNA for KIAA1348 protein, partial cds
10164	20055	35454	1.85	6.0E-01	AB037708.1	NT	Stegomyia aegypti gene for beta-glucosidase, exons 1-4
11529	24439	37897	2.17	6.0E-01	AJ275975.1	NT	Stegomyia aegypti gene for beta-glucosidase, exons 1-4
11529	24439	37899	2.17	6.0E-01	AJ275975.1	NT	Mus musculus zinc finger protein (Zfp3) mRNA, complete cds
11554	24463	37928	2.85	6.0E-01	AF030593.1	NT	Mus musculus zinc finger protein (Zfp3) mRNA, complete cds
11554	24463	37929	2.85	6.0E-01	AF030593.1	NT	Propeller gamma-actin M2 transition initiation factor ZC11A (G14C) mRNA, complete cds
11745	24648	38128	1.30	6.0E-01	AF184151.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RP528, NADH oxidoreductase, NG29, KPC1, Fas-binding protein, BING1, Ispasin, RAG3S-like, KE2, BING4, beta 1.3-galactosyl transferase, and P4-918 genes, complete cds; Sarcos21 gene, partial>
12035	24977	38362	1.46	6.0E-01	AF110530.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RP528, NADH oxidoreductase, NG29, KPC1, Fas-binding protein, BING1, Ispasin, RAG3S-like, KE2, BING4, beta 1.3-galactosyl transferase, and P4-918 genes, complete cds; Sarcos21 gene, partial>
12035	24977	38363	1.46	6.0E-01	AF110530.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RP528, NADH oxidoreductase, NG29, KPC1, Fas-binding protein, BING1, Ispasin, RAG3S-like, KE2, BING4, beta 1.3-galactosyl transferase, and P4-918 genes, complete cds; Sarcos21 gene, partial>
518	13410	20438	24.03	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B cells 1 (NF-kB1) gene, complete cds
350	13446	28358	25.85	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NF-kB1) gene, complete cds

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Meet Similar (Top) hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1828	14846		1.17	6.7E-01	M12132.1	NT	Qual test skeletal muscle troponin I gene, complete cds
2181	15173	28177	2.08	6.7E-01	AA451864.1	EST_HUMAN	contains element TARI repetitive element
2179	15918	28107	3.88	6.7E-01	AF160793.1	NT	Drosophila melanogaster MetSdc gene, complete cds; NMDVC isoform (Nincho) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds
3339	16091	28083	4.6	6.7E-01	6697890	NT	Mus musculus Wlded-Medich syndrome protein (Wasp), mRNA
4883	17071	30434	0.97	6.7E-01	U74742.1	EST_HUMAN	S.ubacronimus Hsp70 for glucose-6-phosphate dehydrogenase
5300	18971	30628	1.11	6.7E-01	AF0470110.1	EST_HUMAN	hsp65121c1 INCL COAP- Cyt7 Homo sapiens cDNA clone IMAGE2874968.3
5589	18772	31700	0.87	6.7E-01	U42485.1	NT	M. luteus ATPase alpha and beta subunit (aba and abp) genes, complete cds
6658	18782	31701	0.87	6.7E-01	U42486.1	NT	M. luteus ATPase alpha and beta subunit (aba and abp) genes, complete cds
6189	19248	32382	1.69	6.7E-01	AE001468.1	NT	Helicobacter pylori strain J99 J81 section 47 of 132 of the complete genome
5378	19240	32604	1.86	6.7E-01	9202039	NT	Caldit temperature 2, complete genome
5579	19520	32605	1.66	6.7E-01	9202039	NT	Caldit temperature 2, complete genome
5657	19397	33155	1.66	6.7E-01	BE96041.2	EST_HUMAN	P01581/7741 NIH_JMC_71 Homo sapiens cDNA clone IMAGE3365778.3
5657	19397	33155	0.48	6.7E-01	BE96041.2	EST_HUMAN	P01581/7741 NIH_JMC_71 Homo sapiens cDNA clone IMAGE3365778.3
5657	19397	33155	0.48	6.7E-01	BE96041.2	EST_HUMAN	Homo sapiens saccharinase (SI), section 47 of 132 of the complete genome
7098	20051		3.77	6.7E-01	AE004468.1	NT	Helicobacter pylori strain J99 J81 section 47 of 132 of the complete genome
7728	20328	33635	0.98	6.7E-01	AE001468.1	NT	Helicobacter pylori strain J99 J81 section 47 of 132 of the complete genome
10042	20526		0.98	6.7E-01	U35045.1	NT	hsp65121c1 INCL COAP- Cyt7 Homo sapiens cDNA
11382	24363	37754	2.28	6.7E-01	U35045.1	EST_HUMAN	hsp65121c1 INCL COAP- Cyt7 Homo sapiens cDNA
11891	27300	37740	3.28	6.7E-01	U35045.1	EST_HUMAN	hsp65121c1 INCL COAP- Cyt7 Homo sapiens cDNA
2324	15328	28528	1.41	6.6E-01	AF193363.1	SWISSPROT	Homo sapiens SLT1 protein (SLT1) mRNA, partial cds
2751	17942	28731	1.44	6.6E-01	AF193363.1	NT	Homo sapiens SLT1 protein (SLT1) mRNA, partial cds
3549	19599	29421	1.26	6.6E-01	4509880	NT	Homo sapiens semaphorin, seven transmembrane repeats (types 1 and type 1 like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
3728	19648	29546	2.9	6.6E-01	U07005.1	NT	G.alkalies random DNA marker, 282bp
6167	18169	31007	0.93	6.6E-01	U28833.1	NT	M. saccharinus (HLB 5-2-4) DNA from parental PNA1
5167	18169	31008	0.93	6.6E-01	U28833.1	NT	M. saccharinus (HLB 5-2-4) DNA from parental PNA1
5968	19030	32612	4.18	6.6E-01	6805577	NT	Mus musculus Ibrexin light chain 2 (K4c2), mRNA
7482	20223	32701	0.68	6.6E-01	AE004468.1	NT	Pseudomonas aeruginosa PAO1, section 18 of 620 of the complete genome
7482	20223	32702	0.68	6.6E-01	AE004468.1	NT	Pseudomonas aeruginosa PAO1, section 18 of 620 of the complete genome
8168	21047	34373	3.09	6.6E-01	AF069036.1	EST_HUMAN	AF069036 G1C Homo sapiens cDNA clone G1C004.3
9129	20290	35417	0.72	6.6E-01	AF070700.1	EST_HUMAN	AF070700 A0C Homo sapiens cDNA clone A0C04.11.5'
10169	20290		1.14	6.6E-01	AL1728.2	NT	Homo sapiens chromosome 21 segment H521C0708

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expressed Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
647	13706	26615	1.33	6.5E-01	U76140.1	NT	4. Ulgans NucleoATPase alpha subunit mRNA, complete cds
647	13706	26616	1.33	6.5E-01	U76140.1	NT	4. Ulgans NucleoATPase alpha subunit mRNA, complete cds
3464	16533	29433	0.86	6.5E-01	AB041238.1	NT	Ulgans NucleoATPase alpha subunit mRNA, complete cds
4121	17144	30017	1.01	6.5E-01	U404832.1	NT	Ulgans NucleoATPase alpha subunit mRNA, complete cds
4560	17394	30298	4.78	6.5E-01	AJ72205.1	NT	Ulgans NucleoATPase alpha subunit mRNA, complete cds
5697	48169	34030	2.9	6.5E-01	U28231.1	NT	Phaeodactylum ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5915	18964	32103	0.68	6.5E-01	U193249.2	NT	Human aquaporin 21, secreted (S21G49)
7020	20052	33294	1.31	6.5E-01	U433438.1	NT	Human aquaporin 21, secreted (S21G49)
8026	20941	34256	0.78	6.5E-01	U04709.1	NT	Human aquaporin 21, secreted (S21G49)
8119	21030	34357	0.9	6.5E-01	AJ769932.1	EST HUMAN	Human aquaporin 21, secreted (S21G49)
10362	23241	38943	0.65	6.5E-01	U78904.1	EST HUMAN	Human aquaporin 21, secreted (S21G49)
10328	23709	37136	4.51	6.5E-01	AJ710676.1	NT	Human aquaporin 21, secreted (S21G49)
11079	24011	37452	2.87	6.5E-01	AJ75833.1	EST HUMAN	Human aquaporin 21, secreted (S21G49)
11228	24068	37654	3.7	6.5E-01	AJ691287.1	EST HUMAN	Human aquaporin 21, secreted (S21G49)
11230	24166		3.97	6.5E-01	AJ138078.1	EST HUMAN	Human aquaporin 21, secreted (S21G49)
12020	24871	38374	2.3	6.5E-01	AF041115.1	NT	Human aquaporin 21, secreted (S21G49)
12000	25031		4.15	6.5E-01	BE465050.1	EST HUMAN	Human aquaporin 21, secreted (S21G49)
12828	25716		2.67	6.5E-01	U77445.1	NT	Human aquaporin 21, secreted (S21G49)
271	13306	26282	6.03	6.5E-01	U48548.1	NT	Human aquaporin 21, secreted (S21G49)
2626	18024	28677	1.03	6.5E-01	AF161184.1	NT	Human aquaporin 21, secreted (S21G49)
3516	18064	29445	1.4	6.5E-01	U48554.2	NT	Human aquaporin 21, secreted (S21G49)
3028	18566	29838	1.39	6.5E-01	AB048327.1	NT	Human aquaporin 21, secreted (S21G49)
4358	17372		0.96	6.5E-01	U77155.1	NT	Human aquaporin 21, secreted (S21G49)
4606	17913	30473	0.75	6.5E-01	U712483.1	NT	Human aquaporin 21, secreted (S21G49)
4606	17913	30474	0.75	6.5E-01	U712483.1	NT	Human aquaporin 21, secreted (S21G49)
6066	18062	30005	1.01	6.5E-01	AC298978.1	NT	Human aquaporin 21, secreted (S21G49)
9173	22101	39441	1.78	6.5E-01	AE001247.1	NT	Human aquaporin 21, secreted (S21G49)
10351	23477	38905	10.78	6.5E-01	U62528.1	NT	Human aquaporin 21, secreted (S21G49)
10005	23497	38920	1.35	6.5E-01	U670405.1	EST HUMAN	Human aquaporin 21, secreted (S21G49)
12718	25368		12.64	6.5E-01	AJ759212.1	EST HUMAN	Human aquaporin 21, secreted (S21G49)
457	13359	29402	5.03	6.5E-01	U05528.1	SWISSPROT	Human aquaporin 21, secreted (S21G49)

Table 4

Expression

Single Exon Probes Expressed in Adult Liver

[illegible]

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9281	21939	34676	1.67	6.2E-01	NC656087.1	EST HUMAN	6013261461 NIH_MGC_44 Homo sapiens cDNA IMAGE:346010.5
10041	22341		3.87	6.2E-01	M21491.1	NT	Human pulmonary surfactant-associated protein SP-B (SP-B) mRNA, complete cds
10050	22456	36891	7.87	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 28
10717	23633	37031	0.6	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
10717	23603	37032	0.6	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
11015	23959	37335	5.73	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE; T-HIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
11015	23999	37336	5.73	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE; T-HIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2417	15421		7.14	6.1E-01	6975076	NT	Mus musculus secreted acidic crystallin glycoprotein (Sparc), mRNA
4951	17657	30523	12.86	6.1E-01	4957338	NT	Caenorhabditis elegans H2 OaMyo2 (Hh-1) alternative 7 spliced genes, complete cds
5726	18709	31802	1.27	6.1E-01	M59240.1	NT	Rat TRPM-2 gene, complete cds
7165	20195	33439	3.56	6.1E-01	M84733.1	NT	Rat TRPM-2 gene, complete cds
7165	20165	33440	3.56	6.1E-01	M84733.1	NT	Rat TRPM-2 gene, complete cds
7365	20359	33628	0.67	6.1E-01	AW105553.1	EST HUMAN	xbf0303.1 NC_024603 Homo sapiens cDNA IMAGE:299727.3 similar to gb:U18677.1 mat
7991	20404	35090	0.50	6.1E-01	Q83769	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN); SUSHI REPEAT-CONTAINING PROTEIN IN SARX PRECURSOR (DRS PROTEIN) [DOWN-REGULATED BY V-SRC]
8911	21741	35090	3.79	6.1E-01	AF035955.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
9353	22281	35641	1.39	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4 (MAP4K4), mRNA
9353	22281	35642	1.39	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4 (MAP4K4), mRNA
9049	23554	36241	23.9	6.1E-01	AF298117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9049	23554	36242	23.9	6.1E-01	AF298117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
10057	23246	36065	1.08	6.1E-01	AF004492.1	NT	Pseudomonas aeruginosa PAO1, section 13 of 528 of the complete genome
10549	23453	36895	1.48	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
12156	24555	36494	2.24	6.1E-01	S8182.1	NT	yeast nuclear-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12156	24565	36495	2.24	6.1E-01	S8182.1	NT	yeast nuclear-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
9171	18367	25650	6.03	6.0E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
9171	18367	25650	6.03	6.0E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1389	14420	27375	1.67	6.0E-01	AF066333.1	NT	Homo sapiens adenovirus-related protein complex 3, mu 2 subunit (GLA20), mRNA
1389	14420	27375	1.67	6.0E-01	AF066333.1	NT	Homo sapiens adenovirus-related protein complex 3, mu 2 subunit (GLA20), mRNA

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe Seq ID Seq ID	Exon Seq ID NO.	ORF-SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5885	18914	29709	0.83	6.0E-01 A123326.1	NT	NT	Viral haemorrhagic septicaemia virus N P. M. G. No. L genes, French strain 01/71
5463	18544	31984	3.6	6.0E-01 P02088	SWISSPROT	EST_HUMAN	D(2)DOFAMINE RECEPTOR
5925	18701	31690	2.44	6.0E-01 AW139743.1	EST_HUMAN	EST_HUMAN	U1-HB1-est-ab-103-0-J11 NCL_OGAP_Sabot Homo sapiens cDNA clone IMAGE2716619.3
6816	19851	33532	2.6	6.0E-01 U36813.1	NT	NT	Musca domestica lysocidine-succinylate chain voltage-sensitive sodium channel mRNA, complete cds
6955	19884	33208	0.79	6.0E-01 Q04912	SWISSPROT	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P168-0N)
7127	20331	33564	0.82	6.0E-01 L0284.1	NT	NT	(CDW136) (CD186 ANTIGEN)
7127	20331	33564	0.82	6.0E-01 L0284.1	NT	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
7742	20973	33971	6.6	6.0E-01 A1277691.1	NT	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
9701	21632	34977	4.43	6.0E-01 P02635	SWISSPROT	SWISSPROT	Homo sapiens paria LM01 gene for LIM domain only1 protein, exon 1
6701	21632	34978	4.43	6.0E-01 P02635	SWISSPROT	SWISSPROT	SEGMENTATION PROTEIN RUSHI TARAZU
10335	23227	39843	1.79	6.0E-01 A0906193.1	NT	NT	SEGMENTATION PROTEIN RUSHI TARAZU
10769	23952		1.95	6.0E-01 Q01467	SWISSPROT	SWISSPROT	Homo sapiens gene for sulcitiene B4 receptor BLT2, sulcitiene B4 receptor BLT1, complete cds
10871	23757		0.52	6.0E-01 BEA31779.1	EST_HUMAN	EST_HUMAN	PEROXISOMAL MEMBRANE PROTEIN PER3 (PEROXIN-3)
11497	24408	37642	1.77	6.0E-01 A131862.1	NT	NT	RC2-FN0054-190700-017-d09 FN0054 Homo sapiens cDNA
11497	24408	37643	1.77	6.0E-01 A131862.1	NT	NT	Gallus gallus mRNA for tyrosine protein, 419 KD isoform
11984	24827	38324	3.16	6.0E-01 A120028.1	EST_HUMAN	EST_HUMAN	Gallus gallus mRNA for tyrosine protein, 419 KD isoform
12088	25345	31828	1.52	6.0E-01 11421093	NT	NT	Homo sapiens nuclear factor (cytochrome-derived 2)-like 3 (NFE2L3), mRNA
12920	25771	31576	2.29	6.0E-01 9355093	NT	NT	Homo sapiens cGMP-inhibited phosphodiesterase (Pde3a), mRNA
12969	25709		5.41	6.0E-01 BE167617.1	EST_HUMAN	EST_HUMAN	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
1028	14791	27017	0.95	6.0E-01 U32701.1	NT	NT	RC1-HY075-09030-015-033 HY075 Homo sapiens cDNA
1427	14468	27411	1.18	6.0E-01 6980232	NT	NT	Hemophilus influenzae Rd action 16 of 163 of the complete genome
3314	15361	29281	6.06	6.0E-01 AL163397.2	NT	NT	Mus musculus 3-hydroxy-3-methylglutaryl-Coenzyme A lyase (Hmgsl), mRNA
3314	15361	29282	6.06	6.0E-01 AL163397.2	NT	NT	Homo sapiens chromosome 21 segment 162510667
4319	17833		3.5	6.0E-01 AF162795.1	NT	NT	Rattus norvegicus chromosome 21 segment 162510667
9258	18273	31072	2.12	6.0E-01 U27316.1	NT	NT	Oryzias latipes chromosome 21 segment 162510667
9326	18310	31160	2.5	6.0E-01 AF024966.1	NT	NT	Oryzias latipes chromosome 21 segment 162510667
6738	19772	33869	2.3	6.0E-01 AF064440.2	NT	NT	One area SRY gene promoter region
7042	20577	33871	3.8	6.0E-01 AF064440.2	NT	NT	Homo sapiens low density lipoprotein receptor related protein II (LRP2) gene, exon 1 and partial cds
7765	20724		0.36	6.0E-01 X08601.1	NT	NT	Homo sapiens gene for histone H2, nucleolar promoter region and complete cds
8275	21398	34655	0.31	6.0E-01 X08601.1	NT	NT	Gallus gallus gene for nucleolar ribosomal protein L25
8275	21398	34655	0.31	6.0E-01 X08601.1	NT	NT	Synovioyctis gus, P06863 complete genome, 10/27, 1575563, 1719643

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9187	22125	35481	0.54	5.8E-01	D12022.1	NT	Legionella pneumophila gene for iron superoxide dismutase, complete cds
10072	22987	33832	0.50	5.8E-01	AF062304.2	NT	Chlamidia trachomatis strain: KUW31/Ox, major outer membrane protein (omp) gene, complete cds
10424	23313	37401	0.6	5.8E-01	P06438	SW/ISSPROT	EGF PROTEIN
10985	23871	37001	1.02	5.8E-01	P55284	SW/ISSPROT	VASCULAR ENDOTHELIAL CADHERIN PRECURSOR (VE-CADHERIN) (CDH31-5)
11115	24045	37481	2.77	5.8E-01	Q02013	SW/ISSPROT	THYMIDYLATE KINASE (TMP KINASE)
11398	24310	37485	1.7	5.8E-01	AF187844.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
11398	24310	37760	3.48	5.8E-01	AF187775.1	EST HUMAN	PXI-D1041-100100-002-003 D1041 Homo sapiens cDNA
11639	24545	38015	2.85	5.8E-01	AF094528.1	NT	Mus musculus strain SPRET/EJ CD44 antigen (CD44) gene, partial cds
11909	24757	35251	1.47	5.8E-01	P47135	SW/ISSPROT	JSNT PROTEIN
12378	25159	31870	1.47	5.8E-01	P47135	SW/ISSPROT	JSNT PROTEIN
12593	25259	31870	1.6	5.8E-01	L42230.1	NT	Cryptosporidium parvum alpha 1 anti-lysozyme (alpha 1 AT) gene, promoter region
12784	25421	31870	3.38	5.8E-01	AB017705.1	NT	Aspergillus niger pyrG gene for orotidine-5-phosphate decarboxylase, complete cds
12925	14945	27922	1.05	5.8E-01	P34628	SW/ISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A (CONTAINS: MAP1 LIGHT CHAIN L2)
4059	17095	29878	1.22	5.8E-01	PA0472	SW/ISSPROT	SMY PROTEIN
4835	17951	30504	5.31	5.8E-01	AB000077.1	NT	Vigna radiata mRNA for protein phosphatase, complete cds
4912	17911	30504	1.23	5.8E-01	AF110846.1	NT	Megastelia scalaris sex-related homolog (Megs2) gene, partial cds, alternatively spliced products
5559	18507	31880	0.82	5.8E-01	AE002152.1	NT	Ureaplasma urealyticum section 83 of 89 of the complete genome
5721	18794	31880	3.59	5.8E-01	Q10059	SW/ISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6429	18472	32345	2.19	5.8E-01	D78639.1	EST HUMAN	HUM606068 Human placenta polyA ⁺ (T7-lyuwa) Homo sapiens cDNA clone GEN-300506 3'
6567	18608	32793	0.7	5.8E-01	D60501.1	NT	Cyclic AMP-regulated phosphoprotein (Pats, mRNA, 1033 nt)
7124	20328	32793	2	5.8E-01	S65091.1	NT	Shigella sonnei DNA for 2S ORF, complete cds
8467	21368	34635	2.69	5.8E-01	HA1571.1	EST HUMAN	Y61500.51 Homo adult brain N25B1955Y Homo sapiens cDNA clone IMAGE:175767 3' similar to
8865	21595	34635	0.78	5.8E-01	AI280041.1	EST HUMAN	68-376187 ALPHASE INDUCED PHOSPHATASE 2 (HUMAN)
8865	21595	34636	0.78	5.8E-01	AI280041.1	EST HUMAN	68-376187 ALPHASE INDUCED PHOSPHATASE 2 (HUMAN)
8768	21668	35042	2.74	5.8E-01	P14328	SW/ISSPROT	SPICE COAT PROTEIN SP96
8768	21668	35043	2.74	5.8E-01	P14328	SW/ISSPROT	SPICE COAT PROTEIN SP96
9448	22375	35759	11.31	5.8E-01	AI270744.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor 4, exon 3-11
9524	22451	35814	1.05	5.8E-01	Q27306	SW/ISSPROT	TRANSCRIPTION FACTOR TCF-4
10123	23074	37769	0.54	5.8E-01	AF031306.1	EST HUMAN	HO153747/1 NF1-MC-30 Homo sapiens cDNA clone IMAGE:382728 9'
11428	24344	37769	7.76	5.8E-01	AI242313.1	NT	Homo sapiens NF1-MC-30 Homo sapiens cDNA clone IMAGE:1985779 3'
11475	24386	37769	3.97	5.8E-01	BF700052.1	EST HUMAN	HO212797/1 NF1-MC-30 Homo sapiens cDNA clone IMAGE:428443 9'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
11582	24491		1.97	5.9E-01	BF703022.1	EST_HUMAN	60212577.F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4284403 5'
1912	14583	27504	1.03	5.7E-01	PC02727	SWISSPROT	ALP-UP-PROTEIN (ALP) [EC:3.6.1.3] (ALP-UP)
1912	14583	27505	0.96	5.7E-01	PC02727	SWISSPROT	ALP-UP-PROTEIN (ALP) [EC:3.6.1.3] (ALP-UP)
3593	101411		1.36	5.7E-01	6759253	SWISSPROT	Man nucleoside diphosphate kinase, cytosolic isoform 1 (PDK1) mRNA
3270	13518	22221	1.36	5.7E-01	Q3971.2	SWISSPROT	POTASSIUM TRANSPORT FACTOR OVO-ONE 1 (MOV01) (MOV01A)
3591	16558		3.23	5.7E-01	AB039503.1	NT	Populus americana pectus-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
6513	20934	32838	0.76	5.7E-01	BF054513.1	EST_HUMAN	60145463.F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:3858590 5'
7008	103545	33268	0.76	5.7E-01	AA194201.1	EST_HUMAN	2298200.1 Soares, NCI-IMP, S1 Homo sapiens cDNA clone IMAGE:485874 5'
7163	18465	31325	1.24	5.7E-01	AL111440.1	NT	Boyle's chimeric strain T4 cDNA library under conditions of nitrogen deprivation
8283	21435	34470	2	5.7E-01	PC0073	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) [P50 REDUCTASE]
8548	21476		0.57	5.7E-01	A251835.1	NT	Mus musculus Kcm1, L1mp3, Mant2, Tace-1, Tace-2 and "scd3" genes, alternative transcripts
8691	21881		0.94	5.7E-01	AD065011.1	EST_HUMAN	HQ0065 Human fetal liver cDNA library Homo sapiens cDNA
10316	23205	38615	1.24	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10316	23205	38616	1.24	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
11048	23232	37372	1.07	5.6E-01	BF050362.1	EST_HUMAN	602007712.F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:405610 5'
3419	18461	22687	1.11	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3982	16980	29654	0.85	5.6E-01	AL161501.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
8156	21095	34395	0.41	5.6E-01	LA4913.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
6991	22295	39554	4.78	5.6E-01	AV684703.1	EST_HUMAN	HUMES7489 Human thymus N8TH II Homo sapiens cDNA
6991	22295	39555	4.78	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GRK Homo sapiens cDNA clone GRCFSP09 5'
9914	22502	38265	1.51	5.6E-01	AB039782.1	NT	Homo sapiens MUC3A, gene for trisialid mucin, partial cds
12244	22068		3.83	5.6E-01	BE466280.1	EST_HUMAN	601514007.F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3915457 5'
12986	16990	29654	3.48	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12715	23595		2.96	5.6E-01	PF05005	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
13074	23598		3.35	5.6E-01	BF073823.1	EST_HUMAN	Rattus norvegicus Proton Pump Cytochrome A, carboxylase, beta polypeptide (Pccb) mRNA
1230	14276	27218	1.54	5.5E-01	88098712	NT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P14; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2752	15743	28738	4.81	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P14; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2861	15013	23911	1.09	5.5E-01	5502055	NT	Homo sapiens nucleolar viral-like protein 2 (S. cerevisiae homologue) (SVL2) mRNA
3174	19155		1.76	5.5E-01	HA4218.1	EST_HUMAN	AF0810.1 Soares adult brain M2251657 Homo sapiens cDNA clone IMAGE:172606 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7721	20530	33540	0.86	5.4E-01	Z21618.1	NT	S cerevisiae RIB6 gene encoding 60S ribosomal protein L16
7729	20535	33602	1.87	5.4E-01	Q64438	SWISSPROT	MITOCHONDRIAL LONG-CHAIN ENOYL-CoA HYDROLYASE (TP-ALPHA)
10409	23334	23335	2.35	5.4E-01	BF972293.1	EST_HUMAN	INCLUDES LONG-CHAIN ENOYL-CoA HYDROLYASE; LONG CHAIN 3-HYDROXYACYL-CoA DEHYDROGENASE
11116	24426	37860	2.6	5.4E-01	Q68845	SWISSPROT	0020784457 NH1M02_22 Homo sapiens cDNA clone IMAGE:424360 5'
12045	24686	38360	2.68	5.4E-01	Q60575	SWISSPROT	NITRATE REDUCTASE NADPH(NR)
12045	24686	38361	2.68	5.4E-01	Q60575	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ 11 CHAIN) (MEROSIN HEAVY CHAIN)
12101	19470	32650	2.55	5.4E-01	AB026017.1	NT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ 11 CHAIN) (MEROSIN HEAVY CHAIN)
12101	19470	32650	2.55	5.4E-01	AB026017.1	NT	Radon neovascular gene for 18311 complete cds
12301	25110		3.13	5.4E-01	AB050981.1	EST_HUMAN	hM7564.1 NCL CGAP_UH1 Homo sapiens cDNA clone IMAGE:2427120 3' similar to gb:M15422 LAMIN A (HUMAN)
630	19018	26518	2.16	5.3E-01	AF019413.1	NT	Homo sapiens HLA class II region containing leucidin X (leucidin-X) gene, partial cds; oycanoma P460 21-hydroxylase (CYP21B), complement component C4 (C4B) (31), helicase (SK21W), RU, complement factor H (B), and complement component C2 (C2) genes; >
2154	15169	28168	0.94	5.3E-01	AF113816.1	NT	Basaloid adenoma var. capitate phospholipase D2 (PLD2) gene, complete cds
2154	15169	28169	0.94	5.3E-01	AF113816.1	NT	Basaloid adenoma var. capitate phospholipase D2 (PLD2) gene, complete cds
2833	15822	28817	7.36	5.3E-01	4500328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2833	15822	28818	7.36	5.3E-01	4500328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3216	16330	29239	4.03	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (SCLC), gene, complete cds
4307	17321		2.5	5.3E-01	U95957.1	NT	Myxodermia genitalium section 9 of 51 of the complete genome
8043	16718	31621	1.43	5.3E-01	AB020921.1	EST_HUMAN	245012.0 Scores every 1000 nt Homo sapiens cDNA clone IMAGE:740711 5'
8043	16718	31622	1.43	5.3E-01	AB020921.1	EST_HUMAN	245012.0 Scores every 1000 nt Homo sapiens cDNA clone IMAGE:740711 5'
8745	18818	31814	0.85	5.3E-01	AA110672.1	EST_HUMAN	274509.71 Scores NHHMPU_31 Homo sapiens cDNA clone IMAGE:096112 5'
8745	18818	31815	0.85	5.3E-01	AA110672.1	EST_HUMAN	274509.71 Scores NHHMPU_31 Homo sapiens cDNA clone IMAGE:096112 5'
5642	18913	32029	1.83	5.3E-01	BE146620.1	EST_HUMAN	767612.41 NCL CGAP_7728 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J2783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN)
5642	18913	32030	1.83	5.3E-01	BE146620.1	EST_HUMAN	767612.41 NCL CGAP_7728 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J2783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN)
9461	22380		1.81	5.3E-01	U01690.2	NT	Rattus norvegicus ribonuclease 1-5'-phosphatase catalyzase (rbc2) gene, partial cds; chloroplast gene for ribonuclease
9510	22437	35801	0.84	5.3E-01	BF433656.1	EST_HUMAN	7071012.1 NCL CGAP_L242 Homo sapiens cDNA clone IMAGE: 3' similar to cyp19a1 element MER20
9510	22437	35802	0.84	5.3E-01	BF433656.1	EST_HUMAN	7071012.1 NCL CGAP_L242 Homo sapiens cDNA clone IMAGE: 3' similar to cyp19a1 element MER29

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Delicious Source	Top Hit Description
10707	23593	37020	0.6	5.3E-01	AF94210.1	EST_HUMAN	hsp400.21 NC1 CGAP. M416 Homo sapiens cDNA clone IMAGE:256,273.3 similar to
10721	23957	37803	0.52	5.3E-01	U114285.3	NT	SW_C02A_HUMAN Z0074 CYTOCHROME C CONSDASE POLYPEPTIDE VA PRECURSOR ;
11993	24836	38333	6.76	5.3E-01	BE550291.1	EST_HUMAN	Homo sapiens nucleophin 214307 (CAN) (NP214). mRNA
12298	25769		4.27	5.3E-01	AA910053.1	EST_HUMAN	933095 at NC1 CGAP. B7 Homo sapiens cDNA clone IMAGE:3382168.8
841	13466	26833	13.56	5.2E-01	U30770.1	NT	APOLIPROTEIN D PRECURSOR (HUMAN)
1191	14230	27169	7.93	5.2E-01	Q9WY30	SW/SSPROT	Drosophila melanogaster hsp400-hsp400 mRNA, complete cds
1219	14257	27197	2.31	5.2E-01	AF224622.1	NT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5) (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1009	14927		2.81	5.2E-01	AL102365.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
2190	16172	28176	2.02	5.2E-01	A8016293.2	NT	Homo sapiens chromosome 21 segment H52TC385
3164	16214	29103	1.49	5.2E-01	U95642.1	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3455	16505		1.84	5.2E-01	AL116790.1	NT	Chlamydomonas reinhardtii strain S2603 POMEYIA and POMEYIA precursor, genes, complete cds
3505	16543	29449	2.23	5.2E-01	AA954195.1	EST_HUMAN	Bovine gamma strain T4 cDNA library under conditions of nitrogen deprivation
3699	16731		1.03	5.2E-01	AF002096.1	NT	en17p05.11 Stragene scdbio brein S11 Homo sapiens cDNA clone IMAGE:161604.3
4717	17722	30584	0.69	5.2E-01	AF025947	NT	Marriage saliv chloroplast islet dehydrogenase precursor (11000) mRNA, nuclear gene encoding chloroplast protein, complete cds
5850	18821	32035	0.52	5.2E-01	AA284201.1	EST_HUMAN	Mus musculus acetylcholine receptor beta (Acb), mRNA
10251	26903	39540	0.82	5.2E-01	X02218.1	NT	zc44009177 Soare, senescent fibroblasts NB18F Homo sapiens cDNA clone IMAGE:328169.3
10530	23416	36830	1.29	5.2E-01	AF143952.2	NT	Chicken duplicated genes for histone H2A, H4 and a histone H9 gene
13061	25583		4.1	5.2E-01	PF16516	SW/SSPROT	Chicken duplicated genes for histone H2A, H4 and a histone H9 gene
640	13701	29608	1.89	5.1E-01	MA9505.1	NT	Homo sapiens ACETOACETIC ACID RECEPTOR DELTA (RAR-DELTA)
671	13733	29644	3.68	5.1E-01	AA23944.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
671	13733	29645	3.66	5.1E-01	AA23944.1	NT	Polymorphism (strain P1 vt) 103 rRNA gene
1679	14709		1.09	5.1E-01	X07855.1	NT	Polymorphism (strain P1 vt) 103 rRNA gene
4163	17184	30557	5.45	5.1E-01	AF936458.1	EST_HUMAN	R. no. sapiens mRNA for mammalian tissue protein
4283	17297	31103	3.64	5.1E-01	AF93630	SW/SSPROT	W8381241 NC1 CGAP. D11 Homo sapiens cDNA clone IMAGE:2427263.3
6407	19512	32687	0.64	5.1E-01	BE541008.1	EST_HUMAN	ADRENOCORTICOTROPIC HORMONE COUPLING FACTOR (RCPT)
6520	19572		0.31	5.1E-01	AF171228.1	EST_HUMAN	ADRENOCORTICOTROPIC HORMONE COUPLING FACTOR (RCPT)
7240	20155	33936	1.13	5.1E-01	BE6673.1	EST_HUMAN	ADRENOCORTICOTROPIC HORMONE COUPLING FACTOR (RCPT)
8550	21785	35153	0.32	5.1E-01	BE7202.1	EST_HUMAN	ADRENOCORTICOTROPIC HORMONE COUPLING FACTOR (RCPT)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6136	22093	35422	0.81	5.1E-01	AF063681.1	EST_HUMAN	G14510293-180000-175-401 ST0023 Homo sapiens cDNA
9136	22093	35423	0.81	5.1E-01	AF063681.1	EST_HUMAN	G14510293-180000-175-401 ST0023 Homo sapiens cDNA
10369	23100	35500	4.79	5.1E-01	J05912.1	EST_HUMAN	H12912 Homo sapiens cDNA (918 bp)
10211	23102	35533	1.35	5.1E-01	U72292.1	EST_HUMAN	IGF1 Human cDNA, T34-24, 2nd full-length Homo sapiens cDNA, not directional
10369	23425	35975	1.02	5.1E-01	U72292.1	EST_HUMAN	Homo cathepsin ester (HACE) gene, complete cds
12434	23702		2.68	5.1E-01	BF032207.1	EST_HUMAN	h01599363F1 NH, MGC, 58 Homo sapiens cDNA clone IMAGE382977.8
12864	25395		1.86	5.1E-01	BF135682.1	EST_HUMAN	h025110-1 NC1, CGAP, Bm23 Homo sapiens cDNA clone IMAGE34027.8 3' similar to contains element TARI repeat-like element
2148	15151	20162	0.58	5.0E-01	4845542	NT	Homo sapiens polyomavirus segment increased 2-like 9 (PMS2L9), mRNA
2148	15151	20163	0.68	5.0E-01	4845542	NT	Homo sapiens polyomavirus segment increased 2-like 9 (PMS2L9), mRNA
2159	15171	20174	1.28	5.0E-01	AF003210.1	NT	Bufo marinus apolipoprotein fragment containing (cholesterol Hc40) gene, DNA biosynthesis initiating protein (hsc40), ATP operon (ap003210HFB), and putative chromosome replication protein (gda) genes, complete cds; and termination factor Rho (rho) gene
2159	15171	20175	1.20	5.0E-01	AF003210.1	NT	Bufo marinus apolipoprotein fragment containing (cholesterol Hc40) gene, DNA biosynthesis initiating protein (hsc40), ATP operon (ap003210HFB), and putative chromosome replication protein (gda) genes, complete cds; and termination factor Rho (rho) gene
3604	19633	29812	1.11	5.0E-01	L38483.1	NT	Rattus norvegicus jagged protein mRNA, complete cds
3542	19570	29852	3.60	5.0E-01	AB033070.1	NT	Spontaneous auricular gaudinotrophin-releasing hormone (GDRH) precursor mRNA, complete cds
6778	18848	31952	0.44	5.0E-01	U03020.1	NT	Spontaneous auricular gaudinotrophin-releasing hormone (GDRH) precursor mRNA, complete cds
6778	18848	31953	0.44	5.0E-01	U03020.1	NT	Spontaneous auricular gaudinotrophin-releasing hormone (GDRH) precursor mRNA, complete cds
8535	19495		0.62	5.0E-01	RF579186.1	EST_HUMAN	IG0212042F1 NH, MGC, 51 Homo sapiens cDNA clone IMAGE427189.8
7029	20055	33288	0.65	5.0E-01	AF02846.1	NT	Homo sapiens EMPKIN gene, promoter and exon 1
8115	21025	34351	0.73	5.0E-01	AF101549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4b
8115	21025	34352	0.73	5.0E-01	AF101549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4b
8371	21278		0.44	5.0E-01	Z71690.1	NT	S cerevisiae chromosome XIV reading frame ORF YNL094c
8094	22023		1.97	5.0E-01	M62304.1	NT	Xenopus laevis smooth muscle beta-topomyosin mRNA, complete cds
9278	22165	35500	0.68	5.0E-01	BF107948.1	EST_HUMAN	h01599363F1 NH, MGC, 79 Homo sapiens cDNA clone IMAGE408488.3
9900	27148	34682	3.39	5.0E-01	BF317212.1	EST_HUMAN	h01599363F1 NH, MGC, 19 Homo sapiens cDNA clone IMAGE4130652.8
10191	20042	35441	1.83	5.0E-01	P95573	SWISSPROT	GLYOXYL DEBRANCHING ENZYME (GLYOXYL DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (GLUGO-4-4-4-GLUCANOTRANSFERASE), AMYLO-1,6-GLUCOSIDASE (DEXTRAN 6-ALPHA-D-GLUCOSIDASE)]
10191	20042	35442	1.93	5.0E-01	P95573	SWISSPROT	GLYOXYL DEBRANCHING ENZYME (GLYOXYL DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (GLUGO-4-4-4-GLUCANOTRANSFERASE), AMYLO-1,6-GLUCOSIDASE (DEXTRAN 6-ALPHA-D-GLUCOSIDASE)]

Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9484	24146	34752	1.2	4.8E-01	AK20744.1	EST_HUMAN	17710.01 Source: human 2N4H81 Homo sapiens cDNA, clone IMAGE:14795.5 similar to carboxyl element
9757	27751		1.35	4.8E-01	BE155148.1	EST_HUMAN	MEF2, myocyte enhancer factor 2
10313	25400		0.88	4.8E-01	BE389038.1	EST_HUMAN	PAH-1101659.0125504-004.H10550 Homo sapiens cDNA
11270	26098		2.4	4.8E-01	XB3393.1	EST_HUMAN	021824PFT NIH_MGC_42 Homo sapiens cDNA, clone IMAGE:400943.8
12257	25149		1.68	4.8E-01	AI163272.2	NT	S. cerevisiae ORF5, Euro. chromosome X
12651	25735		1.68	4.8E-01	AF122368.1	NT	Homo sapiens chromosome 21, segment H8.21, C027
3123	16174		0.74	4.8E-01	AF123387.1	NT	Typhlocyba crux transposon VPI T1 SIRE repeat region
9753	19029	33036	8.84	4.7E-01	BP211783.1	EST_HUMAN	Falls cells, falls leukemia virus subgroup C receptor (FVCR) mRNA, complete cds
7592	20051	33325	0.74	4.7E-01	AI094374.1	EST_HUMAN	80188380PFT NIH_MGC_57 Homo sapiens cDNA, clone IMAGE:400387.5
8446	21378	34719	0.88	4.7E-01	U11414.1	EST_HUMAN	472405.01 Source: testis, NIH Homo sapiens cDNA, clone IMAGE:175584.3
8446	21378	34720	0.88	4.7E-01	U11414.1	EST_HUMAN	h28311 Human pancreatic islet: Homo sapiens cDNA, clone h28311.5 and
11262	24323		5.26	4.7E-01	AF102675.1	NT	h28311 Human pancreatic islet: Homo sapiens cDNA, clone h28311.5 and
11525	24435	37893	2.11	4.7E-01	U41059.1	NT	Influenza A virus isolate H3N1977 Hemagglutinin (HA) gene, partial cds
11728	24800	39110	1.4	4.7E-01	BF52006.1	NT	Human collagen alpha2(XI) (COL11A2), gene, across 6 through 16, and partial cds
11815	24726	39227	1.38	4.7E-01	AY168948.1	EST_HUMAN	60243889PFT NIH_MGC_57 Homo sapiens cDNA, clone IMAGE:4191503.5
12493	25210		2.05	4.7E-01	BE897763.1	EST_HUMAN	RO5-NT0025-25040-011-E08 NT0029 Homo sapiens cDNA
3905	18837	25723	2.16	4.8E-01	BF65300.1	EST_HUMAN	001611333PFT NIH_MGC_71 Homo sapiens cDNA, clone IMAGE:391248.5
3905	18837	25724	2.16	4.8E-01	BF65300.1	EST_HUMAN	002081103PFT NIH_MGC_81 Homo sapiens cDNA, clone IMAGE:4245481.5
6004	18960	31557	0.83	4.8E-01	BF13568.1	EST_HUMAN	002081103PFT NIH_MGC_81 Homo sapiens cDNA, clone IMAGE:4245481.5
6004	18960	31558	0.83	4.8E-01	BF13568.1	EST_HUMAN	001600224PFT NIH_MGC_19 Homo sapiens cDNA, clone IMAGE:4126472.5
6059	19733	31639	3.46	4.8E-01	Q06043	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
6059	19733	31640	3.46	4.8E-01	Q06043	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5737	18810	31904	2.35	4.8E-01	BE734781.1	EST_HUMAN	001668795PFT NIH_MGC_21 Homo sapiens cDNA, clone IMAGE:3843937.5
5751	18824	31921	2.32	4.8E-01	AI247676.1	EST_HUMAN	469002.01 Source: fetal liver, spleen, INFLS, S1 Homo sapiens cDNA, clone IMAGE:1849011.3 similar to
5751	18824	31922	2.32	4.8E-01	AI247676.1	EST_HUMAN	TR-OT10308 OT10308 BUT PROPHILIN, ;
5759	18852	31935	1.52	4.8E-01	P20000	SWISSPROT	MEF1CIS SPECIFIC PROTEIN HOP1
9643	18514		0.86	4.8E-01	AF17124.1	NT	Yeast, schwann cytochrome b gene, partial cds, mitochondrial, all product
9643	18514		0.86	4.8E-01	AF17124.1	NT	Yeast, schwann cytochrome b gene, partial cds, mitochondrial, all product
6117	15776	32311	0.48	4.8E-01	U02415.1	NT	Human mitochondrial 16S rRNA gene encoding 16S ribosomal RNA
6506	19560	32730	0.95	4.8E-01	AE100384.1	NT	Metaphase chromatin: human metaphase chromatin from tissues 1107501 to 1107528 (section 100 of 148) of the

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Sim ¹ /n (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7020	20046	35291	0.45	4.6E-01	AF115340.1	NT	Bacillus subtilis Elmsa (bmsa) gene, complete cds
7073	20279	35833	1.66	4.6E-01	U62332.1	NT	Emricaplin ribulose NEIMPA, (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7073	20279	35834	1.66	4.6E-01	U62332.1	NT	Emricaplin ribulose NEIMPA, (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7630	20572	35824	0.63	4.6E-01	U73230.1	NT	Murine cytochrome oxidase c1 protein gene, complete cds
8192	21039	34429	0.74	4.6E-01	AA463577.1	EST_HUMAN	nt64005.s1 NCL_GGAP_Tbv1 Homo sapiens cDNA clone IMAGE:543353 similar to contains Alu repetitive element; contains element L1 repetitive element
8228	21131		0.45	4.6E-01	Q6006B	SW/SSPROT	GENOME POLYPROTEIN COMPLEX: NUCLEAR PROTEIN (P1)-HELPER COMPONENT
8300	21204		0.55	4.6E-01	A5004031.1	NT	PROTEINASE (HC-PRO): PROTEIN P3; 6 KD PROTEIN 1 (6K1): CYTOSOLIC INCLUSION PROTEIN A (C1); 8 KD PROTEIN 2 (6K2); GENOME-LINKED PROTEIN (VFO); NUCLEAR INCLUSION PROTEIN A (NHA) (N1)
8895	21325	35177	19.05	4.6E-01	BF697399.1	EST_HUMAN	Xyella fastidiosa, section 177 of 229 of the complete genome
9305	22234	35594	0.51	4.6E-01	AA82237.1	EST_HUMAN	602135933.s1 NCL_GGAP_Kid6 Homo sapiens cDNA clone IMAGE:4287623.5
9305	22234	35595	0.51	4.6E-01	AA82237.1	EST_HUMAN	6076008.s1 NCL_GGAP_Kid6 Homo sapiens cDNA clone IMAGE:157287.3 similar to gs:358341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);
9841	22746	36128	1.04	4.6E-01	PE5202	SW/SSPROT	6076008.s1 NCL_GGAP_Kid6 Homo sapiens cDNA clone IMAGE:157287.3 similar to gs:358341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);
9841	22746	36129	1.04	4.6E-01	PE5202	SW/SSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (QUANYLYATE CYCLASE)
10482	23370	36782	1.64	4.6E-01	A016634.1	EST_HUMAN	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (QUANYLYATE CYCLASE)
10482	23370	36783	1.64	4.6E-01	A016634.1	EST_HUMAN	wg75612.x1 Soares_NSP_F8_3W_OT_FPA_P_51 Homo sapiens cDNA clone IMAGE:2310768.3
11429	24345		2.76	4.6E-01	P98163	SW/SSPROT	wg75612.x1 Soares_NSP_F8_3W_OT_FPA_P_51 Homo sapiens cDNA clone IMAGE:2310768.3
11438	24354	37601	5.19	4.6E-01	BE18549.1	EST_HUMAN	POTENTIAL VITELLO GENIN RECEPTOR PRECURSOR (VL)
11438	24354	37602	5.19	4.6E-01	BE18549.1	EST_HUMAN	IL4H10730-10500-075-g55 H10730 Homo sapiens cDNA
11903	24303	37442	5.92	4.6E-01	AF916306.1	EST_HUMAN	Human thapsigargin methanesterase (THM) gene, exon 10 and complete cds
11903	24303	37443	5.92	4.6E-01	AF916306.1	EST_HUMAN	Human thapsigargin methanesterase (THM) gene, exon 10 and complete cds
12250	25043	38516	1.43	4.6E-01	U62330.1	NT	Human thapsigargin methanesterase (THM) gene, exon 10 and complete cds
1333	14760		1.86	4.6E-01	EST11403.1	EST_HUMAN	Human thapsigargin methanesterase (THM) gene, exon 10 and complete cds
1927	14648	27624	1.86	4.6E-01	BE18549.1	EST_HUMAN	601142108.F1 NCL_GGAP_Kid6 Homo sapiens cDNA clone IMAGE:356569.5
1927	14648	27625	1.86	4.6E-01	BE18549.1	EST_HUMAN	601142108.F1 NCL_GGAP_Kid6 Homo sapiens cDNA clone IMAGE:356569.5
2013	15590	28959	5.96	4.6E-01	AA67305.1	EST_HUMAN	Oncomycobacterium R1 section 69 of 229 of the complete chromosome 1
2013	15590	28959	5.96	4.6E-01	AA67305.1	EST_HUMAN	3550802.x1 Soares_beta_yeast_splasm_1NCL_S_51 Homo sapiens cDNA clone IMAGE:454179.3

Single Exon Probes Expressed in Adult Liver

Single Exon Probes Expressed in Adult Liver

[illegible]

Single Exon Probes Expressed in Adult Liver

Single Exon Probes Expressed in Adult Liver

[illegible]

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7016	20043	33277	0.68	4.1E-01	U02388.1	NT	Mus musculus NR1373 chemokine series (Sly5a) gene, complete cds
7036	20764	34007	2.97	4.1E-01	U67935.1	NT	Melanocortin (melanocyte) receptor 77 of 130 of the complete genome
8387	21291		0.47	4.1E-01	M84384.1	NT	Homo sapiens anemic acid dehydrogenase gene, exon 4
8613	21844	34685	1.60	4.1E-01	BFF54694.1	EST_HUMAN	302133361F1 NR1_MGC_81 Homo sapiens cDNA clone IMAGE-286328 5'
8636	22582	35832	1.34	4.1E-01	6755321	NT	Mus musculus signaling intermediate in Toll pathway/conditionally conserved (Stress-ponding), mRNA
10064	22944		0.84	4.1E-01	AF160597.1	NT	Volvo gene cytochrome b (cyb) gene, complete cds; mitochondrial gene for mitochondrial product
10756	23842		1.32	4.1E-01	AL136078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 3/8
10895	23780	37207	1.13	4.1E-01	AV865970.1	EST_HUMAN	AV865979 GLC Homo sapiens cDNA clone GLC08/012 3'
10895	23850	37207	0.86	4.1E-01	P16884	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (56 KDA IMMUNOGENIC PROTEIN) (SK56)
10895	23850	37208	0.86	4.1E-01	P16884	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (56 KDA IMMUNOGENIC PROTEIN) (SK56)
11051	25845		1.01	4.1E-01	BF349882.1	EST_HUMAN	CM2HT0107-200699-010-008 HT0137 Homo sapiens cDNA
11277	24199	37651	89.3	4.1E-01	Q38700.1	NT	Zea mays ZMPSK22 gene for 19 kDa zein protein
11830	23965	37400	2.12	4.1E-01	Q39470.1	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL, PROTEIN KV1.1 (HKV1)
12803	25912		2.83	4.1E-01	D67875.1	NT	Homo sapiens DNA for myoblast precursor protein, complete cds
1461	19587		3.81	4.0E-01	AN647123.1	EST_HUMAN	Leucine rich repeat domain, complete genome
10951	14108	27046	0.87	4.0E-01	8404665	NT	Drosophila melanogaster Dalmatian (dmt) mRNA, complete cds
1307	14396	27553	1.49	4.0E-01	AF204475.1	NT	Mus musculus placental derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
1603	14534		5.87	4.0E-01	6679268	NT	Homo sapiens chromosome 21 segment H52TC08
2852	13247	28189	1.45	4.0E-01	6679460	NT	Homo sapiens chromosome 21 segment H52TC08
3009	10561	28604	1.35	4.0E-01	AL103280.2	NT	Homo sapiens chromosome 21 segment H52TC08
3009	10601	28695	1.35	4.0E-01	AL103280.2	NT	Homo sapiens chromosome 21 segment H52TC08
3190	16702	28883	2.47	4.0E-01	AF068033.1	NT	Streptococcus pneumoniae TIC (MIC), Y10 (MIC), penicillin-binding protein 2c (pbp2c), and undecaprenyl-phosphate-UDP-N-acetyl-pentapeptide phospho-MurNAc-pentapeptide transferase (mraF) genes, complete cds
3601	15530	29838	4.68	4.0E-01	AJ227571.1	NT	Oryz sativa partial cDNA genes for 1 cell receptor delta chain (TCRD.2), exon 1
3601	15530	29838	4.68	4.0E-01	AJ227571.1	NT	Oryz sativa partial cDNA genes for 1 cell receptor delta chain (TCRD.2), exon 1
4631	17830		11.58	4.0E-01	Q330468	SWISSPROT	NADPH (IS)OQUINONE DEHYDROGENASE CHAIN, CYTOCHROME C
8130	19188	33325	1.08	4.0E-01	AF470010.1	EST_HUMAN	SWISSPROT IMAGE-286328 Homo sapiens cDNA
8706	16742	32944	0.76	4.0E-01	P27285	SWISSPROT	STRUCTURAL PROTEIN (P749) (CONFININ, COAT PROTEIN C, SPIKE GLYCOPROTEIN C, E2 AND E1.6 KD PEPTIDE)
8907	21438	34778	0.61	4.0E-01	HEC02034.1	EST_HUMAN	MRP-TN0110-100500-202-002 TN0110 Homo sapiens cDNA
8920	21521	34625	1.11	4.0E-01	AS016625.1	NT	Homo sapiens DCIN2 gene, complete cds

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NC:	Exon SEQ ID NC:	ORF SEQ ID NC:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
5638	25486	35845	1.37	4.9E-01	AA32398.1	EST_HUMAN	EST_29098 Corabulum II Homo sapiens cDNA 5' and similar to EST containing Alu repeat
13043	26043		2.50	4.9E-01	BF339262.1	EST_HUMAN	90159235F1 NH1 MG3. 58 Homo sapiens cDNA clone IMAGE:383592 5'
12146	27382		2.50	4.9E-01	U73093.1	EST_HUMAN	Synchrp35F10 PQG 0413 transposase gene, complete cds
14034	14335	27391	1.86	4.9E-01	AL103300.2	NT	Homo sapiens chromosome 21 segment HS21G100
26900	16634	26933	1.86	3.9E-01	AF220419.1	NT	Oryzla pallidus carboxypeptidase (CEP) gene, complete cds
2755	16748	28741	0.31	3.9E-01	AF303019.1	NT	Homo sapiens mRNA for KIAA1183 protein partial cds
2755	16748	28741	0.31	3.9E-01	X83032.1	NT	H. sapiens Bmyb gene
3144	15194	28687	6.19	3.9E-01	AB225661.1	NT	Sinorhizobium meliloti tol, sye22, cys3 genes and orfs
4196	17167	30060	1.82	3.9E-01	BF552611.1	EST_HUMAN	761681.x1 NCI CGAP. B16 Homo sapiens cDNA clone IMAGE:3339169 3'
5112	18109	30364	1.59	3.9E-01	BE726667.1	EST_HUMAN	90156039B1 NH1 MG3. 20 Homo sapiens cDNA clone IMAGE:3833699 5'
6157	18215	32455	4.8	3.9E-01	BF226536.1	EST_HUMAN	90186236Z1 NH1 MG3. 33 Homo sapiens cDNA clone IMAGE:4082058 5'
6532	19578	32759	0.50	3.9E-01	U62965.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORP), and biglycan (BGN) genes, complete cds; and plasmin membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8532	21463	34803	1.02	3.9E-01	U79415.1	NT	Homo sapiens proso domain1 peptidase (DPP-), gene, complete cds
8420	22448	35713	0.83	3.9E-01	AW177011.1	EST_HUMAN	CM3.C10105-170659-004-b08 OTD103 Homo sapiens cDNA
8428	22395		0.76	3.9E-01	BF346034.1	EST_HUMAN	60207994F1 NCI CGAP_Bme7 Homo sapiens cDNA
8770	22700	39066	1.93	3.9E-01	AW195683.1	EST_HUMAN	cd8604.x1 Soares, NF1_T_OEG_S1 Homo sapiens cDNA clone IMAGE:4165222 5'
10074	23469	36884	1.86	3.9E-01	AB57337.1	EST_HUMAN	064821 KIAA0713 PROTEIN ; NP75062.x1 NCI CGAP. Bme3 Homo sapiens cDNA clone IMAGE:2497668 9' similar to SW RFX5_HUMAN P43832 BINDING REGULATORY FACTOR. ; Human dendrin 27 gene, exons 10 and 11, and L1 and AU repeats
10852	23548	36902	0.71	3.9E-01	U68722.1	NT	Nucleolar tetratricorn mRNA for TATA binding protein (TBP), complete cds
10940	23728	37149	1.14	3.9E-01	BF357686.1	EST_HUMAN	CM2.INN0034-00000-215-104 INN034 Homo sapiens cDNA
10940	23728	37150	1.14	3.9E-01	BF357686.1	EST_HUMAN	CM2.INN0034-00000-215-104 INN034 Homo sapiens cDNA
11088	25652	37387	0.95	3.9E-01	MT8440.1	NT	Human beta-62-crystallin (B2-1) gene, exon 4, partial cds
12250	24182		2.04	3.9E-01	AF555697.1	EST_HUMAN	AV702637.4 CTC Homo sapiens cDNA clone GDC00011 5'
12250	25006	38509	1.61	3.9E-01	AF702637.1	EST_HUMAN	AV702637.4 CTC Homo sapiens cDNA clone AD08036 5'
12395	25951		3.39	3.9E-01	AF304354.1	NT	Homo sapiens prolargin-3 (PRG3) gene, complete cds
12888	25490		1.63	3.9E-01	U145335	NT	Homo sapiens hypothetical protein LU10583 (LU10583), mRNA
1770	13271		3.98	3.9E-01	U704988	NT	Homo sapiens protein kinase C delta (PKCdelta), mRNA
5228	13307		4.96	3.9E-01	AB023299.1	NT	Homo sapiens protein kinase C delta (PKCdelta), mRNA
1863	14614		1.11	3.9E-01	AF203510.1	NT	XylinA1 testis-like, section 16 of 22 of this complete genome

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon: SEQ ID NO:	ORF SEQ ID NO:	Exposition Signal	Mean Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Disease Source	Top Hit Descriptor
2508	15504	25498	1.22	3.8E-01	AF24117.1	NT	Arachidonic acidase c-type like transcription factor (MORF-3) mRNA, complete cds
2519	15503	25497	5.41	3.8E-01	U057602	NT	Mus musculus polyoma virus family 1, member 8 (Sic165) mRNA
3046	16038	25495	23.31	3.8E-01	AF251637.1	NT	Human immunodeficiency virus 39c8 provirus genome (cdna) (HIV-213)
3149	17140	25944	21.91	3.8E-01	AF193318.1	NT	Human immunodeficiency virus 39c8 provirus genome (cdna) (HIV-213)
3153	17140	25944	40.92	3.8E-01	AF193318.2	NT	Human immunodeficiency virus 39c8 provirus genome (cdna) (HIV-213)
3814	16556	25485	0.69	3.8E-01	AF072781	EST_HUMAN	Arachidonic acidase DNA chromosome 4, contig fragment No. 30
3814	16556	25485	0.69	3.8E-01	AF072781	EST_HUMAN	Arachidonic acidase DNA chromosome 4, contig fragment No. 30
3814	16556	25485	1.21	3.8E-01	AF072781	EST_HUMAN	Arachidonic acidase DNA chromosome 4, contig fragment No. 30
3820	18850	20734	1.38	3.8E-01	BE154083.1	EST_HUMAN	YF2812.11 Scores: NF_1, GRC S1 Homo sapiens cDNA clone IMAGE:2557653.9
3900	17017	25906	0.98	3.8E-01	BE154083.1	EST_HUMAN	YF2812.11 Scores: NF_1, GRC S1 Homo sapiens cDNA clone IMAGE:2557653.9
5504	18876	31683	1.03	3.8E-01	Q04883	EST_HUMAN	PMO-110336-2004010-201 HT0339 Homo sapiens cDNA
6596	19437	31683	0.81	3.8E-01	Q04883	EST_HUMAN	PMO-110336-2004010-201 HT0339 Homo sapiens cDNA
6614	19444	33163	4.65	3.8E-01	BE072394.1	EST_HUMAN	TRANSCRIPTION FACTOR SOX-10
7095	20271	33527	4.54	3.8E-01	AB74601.1	EST_HUMAN	Arachidonic acidase cDNA
7270	20178	33421	1.15	3.8E-01	AF161513.2	NT	Arachidonic acidase cDNA
7922	20845	34160	4.03	3.8E-01	AA05274.1	EST_HUMAN	Arachidonic acidase cDNA
7938	20841	34160	4.31	3.8E-01	X01597.1	NT	Arachidonic acidase cDNA
8189	21098	34427	0.53	3.8E-01	V00093.1	NT	Arachidonic acidase cDNA
9120	22048	35407	8.24	3.8E-01	AB046881.1	NT	Arachidonic acidase cDNA
8185	22113	35477	0.82	3.8E-01	11412041	NT	Arachidonic acidase cDNA
6576	22304	35965	1.46	3.8E-01	AF153279.2	NT	Arachidonic acidase cDNA
10090	22883	35965	5.51	3.8E-01	T05413.1	EST_HUMAN	Arachidonic acidase cDNA
10190	23081	35462	0.94	3.8E-01	AF726518	NT	Arachidonic acidase cDNA
11235	24161	35462	1.72	3.8E-01	AF726518	NT	Arachidonic acidase cDNA
11995	24868	35461	3.55	3.8E-01	BE776219.1	EST_HUMAN	Arachidonic acidase cDNA
12117	24968	35461	2.41	3.8E-01	IR42550.1	EST_HUMAN	Arachidonic acidase cDNA
12117	24968	35462	2.41	3.8E-01	IR42550.1	EST_HUMAN	Arachidonic acidase cDNA
12492	25233	35462	2	3.8E-01	AF011124.1	NT	Arachidonic acidase cDNA
12606	25870	35462	1.71	3.8E-01	U04788.1	EST_HUMAN	Arachidonic acidase cDNA
12720	25358	35462	1.89	3.8E-01	BE052995.1	EST_HUMAN	Arachidonic acidase cDNA
3504	15905	25857	10.48	3.7E-01	AF037631.1	NT	Arachidonic acidase cDNA
3521	15955	25461	12.37	3.7E-01	AF036584.1	NT	Arachidonic acidase cDNA
3538	15957	25850	0.94	3.7E-01	AA336482.1	EST_HUMAN	Arachidonic acidase cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1340	14573	27326	4.1	3.E-01	U02056.1	EST_HUMAN	cd320.65.1 Source: fetal liver, 10E1 Homo sapiens cDNA clone IMAGE:24443.5
1632	14653	27329	5.21	3.E-01	U02056.1	EST_HUMAN	U02056.1 NC1 CGAP_C03 Homo sapiens cDNA clone IMAGE:2047419.3
1932	14653	27330	5.21	3.E-01	U02056.1	EST_HUMAN	U02056.1 NC1 CGAP_C03 Homo sapiens cDNA clone IMAGE:2047419.3
1985	14654	27358	4.53	3.E-01	A1215207.1	NT	Male placenta (fetal) protein S10 (P15.10) gene, complete cds
2285	15359		1.50	3.E-01	A030224.1	NT	Human RPLP0 (for RPLP0) gene, partial cds
2413	15477	28459	2.44	3.E-01	U02056.1	NT	Human P280.0 gene for protein, partial cds
2457	15459	28500	1.31	3.E-01	U02056.1	NT	Human P280.0 gene for protein, partial cds
2497	15459	28500	1.31	3.E-01	U02056.1	NT	Human P280.0 gene for protein, partial cds
2510	15511	28514	1.77	3.E-01	U02056.1	EST_HUMAN	Human P280.0 gene for protein, partial cds
2671	15573	28571	1.69	3.E-01	P24206	SWISSPROT	PROTEIN-ISOASPARTATE 2-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEIN-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2672	15629	28571	1.69	3.E-01	A169445.1	NT	SwissProt: PROTEIN CARBOXYL METHYLTRANSFERASE
3530	16548	29471	1.62	3.E-01	U02056.1	NT	Human P280.0 gene for protein, partial cds
3530	16548	29472	1.62	3.E-01	U02056.1	NT	Human P280.0 gene for protein, partial cds
4514	17523	30388	1.24	3.E-01	B5707883.1	EST_HUMAN	RC1-H10545-150000-014-512 H10543 Homo sapiens cDNA
4594	17526	30721	0.8	3.E-01	A1335959.1	NT	Brassica napus mRNA for MAPK4 alpha2 protein
5151	18127	30959	3.83	3.E-01	A1335959.1	EST_HUMAN	h202p04.x1 NC1 CGAP_L024 Homo sapiens cDNA clone IMAGE:2872265.3
5240	18227	31075	0.68	3.E-01	B5307694.1	EST_HUMAN	MR4-B10358-270200-005-c10 B10358 Homo sapiens cDNA
5527	18545	31523	0.76	3.E-01	A100565.1	NT	Homo sapiens type gene intron 5
6323	15373	32541	0.92	3.E-01	P18491	SWISSPROT	FORMATE HYDROGENYLASE SUBUNIT 5 PRECURSOR (PFL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)
6752	15746	32956	1.50	3.E-01	U01096.1	NT	Homo sapiens PHEX gene
7509	20447		3.84	3.E-01	R94090.1	EST_HUMAN	U02056.1 Source: fetal liver, 10E1 Homo sapiens cDNA clone IMAGE:27697.5
7622	20596	33695	1.47	3.E-01	A1002174.1	EST_HUMAN	U02056.1 Source: fetal liver, 10E1 Homo sapiens cDNA clone IMAGE:27697.5
8270	21176	34510	0.47	3.E-01	A1070900.1	EST_HUMAN	U02056.1 Source: fetal liver, 10E1 Homo sapiens cDNA clone IMAGE:27697.5
8802	21732	35531	0.74	3.E-01	P08167	SWISSPROT	U02056.1 Source: fetal liver, 10E1 Homo sapiens cDNA clone IMAGE:27697.5
9355	21785	35734	8.06	3.E-01	A101583.2	NT	MEIO repeat element
9500	22457	35819	0.57	3.E-01	U01528.1	NT	Human hereditary haemochromatosis region, Hs20-like protein gene, hereditary haemochromatosis (Hs20) gene, and sodium phosphate transporter (NPT-2) gene, complete cds

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Probe SEQ ID No.	Exon SEQ ID No.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Disease Source	Top Hit Descriptor
9503	22457	35820	0.57	3.6E-01	U91328.1	NT	Human heterodityl (homodityl) phosphatase gene, heterodityl (homodityl) (HMA-H) gene, RefSeq gene, and eukaryotic phosphatase (NPT3) gene, complete cds
6954	22481	35840	3.22	3.6E-01	4504850	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
6954	22481	35841	3.22	3.6E-01	4504850	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9743	22659	36042	1.47	3.6E-01	AL162844.2	NT	Homo sapiens chromosome 21 segment H521C004
9935	22840	36228	1.05	3.6E-01	X17550.1	NT	D. melanogaster elongated gene, exons 3, 4, 5 & 6
9935	22840	36229	1.05	3.6E-01	X17550.1	NT	D. melanogaster elongated gene, exons 3, 4, 5 & 6
10032	22816		0.7	3.6E-01	X62026.1	NT	C. parvulus p16 gene for phosphatase C upstream region containing bent DNA fragment
10377	23266	36988	20.27	3.6E-01	Q3164	SWISSPROT	PROBABILE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4T5
11383	24250	37745	1.64	3.6E-01	BE002390.1	EST_HUMAN	651676418F1 NH_1MAGC_21 Homo sapiens cDNA clone IMAGE356597 5'
11550	24450	37022	3.81	3.6E-01	AB004293.1	NT	Arabidopsis thaliana mRNA for SigA, complete cds
12176	25439		1.81	3.6E-01	11432598	NT	Methanococcus thermophilus (Methanococcus) from basins 702375 to 714311 (section 62 of 148) of the complete genome
1161	13227	26139	1.40	3.5E-01	AL101506.2	NT	Arabis thaliana DNA chromosome 4, coding fragment No. 30
222	13321	26237	2.31	3.5E-01	6978803	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
701	13769	26677	4.76	3.5E-01	AL16156.2	NT	Arabis thaliana DNA chromosome 4, coding fragment No. 77
748	13805	26750	1.48	3.5E-01	7706758	NT	Homo sapiens GAP-like protein (LOC51836), mRNA
748	13805	26751	1.48	3.5E-01	7706758	NT	Homo sapiens GAP-like protein (LOC51836), mRNA
800	13802	26767	3.87	3.5E-01	BF139798.1	EST_HUMAN	651671005F1 NH_1MAGC_40 Homo sapiens cDNA clone IMAGE485851 3'
1542	14573	27638	1.36	3.5E-01	BF130683.1	EST_HUMAN	507649433F2 NH_1MAGC_19 Homo sapiens cDNA clone IMAGE412424 5'
1686	14686	27656	0.56	3.5E-01	U85763.1	NT	Rattus norvegicus ADP-adenosine triphosphatase activating protein mRNA, complete cds
2302	15310	28316	0.86	3.5E-01	P05766	SWISSPROT	HOMEOBOX PROTEIN HOXA-1 (HOXA-1) (HLS)
2648	15926	28643	1.14	3.5E-01	AA223824.1	EST_HUMAN	3016409.51 Simulium NT2 essential protein 927250 Homo sapiens cDNA clone IMAGE480872 3'
3873	18922		0.91	3.5E-01	AA462138.1	EST_HUMAN	m38603.51 GNA_G5AP_2_yr3 Homo sapiens cDNA clone IMAGE1172957 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4392	1276	30239	2.6	3.5E-01	A571283.1	NT	Danio rerio homeobox protein (Hoxb3b) gene, complete cds
5044	18041	30697	4.68	3.5E-01	M43436.1	NT	Rattus norvegicus myoglobin (LOC) gene, exon 1 through 5
4328	18312	31141	1.27	3.5E-01	H73264.1	EST_HUMAN	Human c-myc complementary DNA clone IMAGE:78113
5517	18560	31444	1.31	3.5E-01	Q09697	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5517	18560	31445	1.31	3.5E-01	Q09697	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5741	18814	31910	1.31	3.5E-01	D20443.1	EST_HUMAN	Human mRNA for KIAA0888 gene, complete cds
8485	19530		1.02	3.5E-01	AU88396.1	EST_HUMAN	PIM-5/0012/33407-207-a-11 SN9012 Homo sapiens cDNA
8673	19710	32003	0.58	3.5E-01	A4431853.1	EST_HUMAN	3270903.1 Source: testis, NIH. Homo sapiens cDNA clone IMAGE:782429 5' similar to R/G105935
8721	19757	32904	0.64	3.5E-01	U37150.1	NT	G1008935 F0421.1
8958	19997	33211	0.62	3.5E-01	Q24357	SWISSPROT	Box fusus padina medullary sulfide reductase (meA) mRNA, complete cds
7409	20108		2.9	3.5E-01	X86505.1	NT	GLUCOSE-2-PHOSPHATE 1-3-EPIMERASE, CHLOROPLAST PRECURSOR (GPEP)
7971	20803	34205	0.65	3.5E-01	P47281	SWISSPROT	S saccharin mRNA for CUS1 protein (PECAM1)
7971	20803	34206	0.55	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDONE-TRNA LIGASE) (HISRS)
8214	21119	34462	0.54	3.5E-01	X09091.1	NT	HISTIDYL-TRNA SYNTHETASE (HISTIDONE-TRNA LIGASE) (HISRS)
8549	21580		2.72	3.5E-01	11148242	NT	E. coli L-arabinose transport operon with genes araC, araG and araH
8652	21583	34918	0.69	3.5E-01	BF358071.1	EST_HUMAN	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
8035	21905		0.79	3.5E-01	AF051591.1	NT	RC4-E10024-260000-014-307 ET0024 Homo sapiens cDNA
8482	22410	35771	1.34	3.5E-01	4907510	NT	Rattus norvegicus Na+-Ca2+ cotransporter (NCC1) mRNA, complete cds
						NT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
						SWISSPROT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L
						NT	TYPE, ALPHA-1 POLYPEPTIDE ISOMER 5) BRAIN CALCIUM CHANNEL III) (BII)
						NT	Xlaens gene for padina including RPT enhancer
						EST_HUMAN	Q1210577.0001000126-007 F10577 Homo sapiens cDNA
						NT	Cgittus rhodopsin gene for opsin protein
						NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
						NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
						NT	Human leukocyte cluster region (BCR) gene, complete cds
						NT	Y00412.1 Source, multiple sources, ZINC/RIS Homo sapiens cDNA clone IMAGE:200376 5'
						EST_HUMAN	Phospholipase A2 gene for protein (Bart2) gene, exon 1
						NT	Human glucuronidase (GUS) gene, repeat polymorphism
						NT	Schistosoma mansoni strain NMRI chromatin assembly factor 1 small subunit-like protein (RBP49) mRNA, complete cds
						NT	B. laurus ap1 gene for F01(F1)A TP synthase alpha-subunit
						NT	Thermoplasma acidophilum section 86 of 156 of the complete genome
						NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit (Accession No.)	Top 1-Hit Database Source	Top Hit Descriptor
13004	25827	31486	2.82	3.8E-01	H08014.1	EST_HUMAN	yesH17.1.7 Sources ratine NZbAHR Homo sapiens cDNA clone IMAGE:216957.5
13064	25827	31487	2.82	3.8E-01	H08014.1	EST_HUMAN	yesH17.1.7 Sources ratine NZbAHR Homo sapiens cDNA clone IMAGE:216957.5
730	13781		1.78	3.4E-01	U22869.1	NT	Homo sapiens partial N-myc (won 3), HPV48 L2, HPV46 L1, HPV48 E6, HPV46 E7 and HPV46 E1 genes Isolated from T4 cervical carcinoma cell line
1002	14091	29605	5.28	3.4E-01	U07894.2	EST_HUMAN	Pseudomonas fluorescens coR ₂ , cds genes, c7222 and partial nraA gene
1004	14093	29597	21.9	3.4E-01	U08040.20.1	EST_HUMAN	O78-170-281-341199-018-g10 BT0261 Homo sapiens cDNA
1364	14384	27839	1.3	3.4E-01	U00854.1	NT	Arabidopsis thaliana NIA gene for NIA protein (positive regulatory element)
2423	16421	29428	2.72	3.4E-01	U08093.1	EST_HUMAN	Synchohyalis sp. PC06803 complete genome, 1127, 1311295-1430418
3044	16598	29588	0.47	3.4E-01	AL163310.2	NT	Homo sapiens chromosome 21 segment H8370910
3044	16596	29589	0.72	3.4E-01	AL163310.2	NT	Homo sapiens chromosome 21 segment H8370910
3161	16240	28132	0.88	3.4E-01	U06090.1	NT	Synchohyalis sp. PC06803 complete genome, 1127, 1311295-1430418
3201	10282	20148	7.66	3.4E-01	U85008.1	NT	Caris famillaris rat photoreceptor cGMP-gated channel alpha-subunit (CNCG1) mRNA, complete cds
3952	18458	29338	4.91	3.4E-01	U043852.1	NT	Homo sapiens SSI putative protein D1, promoter region, and exon 1
3963	16630	28534	5.01	3.4E-01	U106835.1	NT	Methylophilus sp. strain S31 surfactant protein (gSP), Draik (dnkA), and putative Drau (fnaU) genes, complete cds
3935	16630	28534	5.01	3.4E-01	U106835.1	NT	Human H1 N1 CGAP_Ov18 Homo sapiens cDNA clone IMAGE:597232.3 similar to TR-QU1/15
4356	17197		1.31	3.4E-01	BE449010.1	EST_HUMAN	CG11516.1 N1 CGAP_Pu1 Homo sapiens cDNA clone IMAGE:100034.3
4356	17197		1.31	3.4E-01	BE449010.1	EST_HUMAN	CG11516.1 N1 CGAP_Pu1 Homo sapiens cDNA clone IMAGE:100034.3
490	17622	30458	1.83	3.4E-01	U16884.1	EST_HUMAN	Homo sapiens H1N1 CGAP_H16 (ITC6) genes, exons 12 and exon 2
4745	17623	30022	2.1	3.4E-01	U16884.1	EST_HUMAN	NRH103358.29320-202-60 BT0403 Homo sapiens
4745	17623	30022	2.1	3.4E-01	U16884.1	EST_HUMAN	NRH103358.29320-202-60 BT0403 Homo sapiens
4771	17770	30044	1.42	3.4E-01	BE714058.1	EST_HUMAN	g953545.1 N1 CGAP_G168 Homo sapiens cDNA clone IMAGE:4190958.5
5007	18464		6.1	3.4E-01	U240073.1	EST_HUMAN	g953545.1 N1 CGAP_G168 Homo sapiens cDNA clone IMAGE:1877730.3 similar to contains A1u repetitive element
8266	18464		0.65	3.4E-01	U0687031.1	EST_HUMAN	m75904.1 N1 CGAP_L1 Homo sapiens cDNA clone IMAGE:108955.3 similar to gis-1089770_mel1
5373	16385	31195	1.16	3.4E-01	AW002545.1	EST_HUMAN	KERATIN, TYPE II CYTOSKELETAL 1 (H1JMAN)
5623	19591	32037	2.72	3.4E-01	AL161884.2	EST_HUMAN	WHH42.1 N1 CG GAP_GCG Homo sapiens cDNA clone IMAGE:2916957.3 similar to TRC-3537 C19337
6022	19034		4.93	3.4E-01	U068513.1	NT	Similar to POGO ELEMENT.1
6239	19293		2.27	3.4E-01	U02971.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
6543	19314	32470	0.83	3.4E-01	BE748912.1	EST_HUMAN	212611.1 S1 Sardegna N1T neuron (g937283) Homo sapiens cDNA clone IMAGE:347221.3
6546	19396	32469	0.83	3.4E-01	BE748912.1	EST_HUMAN	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 3A, 3B, 3C, 3D proteins RNA, complete mature capsid and cds
6546	19396	32469	0.83	3.4E-01	BE748912.1	EST_HUMAN	UHHH-seq # 12-01-131 N1 CGAP_S103 Homo sapiens cDNA clone IMAGE:2715552.3

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6462	10527	27705	1.93	3.4E-01	U12844.1	EST_HUMAN	OKF2701A336.11 701 (cpcwpc: bang2) Homo sapiens cDNA clone D426781A.248.9
7047	20073		1.3	3.4E-01	N6323.1	EST_HUMAN	035412.41 Swiss Gene Bank DNH11997 Homo sapiens cDNA clone IMAGE:271423
7279	20232	33462	1.22	3.4E-01	AF46992.1	EST_HUMAN	IMAGE:25.41 NC-CGAP 3m-351 Homo sapiens cDNA clone IMAGE:270240.3 similar to g337451
7413	20112	33346	0.46	3.4E-01	BF02702.1	EST_HUMAN	LAMININ RECEPTOR (HUMAN)
7696	20812	34118	0.41	3.4E-01	BE971696.1	EST_HUMAN	0020630371 NIH MSC_21 Homo sapiens cDNA clone IMAGE: 6248565.9
8445	21416		0.61	3.4E-01	AE020483.1	NT	00105161851 NIH MSC_21 Homo sapiens cDNA clone IMAGE: 3830947.3
8614	21744	35962	0.77	3.4E-01	Y14850.1	NT	Escherichia coli K-12 MG1693 section 333 of 400 of the complete genome
9056	21685		2	3.4E-01	AA337063.1	EST_HUMAN	Homo sapiens TORAY28 gene, allele A4, partial
91708	22039	35793	1.26	3.4E-01	U04690.1	NT	EST 11768 Endometrial tumor Homo sapiens cDNA 3' end
9411	22039	35793	1.61	3.4E-01	U04690.1	NT	Creatulus gireus cholesterol 7 alpha-hydroxylase gene, complete cds
9793	22677	35961	4.32	3.4E-01	P23013	SWISSPROT	Bovine enterovirus strain 12597, complete genome
9793	22677	35962	4.32	3.4E-01	P23013	SWISSPROT	INTEGRIN BETA-3 PRECURSOR
9955	22860		0.83	3.4E-01	AB017510.1	NT	Ephyrae fluviatilis mRNA for PLC-gamma5, complete cds
9979	21337	34972	6.71	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9979	21337	34973	6.71	3.4E-01	U08763.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
10218	23109	36510	0.83	3.4E-01	U08763.1	NT	Glycine max putative transcription factor SOG1-1 (gcol-1) mRNA, complete cds
10401	23280	35713	1.61	3.4E-01	AJ225064.1	NT	Homo sapiens FAI gene, exon 16, 17 and 18
10556	23840		0.74	3.4E-01	AEO04068.1	NT	Vibrio cholerae chromosome 1, section 4 of 251 of the complete chromosome
11485	24571		4.36	3.4E-01	AE000681.1	NT	Methanocaldococcus jannaschii chromosome 1, section 67 of 148 of the complete genome
11491	24603	37864	3.01	3.4E-01	P06925	SWISSPROT	PROBABLE EA PROTEIN
11634	24444	37005	2.43	3.4E-01	AF040691.1	NT	Rattus arseali cytochrome b (cyb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11729	24631	38111	1.62	3.4E-01	M25666.1	NT	Human von Willebrand factor gene, exons 36 and 37
11729	24631	38112	1.62	3.4E-01	M25666.1	NT	Human von Willebrand factor gene, exons 36 and 37
11950	24175	36273	2.47	3.4E-01	AE033507.1	NT	Rattus norvegicus mRNA for 5'-protein/MUC16, complete cds
11958	24801	36296	3.9	3.4E-01	AF191615.2	NT	Rattus norvegicus mRNA for 5'-protein/MUC16, complete cds
12162	25027	38528	1.94	3.4E-01	AF061646.1	EST_HUMAN	IMAGE:27.1 NC-CGAP 3m-351 Homo sapiens cDNA clone IMAGE: 5467646.3
12242	20096		2.48	3.4E-01	U08004.1	NT	Chloris variegata virus putative replicase gene, partial cds
12344	22157		1.48	3.4E-01	Z71052.1	NT	Saccharomyces cerevisiae RIB gene encoding ribosomal synthesis
12433	23753		1.82	3.4E-01	AF238351.1	NT	Saccharomyces pombe Cwp80 (Cwp80) gene, complete cds
12441	26261		12.87	3.4E-01	Z63395.1	NT	Human albumin mRNA, complete cds

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Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Disease Source	Top Hit Descriptor
12966	26768		3.15	3.4E-01	BE218662.1	EST_HUMAN	h42908.at NC1_GCAP_L01 Homo sapiens cDNA clone IMAGE317627 5' similar to contains PFR13
12967	26769		2.97	3.4E-01	BE218662.1	EST_HUMAN	PFR13 repeat region, 5' end
12968	26770		2.97	3.4E-01	BE218662.1	EST_HUMAN	Brain specific, 5' end
12725	26530	31801	1.6	3.4E-01	A122731.1	NT	Brain specific, 5' end
12921	26530		1.65	3.4E-01	A1228346.1	NT	Brain specific, 5' end
13002	26554		2.09	3.4E-01	A701613.1	NT	Homo sapiens ALA class III region encoding hexose X (hexose-X) gene, partial cds, cytochrome P450 2A1
13101	26554		1.82	3.4E-01	A701613.1	NT	Hydroxylase (OYP2B8), complement component C2 (C2) gene, 2' end, complement factor B (BF), and complement component C2 (C2) gene, 2
15	13150	26016	5.42	3.3E-01	X07560.1	NT	Nucleoside diphosphate kinase, complete genome
109	13150	26016	4.93	3.3E-01	X07560.1	NT	Rhizobium leguminosarum sym plasmid pRL5.1 nodX gene
470	13541	26464	0.93	3.3E-01	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
666	13718	26530	2.63	3.3E-01	7662485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1226	14295	27209	3.64	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1333	14307	27317	4.93	3.3E-01	B569550.1	EST_HUMAN	602184016T1 NH_M03_42 Homo sapiens cDNA clone IMAGE300251 3'
1828	14698	27821	1	3.3E-01	6733695	NT	Mus musculus dalminin 5 (Dgms), mRNA
2426	15432		4.65	3.3E-01	4607834	NT	Homo sapiens uridine monophosphate synthetase (cordate phosphoribosyl transferase and cordine-5',-diphosphate) (UMPS) mRNA
2697	18043	28647	1.85	3.3E-01	A1251806.1	NT	Bacteriophage phi7e03-12 complete genome
3000	19112		0.72	3.3E-01	O02743	SWISSPROT	INTERLEUKIN-10 SUBUNIT (IL-10) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 30 NO SUBUNIT) (CMF P03)
3103	19154	25050	0.99	3.3E-01	A1007832.2	NT	Sheepmyces agilis mycophenolate synthase gene
3554	19552	25197	1.71	3.3E-01	A017822.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3977	19506	25787	2.6	3.3E-01	O54645	SWISSPROT	EXODEOXYRIBONUCLEASE VBETA CHAIN
3989	19518	25796	1.01	3.3E-01	P25902	SWISSPROT	GENOME POLYMERASE (POLYMERASE-TERMINAL PROTEIN (P1), HELPER COMPONENT
4049	17075	25661	1.57	3.3E-01	AL161486.2	NT	PROTEINASE (HC-PROT) (PROTEIN P3)
4057	17112	25940	1.92	3.3E-01	A123446.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4359	17403		1.11	3.3E-01	4790025	NT	Hydroxylase (OYP2B8), complement component C2 (C2) gene, 2' end, complement factor B (BF), and complement component C2 (C2) gene, 2
4474	17485		1.79	3.3E-01	O01562.1	NT	Homo sapiens KIAA protein enhancer like 1 (KIAA1100) (KIAA1100) mRNA
4500	17501		1.4	3.3E-01	A183911.1	EST_HUMAN	Kidney specific, 5' end
4602	17630	30608	1.12	3.3E-01	D04003.1	NT	h42908.at NC1_GCAP_L01 Homo sapiens cDNA clone IMAGE2205407 3' similar to gp307562 ANTIGEN PEPTIDE TRANSPORTER (TUMOR)

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Probe SEQ ID NC:	Exon SEQ ID NC:	ORF SEQ ID NO:	Expression Signal	Max Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5254	18337		0.97	3.3E-01	AF095472.2	NT	Basophilic chondrocyte-specific factor 1, 4-mannanase (manF), esterase (esA), transcription regulator (regA), and
5507	18436	31434	2.28	3.3E-01	X62819.1	NT	deficient in the
5507	18556	31435	2.28	3.3E-01	X62819.1	NT	B-1000-specific mRNA for 3UTR of chitinase-like protein
5777	18849	31944	0.97	3.3E-01	P20205	SWISSPROT	DYNAMIN
5777	18849	31955	0.97	3.3E-01	P20205	SWISSPROT	DYNAMIN
5667	19042	32190	0.84	3.3E-01	BF213478.1	EST_HUMAN	801346009F NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078823 5'
6171	19228	32373	1.45	3.3E-01	BF510450.1	EST_HUMAN	801427081F NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875763 3'
6171	19228	32374	1.45	3.3E-01	BF510450.1	EST_HUMAN	801427081F NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875763 3'
6271	19322	32487	49.81	3.3E-01	P05091	SWISSPROT	CROJMSPOK20ITE PROTEIN(CS)
7101	20307	33566	0.69	3.3E-01	AB034233.1	NT	Fluorescent fibroblast cell line for DNA gyrase B subunit, partial cds
7101	20307	33567	0.69	3.3E-01	AB034233.1	NT	Fluorescent fibroblast cell line for DNA gyrase B subunit, partial cds
7218	20216	33482	4.71	3.3E-01	A1628131.1	EST_HUMAN	164401.x1 NCI_LCGAP_K4711 Homo sapiens cDNA clone IMAGE:2265869 3' similar to contains ALU
7218	20216	33483	4.71	3.3E-01	A1628131.1	EST_HUMAN	164401.x1 NCI_LCGAP_K4711 Homo sapiens cDNA clone IMAGE:2265869 3' similar to contains ALU
8288	21161	34644	1.85	3.3E-01	N85146.1	EST_HUMAN	3248BF Human fetal liver1, Lambda ZAP Express Homo sapiens cDNA clone J2488 5' similar to TEGT
8125	22063	35413	21.18	3.3E-01	BF82854.1	EST_HUMAN	002140372F NIH_MGC_46 Homo sapiens cDNA clone IMAGE:301800 5'
8288	22216	35674	0.82	3.3E-01	BF210322.1	EST_HUMAN	501873281F NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097180 5'
8320	22248	35011	0.54	3.3E-01	A1129115.1	EST_HUMAN	AT129115 N28P1T Homo sapiens cDNA clone N28P1T00130 5'
8320	22248	35612	0.54	3.3E-01	A1129115.1	EST_HUMAN	AT129115 N28P1T Homo sapiens cDNA clone N28P1T00130 5'
8698	22594	35655	0.86	3.3E-01	Q52525	SWISSPROT	MITOCHONDRION-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE KINASE 1) (MEK)
8698	22594	35655	0.86	3.3E-01	Q52525	SWISSPROT	KINASE 1 (MEK)
8917	22605	36293	1.28	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET10041-160000-187-410 ET10041 Homo sapiens cDNA
8917	22605	36294	1.28	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET10041-160000-187-410 ET10041 Homo sapiens cDNA
10012	22612	36350	3.15	3.3E-01	N69696.1	EST_HUMAN	226701.x1 Soares_fetal_liver NIH/L15W Homo sapiens cDNA
10031	22814	36262	2.52	3.3E-01	BF370746.1	EST_HUMAN	PC-2-N0077-20080-011-gdb N0077 Homo sapiens cDNA
10497	23358	37359	1.58	3.3E-01	A11044.1	NT	Homo sapiens high-molecular weight phosphoprotein (HMG-C) gene, exon 1-3, complete cds
11194	24032	37549	2.42	3.3E-01	X03633.1	NT	D. mauritiana Adh gene
11194	24032	37549	2.42	3.3E-01	X03633.1	NT	D. mauritiana Adh gene
11452	24519	38061	2.21	3.3E-01	BZ10348.1	EST_HUMAN	10357 Homo sapiens cDNA clone IMAGE:4213085 5'
11452	24519	38061	2.21	3.3E-01	BZ10348.1	EST_HUMAN	10357 Homo sapiens cDNA clone IMAGE:4213085 5'
11688	24584	38061	8.39	3.3E-01	BE219331.1	EST_HUMAN	hg02421 NCI_LCGAP_L022 Homo sapiens cDNA clone IMAGE:378878 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
11785	24707	38109	4.62	3.3E-01	P47953	SWISSPROT	GALECTIN-3 (GALACTOSE SPECIFIC LECTIN-3) (MAG-2 ANTIGEN) (ICE-BINDING PROTEIN) (85 kD LECTIN) (CARBOHYDRATE-BINDING PROTEIN-3) (CBP-3) (AMIN-BINDING PROTEIN) (LECTIN)
12140	24860		3.66	3.3E-01	A418692.1	EST_HUMAN	ab71626.1 NCBI GSP_Q081 Homo sapiens cDNA clone IMAGE:133860 3'
12159	13130	28016	1.87	3.3E-01	X07693.1	NT	Ribosomal leucine transfer RNA synthetase (RLS) gene
12695	26549		25.86	3.3E-01	AF000002.1	NT	Proteinase inhibitor 1 (PI-1) gene
479	13550		1.76	3.2E-01	AF16361.1	NT	Rattus norvegicus EH domain binding protein Eln mRNA, complete cds
741	13799		1.34	3.2E-01	AF161612	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 81
1158	14228	27167	15.88	3.2E-01	AF070713	NT	Fusarium roseum virus 1 (RNA2) putative RNA dependent RNA polymerase gene, complete cds
1308	14341	27289	2.22	3.2E-01	Z62022.1	NT	P. vulgaris acs-1 gene
1417	14448	27402	5.57	3.2E-01	Q48824	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1659	14689		0.86	3.2E-01	AF203790.1	NT	Arabidopsis thaliana cDNA clone RPP13 (RPP13) gene, complete cds
1799	14829	27783	1.19	3.2E-01	Z35041.1	NT	S. cerevisiae chromosome III recombination (RPP13) gene, complete cds
1808	14834	27804	4.71	3.2E-01	AW567194.1	EST_HUMAN	EST168264 IMAGE resequencer, MAGO Homo sapiens cDNA
1808	14834	27805	4.71	3.2E-01	AW567194.1	EST_HUMAN	EST168264 IMAGE resequencer, MAGO Homo sapiens cDNA
1808	14890	27870	1.33	3.2E-01	AF111956.1	NT	Bovine oncosin strain T4 cDNA library under conditions of nitrogen deprivation
2173	15185	28190	2.60	3.2E-01	BF203817.1	EST_HUMAN	601688604F1 NH_MGC-17 Homo sapiens cDNA clone IMAGE:4111512 5'
2572	15570		2.70	3.2E-01	7710079	NT	Mus musculus Pm16000111 homeobox (Pm1601) mRNA
2769	15760	28746	1.72	3.2E-01	AF060558.1	NT	Homo sapiens promyelocytic leukemia trio finger protein (PLZF) gene, complete cds
3871	18704		1.03	3.2E-01	D10872.1	NT	Human NAT1 affects 3,2 gene for 3-oxo-N-acyltransferase
4801	17811	30377	1.71	3.2E-01	N48918.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4387	17895	30483	0.74	3.2E-01	AF111697.2	NT	Homo sapiens Jm domain protein gene, partial cds; cdc gene, complete cds; and unknown gene
4619	17827	30491	1.69	3.2E-01	Q10269	SWISSPROT	HYPOPHOSPHATASE 1 (HPP1) (HPP1) (HPP1) (HPP1) (HPP1) (HPP1) (HPP1) (HPP1) (HPP1) (HPP1)
4850	17852		6.43	3.2E-01	BF563817.1	EST_HUMAN	402081972F1 NH_MGC-91 Homo sapiens cDNA clone IMAGE:426605 5'
5153	18146	30891	0.84	3.2E-01	BF563817.1	EST_HUMAN	402081972F1 NH_MGC-91 Homo sapiens cDNA clone IMAGE:426605 5'
8404	18335	31377	3.04	3.2E-01	BF513034.1	EST_HUMAN	CD44-H1058-00000-259-F101069 Homo sapiens cDNA
6185	18395	32387	0.24	3.2E-01	Z72721.1	NT	Human thymus tissue cDNA library (Homo sapiens) cDNA
1829	18429	32398	0.24	3.2E-01	Z72721.1	NT	Human thymus tissue cDNA library (Homo sapiens) cDNA
6177	18522	32706	0.62	3.2E-01	BF563818.1	EST_HUMAN	402081972F1 NH_MGC-91 Homo sapiens cDNA clone IMAGE:426605 5'
6558	19800	32785	0.76	3.2E-01	AF018494.1	NT	Human thymus tissue cDNA library (Homo sapiens) cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8891	18911	38127	0.67	3.2E-01	AF171603.1	EST HUMAN	ANV18037 R17A1 Homo sapiens cDNA clone R17A181-01 5'
7027	20268		1.44	3.2E-01	A0302069.1	NT	Homo sapiens for KIA03061 gene, KIA03061 protein
4439	21317	34712	0.67	3.2E-01	A1277693.1	NT	Homo sapiens partial UNQ1 gene for LIM domain only 1 protein, exon 1
8160	21890	30020	1.69	3.2E-01	N002095.1	NT	Rat ISO-alpha1b subunit of alpha1b-globulin, complete cds
8842	21722	33119	0.96	3.2E-01	A1231001.1	NT	Rattus norvegicus repeat, map NC8-D1270c1
8859	21969	35227	15.44	3.2E-01	X02098.1	NT	H sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 5' flanking region
8842	21872	35232	15.26	3.2E-01	EF311836.1	EST HUMAN	1807107F1 NH, MGC - 19 Homo sapiens cDNA clone IMAGE128653 5'
8620	21859	37197	1.71	3.2E-01	AF161542.2	NT	Amblystoma tigrinum DNA chromosome 4, contig fragment No. 70
8037	21896	35349	1.42	3.2E-01	BF246771.1	EST HUMAN	601855590F1 NH, MGC - 57 Homo sapiens cDNA clone IMAGE4076527 5'
8037	21896	35349	1.42	3.2E-01	BF246771.1	EST HUMAN	601855590F1 NH, MGC - 57 Homo sapiens cDNA clone IMAGE4076527 5'
8136	22084	35424	1.47	3.2E-01	AE002015.1	NT	Drosophila melanogaster R1 section 152 of 228 of the complete chromosome 1
8229	22167	35570	0.85	3.2E-01	U011028.1	NT	Oryzopsis latifolia g. H-chain pseudogene, V region (VH8-23) gene, partial cds
8229	22167	35571	0.85	3.2E-01	U011028.1	NT	Oryzopsis latifolia g. H-chain pseudogene, V region (VH8-23) gene, partial cds
8919	22545	33919	0.62	3.2E-01	AF163204.2	NT	Homo sapiens chromosome 21 segment H527C004
8925	22551		2.39	3.2E-01	M09511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
8993	22878	35998	0.62	3.2E-01	AF041826.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
8993	22878	35998	0.62	3.2E-01	AF041826.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
10496	23337	37197	3.21	3.2E-01	U04914.1	NT	Bordetia pertussis plasmid p35-2, erpC and erpD genes, complete cds, and unknown genes
10689	23381	37011	0.69	3.2E-01	BC330250.1	EST HUMAN	h06905.41 NC1, CCNP, L204 Homo sapiens cDNA clone IMAGE3181589 3'
10689	23381	37011	0.69	3.2E-01	BC330250.1	EST HUMAN	Homo sapiens gene for AF-3, complete cds
11112	21042	37487	3.28	3.2E-01	U06813.1	EST HUMAN	EST047022 Full brain, Stratagene (cat#936206) Homo sapiens cDNA clone HBD0221
12395	25972		4.89	3.2E-01	O08317	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12844	25466		3.57	3.2E-01	O08317	NT	SWISSPROT
12954	25716		1.71	3.2E-01	AF167095.1	NT	Bos taurus isolated 1,4,5-triphosphate receptor type I mRNA, complete cds
12977	25537		1.49	3.2E-01	38974.1	NT	Homo sapiens deoxyribonuclease domain gene, complete cds
13024	25904	31364	1.48	3.2E-01	BC395576.1	EST HUMAN	601275490F1 NH, MGC - 20 Homo sapiens cDNA clone IMAGE3616766 5'
2720	19753	28712	3.72	3.1E-01	R18051.1	EST HUMAN	y60806.01 Scores feed liver spliced INFL3 Homo sapiens cDNA clone IMAGE12801 5' similar to
2748	18502	28723	3.75	3.1E-01	7091071	NT	gt, M04014 CM PROTEIN (HUMAN)
2748	18502	28734	3.75	3.1E-01	7091071	NT	Homo sapiens KIA00174 gene product: (KIA00174), mRNA
2900	19954		1.33	3.1E-01	AF026050.1	EST HUMAN	H0605.41 Scores, NT_1_1080_51 Homo sapiens cDNA clone IMAGE2875991 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6045	21974	35332	1.63	3.0E-01	BE000933.1	EST_HUMAN	801330797.NIH_MGC_33 Homo sapiens cDNA clone IMAGE3681594.5
6338	22316	39678	0.62	3.0E-01	AF147618.1	NT	Streptomyces sulfidiphilus isopenicillamine N synthase (isfco) gene, partial cds
9439			0.69	3.0E-01	7601689	NT	Homo sapiens DNFZ1860A0122 protein (DNFZ1860A0122), mRNA
9759	22943	39068	1.14	3.0E-01	AF220207.1	NT	Arabidopsis PCOT120 oxytocin-specific DNA methyltransferase (cmm) gene, complete cds; putative anthelmintic phosphotriesterase gene, partial cds; and unknown gene
10102	22993	39370	0.61	3.0E-01	U79349	SWISSPROT	16032747C.HUMAN_58.5 ND PROTEIN IN WZA-ASIA INTERGENIC REGION
10474	23346	39780	0.86	3.0E-01	AF074912.1	EST_HUMAN	HTP23271F.NIH_MGC_31 Homo sapiens cDNA clone IMAGE238833.8
10942	23371	37162	2.27	3.0E-01	AB030021.1	EST	Aspergillus oryzae btpA gene for Bt chaperone Btp, complete cds
12163	23519	38520	2.77	3.0E-01	AF150293.1	EST_HUMAN	pp4k10.1l Soxase fetal liver spleen INF15 Homo sapiens cDNA clone IMAGE184107.5
12163	23519	38521	2.77	3.0E-01	AF150293.1	EST_HUMAN	pp4k10.1l Soxase fetal liver spleen INF15 Homo sapiens cDNA clone IMAGE184107.5
12322	25247		1.64	3.0E-01	FF4660	SWISSPROT	PONTICULIN PRECURSOR
12702	25867		2.67	3.0E-01	A0267931.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gpdh-2 gene)
13005	26071		6.68	3.0E-01	5897769	NT	Mus musculus ribose-5-phosphate isomerase A (RpiA), mRNA
2037	15054	26073	1.22	3.0E-01	A0000736.1	NT	Aquifex acidicus section 08 of 109 of the complete genome
2383	15218	28258	1.03	2.3E-01	AF222718.1	NT	Chrysidomyces synuridis mitochondrion, complete genome
3227	16276	25178	1.4	2.3E-01	AF078111.1	EST	Xeropus laevis testis protein, complete cds
3228	18343	25246	1.16	2.3E-01	AF075423.1	EST_HUMAN	PMH-C70325-171299-001.412 C70328 Homo sapiens cDNA
3236	18343	25247	1.16	2.3E-01	AF075423.1	EST_HUMAN	PMH-C70325-171299-001.412 C70328 Homo sapiens cDNA
3948	18344	25878	0.92	2.3E-01	AF108336.1	EST_HUMAN	9212411.NCI_GADP_Gene4 Homo sapiens cDNA clone IMAGE2188412.3 similar to gpC10080 NII-3A
4175	17184		0.67	2.3E-01	AF060295.2	EST_HUMAN	SWC1 FINGER PROTEIN (HUMAN)containing element L1 negative element
4398	17807	35404	1.16	2.3E-01	A0264488.1	EST_HUMAN	WDF012121.NCI_GADP_G0331 Homo sapiens cDNA clone IMAGE1791391.9 similar to contains Alu repetitive element
4593	17811	35470	0.79	2.3E-01	AF124119.1	EST_HUMAN	Mus musculus SMO1 (Smt1) gene, complete cds
4593	17811	35471	0.79	2.3E-01	AF124119.1	NT	Mus musculus SMO1 (Smt1) gene, complete cds
5132	18128	33970	1.11	2.3E-01	7602169	NT	Homo sapiens KAO0537 gene product (KAO0537), mRNA
5387	19321	35487	1.11	2.3E-01	AF101852.1	NT	Human 18S ribosomal DNA clone 18S, coding fragment (ncs_8)
5387	19321	35488	1.03	2.3E-01	AF101852.1	EST_HUMAN	477612.1 Soares fetal liver 18S rRNA Homo sapiens cDNA clone IMAGE23891.3
5388	19321	35489	1.03	2.3E-01	AF101852.1	EST_HUMAN	477612.1 Soares fetal liver 18S rRNA Homo sapiens cDNA clone IMAGE23891.3
5390	19321	35428	0.82	2.3E-01	AF124100.1	NT	B. subtilis adaptin 100 (p.e. 100) and sacC (partial) genes for nucleoside phosphotransferase system polypeptide P18, 18.28.30, and 100
6072	19308	32169	6.20	2.3E-01	X65008.1	NT	B. subtilis, isopenicillin carboxylase (p.e. 100) and sacC (partial) genes for nucleoside phosphotransferase system polypeptide P18, 18.28.30, and 100
5972	19308	32169	5.26	2.3E-01	X65008.1	NT	system polypeptide P18, 18.28.30, and 100
5985	32176		4.64	2.3E-01	reza008.1	NT	Mus musculus Irf receptor 2b (Irf2b), mRNA

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Probe Seq ID NO.	Exon Seq ID NO.	ORF SEQ ID NO.	Exon Signal	Meat Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6261	19342	32510	1.3	2.9E-01	AA18145.1	EST_HUMAN	2607932.11 Scavenger (HSA)P1, S1 Homo sapiens cDNA clone IMAGE:567711.6'
6533	19377	32759	0.93	2.9E-01	AF070128.1	EST_HUMAN	14627405.41 NC1_GGAP_L104 Homo sapiens cDNA clone IMAGE:2242372.3 similar to contig L1.11
6562	19323	32608	2.65	2.9E-01	U03020.1	NT	Scavenger-related protein, complete cds
6726	19764	32911	0.43	2.9E-01	R09184.1	EST_HUMAN	Bos taurus myosin I mRNA, complete cds
6728	19764	32911	0.43	2.9E-01	R09184.1	EST_HUMAN	X50008.11 Scavenger (HSA)P1, S1 Homo sapiens cDNA clone IMAGE:141613.5'
6728	19764	32912	0.43	2.9E-01	R09184.1	EST_HUMAN	X50008.11 Scavenger (HSA)P1, S1 Homo sapiens cDNA clone IMAGE:141613.5'
7022	20048	32972	0.53	2.9E-01	Z60196.1	NT	D. discoideum gene for 34 kD actin binding protein
7164	20184	33428	0.56	2.9E-01	AF123001.1	NT	Sus scrofa (pig) actin, complete cds
7327	18105	31270	1.57	2.9E-01	AF123001.1	NT	Mus musculus fibronectin (FN) gene, complete cds and L1 protein (L1) gene, partial cds
7455	20395	33606	2.97	2.9E-01	Q34989	SWISSPROT	POTATIVE MULTIPROTEIN OXIDASE YDR030C
7521	20490	33746	1.76	2.9E-01	AF100546.1	NT	Mus musculus major nonkeratin protein (Mnk) gene, complete cds and L1 protein (L1) gene, partial cds
8468	21429	34769	1.76	2.9E-01	BE544122.1	EST_HUMAN	galeosin-like transferase (boar) 3-palmitoyl l-tyrosine
8468	21429	34770	1.76	2.9E-01	BE544122.1	EST_HUMAN	galeosin-like transferase (boar) 3-palmitoyl l-tyrosine
8728	21698	35004	0.65	2.9E-01	AJ227657.1	NT	Bos taurus partial statin A gene, exon 5-19
8728	21698	35005	0.65	2.9E-01	AJ227657.1	NT	Bos taurus partial statin A gene, exon 5-19
8740	21670	35044	1.12	2.9E-01	BE217743.1	EST_HUMAN	601882370F1 NH-LMPC, 5' Homo sapiens cDNA clone IMAGE:1095113.5'
9157	22085	35444	0.77	2.9E-01	AU180910.1	EST_HUMAN	AU180910.1 NT2P22: Homo sapiens cDNA clone NT2P22030001.3
9481	22409	35770	1.11	2.9E-01	AF125508.1	NT	Arabidopsis thaliana sulfonylesterase receptor-like protein mRNA, complete cds
9541	22511	35874	0.80	2.9E-01	MZ2462.1	NT	Balston lymphocyte homing/exit actin receptor mRNA, complete cds
9788	22762	36133	0.94	2.9E-01	AJ242627.1	NT	Pyrococcus abyssi complete genome, segment 516
9788	22762	36134	0.96	2.9E-01	AJ242627.1	NT	Pyrococcus abyssi complete genome, segment 516
11332	24251	37068	1.76	2.9E-01	AF129643.1	NT	Tyrphostin (anti-tyrosine kinase) specific surface glycoprotein gp52 (gp52) mRNA, partial cds
11002	24511	37978	2.08	2.9E-01	V01394.1	NT	Topical californin mRNA encoding scytoskeleton receptor gamma subunit
11602	24811	37979	2.08	2.9E-01	V01394.1	NT	Topical californin mRNA encoding scytoskeleton receptor gamma subunit
12013	24855	38555	1.91	2.9E-01	A065573.1	EST_HUMAN	hNS402.51 NC1_GGAP_P12 Homo sapiens cDNA clone IMAGE:1237379 similar to contig L178.02.L1788
12013	24855	38556	1.91	2.9E-01	A065573.1	EST_HUMAN	hNS402.51 NC1_GGAP_P12 Homo sapiens cDNA clone IMAGE:1237379 similar to contig L178.02.L1788
12013	24855	38557	1.91	2.9E-01	AF129643.1	NT	Topical californin mRNA encoding scytoskeleton receptor gamma subunit
12030	24872	38575	1.80	2.9E-01	U03020.1	NT	Scavenger-related protein, complete cds
12030	24872	38576	1.80	2.9E-01	U03020.1	NT	Scavenger-related protein, complete cds
12030	24872	38577	1.80	2.9E-01	U03020.1	NT	Scavenger-related protein, complete cds
12704	23395	37106	1.65	2.9E-01	AN060591.1	EST_HUMAN	W68806.X1 NC1_GGAP_B1025 Homo sapiens cDNA clone IMAGE:2685921.3 similar to contig element
12704	23395	37106	1.65	2.9E-01	AN060591.1	EST_HUMAN	W68806.X1 NC1_GGAP_B1025 Homo sapiens cDNA clone IMAGE:2685921.3 similar to contig element
12705	23414	37187	2.51	2.9E-01	AF032453.1	NT	Homo sapiens TNF- α inducible RNA binding protein (TIRP) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similarity (Top) Hit BLAST E Value	Top Hit/Accession No.	Top Hit Database Source	Top Hit Description
18293	25142		1.88	2.8E-01	BE76189.1	EST_HUMAN	GGT145255F7 NH_KJC-39 Homo sapiens cDNA clone IMAGE:3804569.8
4890	13885		1.3	2.8E-01	U97128.1	NT	Rattus norvegicus Adipocyte-enriched protein (AEP) mRNA, complete cds
4891	13885		0.72	2.8E-01	U97128.1	NT	Protein tyrosine phosphatase (PTP) gene, partial cds
4892	13885		0.72	2.8E-01	U97128.1	NT	Protein tyrosine phosphatase (PTP) gene, partial cds
1103	14152	27093	1.41	2.8E-01	AF15106.1	EST_HUMAN	Gene expression cloning (GEC) cDNA, partial cds
1303	14326	27293	1.41	2.8E-01	BE512442.1	EST_HUMAN	Gene expression cloning (GEC) cDNA, partial cds
1303	14326	27293	1.41	2.8E-01	BE512442.1	EST_HUMAN	Gene expression cloning (GEC) cDNA, partial cds
1317	14330	27294	0.91	2.8E-01	BE521512.1	EST_HUMAN	Gene expression cloning (GEC) cDNA, partial cds
1317	14330	27294	0.91	2.8E-01	BE521512.1	EST_HUMAN	Gene expression cloning (GEC) cDNA, partial cds
1757	17474	27755	1.65	2.8E-01	AF168020.1	EST_HUMAN	Human mRNA for anti-infective protein (AIP), complete cds
2025	15045	28037	1.41	2.8E-01	AL047620.1	EST_HUMAN	OV1-CT10344.120305-055-055 CT10344 Homo sapiens cDNA
2145	15195	28180	1.16	2.8E-01	AF151198.1	EST_HUMAN	SKP2/680324.1T 555 (synonym: hult) Homo sapiens cDNA clone DKFZ566237.1
2464	14406	26186	2.81	2.8E-01	AE000494.1	EST_HUMAN	h444603.x1 Soares, NFI, T, GAG, S1 Homo sapiens cDNA clone IMAGE:2912333.5
2464	14406	26186	2.81	2.8E-01	AE000494.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2578	15577	26497	2.16	2.8E-01	AL16165.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 95
2714	15705	26703	1.07	2.8E-01	AB020597.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 95
3011	17003	26907	1.62	2.8E-01	AF179400.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 95
3012	16094	26968	2.41	2.8E-01	Z14037.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 95
3012	16094	26968	2.41	2.8E-01	Z14037.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 95
3436	16477	23353	0.96	2.8E-01	AF000004.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 95
4052	17107	28685	2.85	2.8E-01	AE001180.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 95
4220	17235		0.81	2.8E-01	AE004400.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 95
4264	17308		2.84	2.8E-01	AF000888.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 95
4566	17574	30437	1.22	2.8E-01	AL021127.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 95
4571	17575	30441	3	2.8E-01	AF15915	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 95
4936	17982	30792	1.11	2.8E-01	AF070238.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 95
4943	17942	30800	3.86	2.8E-01	AF030154.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 95
4971	17995	30828	1.41	2.8E-01	BF429188.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 95
4994	17990	30840	3.14	2.8E-01	AF27030.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 95
5408	18395	31227	0.91	2.8E-01	AF002686.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 95
5408	18395	31228	0.91	2.8E-01	AF002686.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 95

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Meat Similar (Top) HIT BLAST E Value	Top HIT Accession No.	Top HIT Database Source	Top HIT Descriptor
5454	24628	31418	23.21	2.9E-01	A436297.1	EST_HUMAN	EST-2072 Infant brain Homo sapiens cDNA 5' end
5800	18872	31880	2.50	2.9E-01	A8718625.1	NT	Homo sapiens DCN2 gene, complete cds
6528	19240		0.65	2.9E-01	A1902583.1	EST_HUMAN	GM1-580024-15200-115-012-15N2024 Homo sapiens cDNA
6143	18202	32339	0.54	2.9E-01	A4766296.1	EST_HUMAN	4601965.at NCL CGAP GC051 Homo sapiens cDNA clone IMAGE:100961 3' similar to gb-X124539 F1500- BINDING PROTEIN (HUMAN).
6163	18220		0.61	2.9E-01	A4404576.1	EST_HUMAN	741191.t1 Soares ovary tumor NHOT Homo sapiens cDNA clone IMAGE:724621 5' similar to contains Alu repetitive element.
6417	25976		0.83	2.9E-01	M304068.1	NT	Bovine 680 bp repeated unit of 1729 satellite DNA
6421	19507	32682	1.53	2.9E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-5-phosphate aldolase mRNA, complete cds
6422	19507	32683	1.52	2.9E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-5-phosphate aldolase mRNA, complete cds
7035	20091	33295	9.12	2.9E-01	BF511215.1	EST_HUMAN	U18614-sef-04-DU-1 NCL CGAP Sup8 Homo sapiens cDNA clone IMAGE:308182 3'
7346	20345	33812	0.63	2.9E-01	U68500.1	NT	Orthocorys heterodula cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
7745	20976	33974	0.47	2.9E-01	B6881485.1	EST_HUMAN	6014807.57F1 NH2-MSC_60 Homo sapiens cDNA clone IMAGE:359212 5'
7845	20772		1.02	2.9E-01	U06083.1	NT	Mirafra quindiana ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, chloroplast gene encoding chloroplast protein, partial cds
8412	19220		0.83	2.9E-01	A4404576.1	EST_HUMAN	741191.t1 Soares ovary tumor NHOT Homo sapiens cDNA clone IMAGE:724621 5' similar to contains Alu repetitive element.
8671	21802	34641	1.63	2.9E-01	A1844126.1	EST_HUMAN	464901.x1 NCL CGAP Co8 Homo sapiens cDNA clone IMAGE:1626299 3' similar to gb-X00323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8971	21002	34942	1.59	2.9E-01	A1844126.1	EST_HUMAN	464901.x1 NCL CGAP Co8 Homo sapiens cDNA clone IMAGE:1626299 3' similar to gb-X00323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8971	21717	35065	2.95	2.9E-01	U19168.1	NT	Homo sapiens truncated 14-kDa demethylase cytochrome P450 (CYP51) gene, exon 5
9080	22008	35365	0.83	2.9E-01	AAP11629.1	EST_HUMAN	602605.at NCL CGAP Co12 Homo sapiens cDNA clone IMAGE:1416953 3' similar to gb-X87780.G (SMMK1) CHAIN C REGION (HUMAN);
9151	22076		9.22	2.9E-01	BF37847.1	EST_HUMAN	6022867.1 NCL CGAP Co36 Homo sapiens cDNA clone IMAGE:4156025 5'
8945	22816	36205	1.24	2.9E-01	U17261.1	NT	Neurospora crassa arginine reductase gene, clone-2 (con-2) gene, complete cds
10253	23124	36711	1.24	2.9E-01	U19384.1	NT	Escherichia coli transcription factor T (Tf) gene, complete cds
10303	23385	36712	1.44	2.9E-01	A132778.1	NT	Escherichia coli transcribed intern receptor Tr (tr) gene, complete cds
10403	23385	36712	1.44	2.9E-01	A132778.1	NT	Escherichia coli transcribed intern receptor Tr (tr) gene, complete cds
10457	23345	36762	0.71	2.9E-01	AF294393.1	NT	Rattus norvegicus glycerol 3-phosphate dehydrogenase gene, Promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
10552	23448	36870	5.21	2.9E-01	77006163	NT	Homo sapiens lipocalin-1 (LOC51319), mRNA
10802	23898		1.17	2.9E-01	8820154	NT	Fujinaga sarcosineuria, complete genome

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF-SEQ ID NO.	Expression Signal	Most Similar (To) Hit BLAST E Value	Top-Hit Accession No.	Top-Hit Database Source	Top-Hit Descriptor
11894	24110	31951	2.91	2.8E-01	BF241062.1	EST_HUMAN	601480745F1 NIH MG-63 Homo sapiens cDNA clone IMAGE:4105659 5'
11894	24110	31958	2.61	2.8E-01	BF241062.1	EST_HUMAN	601480745F1 NIH MG-63 Homo sapiens cDNA clone IMAGE:4105659 5'
11211	24197	31957	2.95	2.8E-01	BF95976.1	EST_HUMAN	601480745F1 NIH MG-63 Homo sapiens cDNA clone IMAGE:4105659 5'
11317	24296	31961	2.31	2.8E-01	AF951862.1	NT	000341111 Homo sapiens (H) gene, alternative splicing products, 5' flanking region, exons 1 through 7 and complete cds
11724	24626	31961	3.63	2.8E-01	BF671023.1	EST_HUMAN	601480745F1 NIH MG-63 Homo sapiens cDNA clone IMAGE:4273653 5'
12222	25096	39555	2.02	2.8E-01	R23893.1	EST_HUMAN	A51911.1 Soares, parent N624P Homo sapiens cDNA clone IMAGE:330437 5' similar to contains LTR3 repeat element
12738	25376	31768	12.34	2.8E-01	D53338.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12834	25449	31776	6.3	2.8E-01	BE170869.1	EST_HUMAN	PMH10603-030400-001-c07 T00300 Homo sapiens cDNA
489	13059	26467	4.49	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
639	13907	29902	2.7	2.7E-01	MJ460061.1	EST_HUMAN	z55610.1 Soares, total, testis, N624P Homo sapiens cDNA clone IMAGE:769327 3' similar to contains Alu repetitive element
1289	14321	27267	1.39	2.7E-01	AB004006.1	NT	Ipomoea purpurea transposable element Tnp100 gene for transposase, complete cds
1844	14876	27267	1.92	2.7E-01	X798.1.1	NT	G.lentia SR2 gene
1769	14789	27786	2.77	2.7E-01	W3907.1	EST_HUMAN	z52270.1 Soares, fetal, heart, N624P Homo sapiens cDNA clone IMAGE:341443 5'
1801	14827	27765	1.34	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN (CNSER: INNER COAT PROTEIN P12: CORE PROTEIN P16: CORE SHELL PROTEIN P30: NUCLEOPROTEIN P10)
2149	15917	28367	2.21	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monomeric transporter type 2, promoter region and exon 1
2390	15936	28367	0.89	2.7E-01	Y13668.1	NT	Feline immunodeficiency virus env gene, isolate FTO039PL (M89), partial cds
2479	15491	28462	3.82	2.7E-01	AG10869.1	EST_HUMAN	z453c1.12 NCI, COMP_Luc2 Homo sapiens cDNA clone IMAGE:204939 3' similar to contains element L1 repetitive element
2941	15994	28966	1.32	2.7E-01	AF251276.1	NT	Mus musculus serine protease inhibitor 14 (SP14) mRNA, complete cds
3026	16078	28966	0.81	2.7E-01	BF086294.1	EST_HUMAN	CCNH10875-05000-355-c05 H'0075 Homo sapiens cDNA
3899	16928	29606	0.86	2.7E-01	AF030483.1	NT	Corynebacterium glutamicum metK gene, ORF1 (partial) and ORF 2 (partial)
4097	17122	29966	2.96	2.7E-01	AF026161.1	EST_HUMAN	W62481.1 NCI, CGAP_FUHT Homo sapiens cDNA clone IMAGE:2462828 3'
4108	17132	30066	0.78	2.7E-01	AF210241.1	NT	Drosophila buzzatii apolipoprotein 8 (aP8) gene, partial cds
4108	17132	30077	0.78	2.7E-01	AF210241.1	NT	Drosophila buzzatii apolipoprotein 8 (aP8) gene, partial cds
4113	17139	30310	2.87	2.7E-01	L7799.1	NT	Homo sapiens D-cephe syndrome critical region, genomic end
4177	17197	30667	1.06	2.7E-01	AF70468.1	EST_HUMAN	W62045.1 NCI, COMP_Luc2 Homo sapiens cDNA clone IMAGE:2445626 3' similar to TR-Q1888 Q1888 MP-2 FUNCTION (M69)
5000	17959	30596	3.23	2.7E-01	L27918.1	NT	Human cDNA clone IMAGE:2445626 3' similar to TR-Q1888 Q1888 MP-2 FUNCTION (M69)
5171	18163	31928	0.27	2.7E-01	AF086913.1	EST_HUMAN	R04103088-290300-010-c07 C03038 Homo sapiens cDNA
5191	18183	31928	0.82	2.7E-01	AF027153.1	EST_HUMAN	W11930.1 Soares, NIH_L_G8C_S1 Homo sapiens cDNA clone IMAGE:236024 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hitt BLAST E Value	Top Hitt Accession No.	Top Hitt Database Source
9875	22788	36179	9.77	2.7E-01	Q69909	SWISSPROT
9875	22790		2.76	2.7E-01	P77628	SWISSPROT
10317	23206	36917	0.6	2.7E-01	D99590.1	NT
10553	23469	36985	1.14	2.7E-01	AF591844.1	NT
10616	23504	36936	0.96	2.7E-01	AF597434.1	NT
10743	23628	37060	1.07	2.7E-01	AF156559.1	NT
10743	23659	37061	1.07	2.7E-01	AF156559.1	NT
11010	24364		0.52	2.7E-01	AB011678.1	NT
11251	24175	37622	1.55	2.7E-01	AF705043.1	EST_HUMAN
11251	24175	37623	1.55	2.7E-01	AF705043.1	EST_HUMAN
11251	24184	37633	3.26	2.7E-01	AJ193259.1	NT
12087	28545		2.8	2.7E-01	AF217491.1	NT
492	18545		1.49	2.6E-01	P78411	SWISSPROT
593	13574		1.31	2.6E-01	D18499.1	NT
1420	14451	27405	1.41	2.6E-01	BE84899.1	EST_HUMAN
1456	14488	27448	0.6	2.6E-01	AB013290.1	NT
1514	14935	27911	4.79	2.6E-01	AL191472.2	NT
1514	14935	27912	4.79	2.6E-01	AL191472.2	NT
2105	15151		9.35	2.6E-01	AW733162.1	EST_HUMAN
2167	15175	28185	1.13	2.6E-01	MT1844.1	NT
2577	15576		11.59	2.6E-01	BE272440.1	EST_HUMAN
3641	16677	29575	1.02	2.6E-01	NC2342.1	NT
3711	16743	29633	2.18	2.6E-01	AF229118.1	NT
4190	17210	30016	0.71	2.6E-01	AF195950.1	EST_HUMAN
4252	17258	30157	17.02	2.6E-01	BE195950.1	EST_HUMAN
4449	17427	30336	1.42	2.6E-01	AF175293.1	NT
4511	17619	30381	0.72	2.6E-01	AF195212.1	NT
4511	17619	30482	0.72	2.6E-01	AF521106.1	NT

Table 4

[illegible]

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	QRT SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9453	21414	34751	1.35	2.0E-01	BE14433.1	EST_HUMAN	MRG-1 (195-161) (U09043.4) (F0168) Homo sapiens cDNA
9476	21850	34969	0.83	2.0E-01	70829.1	NT	3' region cDNA for alpha 12 microglobulin (beta)
9715	21850	35467	0.03	2.0E-01	U09043.1	EST_HUMAN	O-mannosyl transferase for alpha 12 microglobulin (beta)
9739	21854	35364	2.16	2.0E-01	U09043.1	EST_HUMAN	O-mannosyl transferase for alpha 12 microglobulin (beta)
9749	21854	35364	2.16	2.0E-01	U09043.1	EST_HUMAN	O-mannosyl transferase for alpha 12 microglobulin (beta)
9753	21860	35633	4.07	2.0E-01	BE830339.1	EST_HUMAN	HYPOPHYSICAL 76.2 NO PROTEIN G112112 IN CHROMOSOME II
9753	22180	35633	4.07	2.0E-01	BE830339.1	EST_HUMAN	HYPOPHYSICAL 76.2 NO PROTEIN G112112 IN CHROMOSOME II
9753	22180	35633	4.07	2.0E-01	BE830339.1	EST_HUMAN	HYPOPHYSICAL 76.2 NO PROTEIN G112112 IN CHROMOSOME II
10009	22817	36206	1.09	2.0E-01	X17054.1	NT	RC6-ET0082.3:05090421-F10 ET0082 Homo sapiens cDNA
10259	23146		0.57	2.0E-01	AF057121.1	NT	S. coelicolors INV gene for live host (EG 3.2.1.26)
10381	23270	35992	1.28	2.0E-01	P07268	SWISSPROT	Lentivir canidensis cytochrome b (cyt b) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10381	23270	35992	1.28	2.0E-01	P07268	SWISSPROT	GREEN-SENSITIVE OPIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KPH-G)
10381	23270	35992	1.28	2.0E-01	P07268	SWISSPROT	GREEN-SENSITIVE OPIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KPH-G)
10897	23573		0.71	2.0E-01	Q28256	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10897	23573		0.71	2.0E-01	Q28256	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10897	23573		0.71	2.0E-01	Q28256	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
11074	23959		0.35	2.0E-01	Y10196.1	NT	Homo sapiens PHEX gene
11805	24705	35106	1.81	2.0E-01	P43280	SWISSPROT	Danio rerio mRNA for RPT-3-like protein
11805	24705	35106	1.81	2.0E-01	P43280	SWISSPROT	CELL DIVISION PROTEIN FTSW HOMOLOG
12330	25142		0.33	2.0E-01	X01755.1	NT	Human lamda-immunoglobulin constant region (germline)
12330	25142		0.33	2.0E-01	X01755.1	NT	Human lamda-immunoglobulin constant region (germline)
12330	25142		0.33	2.0E-01	X01755.1	NT	Human lamda-immunoglobulin constant region (germline)
12520	25262	31841	3.06	2.0E-01	BE83491.1	EST_HUMAN	Mus musculus jerky (JH), mRNA
12520	25262	31841	3.06	2.0E-01	BE83491.1	EST_HUMAN	Mus musculus jerky (JH), mRNA
12520	25262	31841	3.06	2.0E-01	BE83491.1	EST_HUMAN	Mus musculus jerky (JH), mRNA
12594	25464		1.79	2.0E-01	D08425.1	NT	Homo sapiens Nuk-A TPase gamma subunit (PYD2) gene, complete cds, alternatively spliced
12594	25464		1.79	2.0E-01	D08425.1	NT	Homo sapiens Nuk-A TPase gamma subunit (PYD2) gene, complete cds, alternatively spliced
12594	25464		1.79	2.0E-01	D08425.1	NT	Homo sapiens Nuk-A TPase gamma subunit (PYD2) gene, complete cds, alternatively spliced
13038	25575		2.47	2.0E-01	P47295	SWISSPROT	Thermoplasma maritima section 26 of 138 of the complete genome
13038	25575		2.47	2.0E-01	P47295	SWISSPROT	Thermoplasma maritima section 26 of 138 of the complete genome
13038	25575		2.47	2.0E-01	P47295	SWISSPROT	Thermoplasma maritima section 26 of 138 of the complete genome
250	19357	26272	2.76	2.0E-01	4022296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP8D), nuclear gene encoding mitochondrial protein, mRNA
250	19357	26272	2.76	2.0E-01	4022296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP8D), nuclear gene encoding mitochondrial protein, mRNA
250	19357	26272	2.76	2.0E-01	4022296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP8D), nuclear gene encoding mitochondrial protein, mRNA
261	19357	26272	1.71	2.0E-01	4022296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP8D), nuclear gene encoding mitochondrial protein, mRNA
261	19357	26272	1.71	2.0E-01	4022296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP8D), nuclear gene encoding mitochondrial protein, mRNA
261	19357	26272	1.71	2.0E-01	4022296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP8D), nuclear gene encoding mitochondrial protein, mRNA
277	13359		3.99	2.0E-01	U09001.1	NT	Starfish (P. schenckii) cytoplasmic actin gene, complete cds
887	13011	20854	1.35	2.0E-01	U09001.1	NT	Mus musculus CD35/alpha 2-phosphatase dehydrogenase (GapA-S) gene, complete cds
1037	14131		1.24	2.0E-01	AL030436.1	NT	Human transferrin receptor 2 (TF2) of the complete genome
1138	14180	27129	7.22	2.0E-01	U09001.1	EST_HUMAN	Human transferrin receptor 2 (TF2) of the complete genome
1408	14180		0.83	2.0E-01	U09001.1	EST_HUMAN	Human transferrin receptor 2 (TF2) of the complete genome
1408	14180		0.83	2.0E-01	U09001.1	EST_HUMAN	Human transferrin receptor 2 (TF2) of the complete genome
1408	14180		0.83	2.0E-01	U09001.1	EST_HUMAN	Human transferrin receptor 2 (TF2) of the complete genome
1430	14570	27529	1.31	2.0E-01	U110284.1	NT	Scaphytruncus stercoratus 14 cDNA library under conditions of nitrogen deprivation

Table 4
Single Exon Probe Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1798	14785		4.13	2.9E-01	4885406	NT	Homo sapiens hypoxanthine activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
2431	14435		5.17	2.9E-01	AL60075.1	NT	Adult rat testis section 7 of 10 of the complete genome
2518	15519		1.80	2.9E-01	AK25187.1	EST_HUMAN	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
2683	15977	28676	1.68	2.9E-01	AF010101.1	EST_HUMAN	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
3473	16913		4.37	2.9E-01	AF09737.1	EST_HUMAN	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
3688	17495	28544	1.91	2.9E-01	AF09737.1	EST_HUMAN	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
4038	17151		1.94	2.9E-01	P23230	SWISSPROT	Ascaris suum HMG-1, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
4423	17454		0.91	2.9E-01	Q03314	SWISSPROT	Ascaris suum HMG-1, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
4728	17733	30495	0.77	2.9E-01	AF24341.1	NT	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
4843	17865		1.6	2.9E-01	Q27225	SWISSPROT	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
4869	17869	30733	4.63	2.9E-01	AF007788.1	NT	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
4890	17894	30760	2.95	2.9E-01	AE004416.1	NT	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
4918	17917		3.27	2.9E-01	AJ220193.1	NT	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
4947	17940	30304	0.79	2.9E-01	BE967395.1	EST_HUMAN	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
6178	18170	31015	1.08	2.9E-01	AF078388.1	EST_HUMAN	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
6242	18226	31078	0.84	2.9E-01	P27023	SWISSPROT	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
6242	18226	31078	0.84	2.9E-01	P27023	SWISSPROT	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
6500	18588	31437	10.84	2.9E-01	S88350.1	NT	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
6185	18242	32289	0.96	2.9E-01	AJ008345.1	NT	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
6185	18242	32289	0.96	2.9E-01	AJ008345.1	NT	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
6940	18988	32890	0.86	2.9E-01	P22219	SWISSPROT	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
6915	19445	33164	0.86	2.9E-01	AJ251973.1	NT	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
7390	20065	33329	0.71	2.9E-01	8384153	NT	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
7740	20871	33969	0.61	2.9E-01	U18622.1	NT	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
7771	20701		1.46	2.9E-01	AF193181.1	NT	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
8037	20562	34287	0.93	2.9E-01	AF193566.1	NT	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
8056	20567	34377	4.85	2.9E-01	AF193566.1	NT	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
8427	21390	34690	1.71	2.9E-01	BF190460.1	EST_HUMAN	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'
8138	21370	34711	0.74	2.9E-01	BE600712.1	EST_HUMAN	HLH122 mRNA, 5' UTR, cDNA, Homo sapiens cDNA clone IMAGE:384982 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID No.	Exon SEQ ID No.	ORF SEQ ID No.	Expression Signal	Most Similar BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8604	21134	35003	2.25	2.4E-01	AF098285.1	EST HUMAN	60145238F1 NH1.MG.60 Homo sapiens cDNA, clone IMAGE:362809.9
9169	22125	35476	4.48	2.4E-01	H32266.1	EST HUMAN	Xp1807.11 Soares first liver spliced TNE S Homo sapiens cDNA, clone IMAGE:202601.9
9433	22291	35724	1.03	2.4E-01	AB9926.1	NT	Mouse testis-specific protein (TP21.1) gene, exon 10
10047	22963	36341	22.61	2.4E-01	U96951.2	NT	Homo sapiens multi metalloproteinase MAP Rask-1 gene, promoter region
10047	22963	36332	22.61	2.4E-01	U96951.2	NT	Homo sapiens multi metalloproteinase MAP Rask-1 gene, promoter region
10101	22560	36339	1.86	2.4E-01	AF08164.1	NT	Hodarium vulgaris xanthoxanthin-like kinase PRK10 gene, partial cds
10101	22560	36340	1.86	2.4E-01	AF08164.1	NT	Hodarium vulgaris xanthoxanthin-like kinase PRK10 gene, partial cds
10500	22465	36915	1.69	2.4E-01	AF058197.1	EST HUMAN	RC3-ST0166-100100-015-07 ST0166 Homo sapiens cDNA
10530	23716	37141	0.52	2.4E-01	AF058262	NT	Positive purpurin alkaloidase, complete genome
11020	23904	37343	1.77	2.4E-01	AF162346.1	EST HUMAN	Xp400.10.1 NC1_OGAP_LRT Homo sapiens cDNA, clone IMAGE:2830034.3 similar to contains Alu repetitive element; contains element MSRI repetitive element;
11023	23907	37347	1.81	2.4E-01	X88491.1	NT	Mouse L1M LINE DNA
11075	24426	37884	4.42	2.4E-01	U50014.1	NT	Human mRNA for KIAA0124 gene, partial cds
12075	24016		1.81	2.4E-01	AF027183.1	NT	Homo sapiens sodium/hydroxide cotransporter (SCN5A3) gene, complete cds
12290	25101	38676	6.89	2.4E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (CesA-4) cDNA, complete cds
12816	26936		4.23	2.4E-01	AF101541.2	EST HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
873	13543	26950	1.43	2.4E-01	AA803416.1	EST HUMAN	un70244.1 Soares_NFL_T_GBC ST1 Homo sapiens cDNA, clone IMAGE:1662023.3
873	13528	26974	2.49	2.4E-01	BF579124.1	EST HUMAN	60213242F1 NH1.MG.81 Homo sapiens cDNA, clone IMAGE:4271578.9
1330	14384	27312	12.06	2.4E-01	A209890.1	NT	Homo sapiens KIAA0861 gene (partial), XTS gene and LZTF1.1 gene
1330	14384	27313	12.06	2.4E-01	A209890.1	NT	Homo sapiens KIAA0861 gene (partial), XTS gene and LZTF1.1 gene
1411	14442	27395	1.04	2.4E-01	Y17293.1	NT	Homo sapiens FLJ1 gene, partial
1079	14690		17.09	2.4E-01	AF207703.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mct1p mRNA, complete cds
1918	14839	27915	1.72	2.4E-01	AF251703.1	NT	Zoocys thumoides fructose-1,6-bisphosphatase mRNA, complete cds
2162	15164	28166	1.03	2.4E-01	AF111683.2	NT	Homo sapiens serine peptidase (tentative), subtilisin II gene, complete cds, and unknown genes
2181	15192		1.76	2.4E-01	F46394	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (GAT PROTEASE)
2279	16288	28296	1.94	2.4E-01	A200680.1	NT	Artibeus ferox section 12 of 109 of the complete genome
2407	18412	28416	1.44	2.4E-01	BF00271.1	EST HUMAN	702384X1 NC1_OGAP_Con0 Homo sapiens cDNA, clone IMAGE:3510887.3 similar to SW-PRSD_XENLA
2558	18565	28502	1.15	2.4E-01	Z28534.1	NT	Caenorhabditis elegans 28S PROTEINASE REGULATOR SUBUNIT 6A;
2812	18581	28800	2.12	2.4E-01	AF11831.1	NT	S. pombe nup1 gene
2834	18623	28819	4.86	2.4E-01	AF100154.1	NT	Reovirus sigma3 complete genome
3177	19227		3.63	2.4E-01	U72726.1	NT	Oryza indica transmembrane receptor, leucine-like protein, family member D, and subunit (gag/pol) genes, complete cds
3824	19854	29738	0.67	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 460 of the complete genome

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6614	18950	31685	2.08	2.3E-01	AB02400.1	NT	<i>Mus musculus</i> <i>Islup 1</i> mRNA, complete cds
5176	18171	31018	0.5	2.3E-01	AB02400.1	NT	007313220FT NIH_MGC_31 for Homo sapiens cDNA clone IMAGE-4271547 5'
5259	18283	31134	0.62	2.3E-01	AF167480.1	EST_HUMAN	Homo sapiens mRNA for KIAA1812 protein, partial cds
5487	18507	31413	2.27	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1812 protein, partial cds
6614	18950	31685	2.08	2.3E-01	BC069381.1	EST_HUMAN	P303003 g3 NCL-GAP. Ovine Homo sapiens cDNA clone IMAGE-3470698 3' similar to SWI/GAG-SMSAV
5912	18793	31895	4.75	2.3E-01	BC069381.1	EST_HUMAN	P303003 g3 NCL-GAP. Ovine Homo sapiens cDNA clone IMAGE-3470698 3' similar to SWI/GAG-SMSAV
5946	18817	31911	1.14	2.3E-01	BC069381.1	EST_HUMAN	P303003 g3 NCL-GAP. Ovine Homo sapiens cDNA clone IMAGE-3470698 3' similar to SWI/GAG-SMSAV
5938	19026	32116	3.24	2.3E-01	BC069381.1	NT	SHELL PROTEIN P30, NUCLEOPROTEIN P30.1
6166	19223	32296	1.66	2.3E-01	AF108440.1	EST_HUMAN	C-familial rami gene
6166	19222	32297	1.66	2.3E-01	AF108440.1	EST_HUMAN	Vf8086a concanavalin anti-subunit ribosomal RNA gene
6849	19878	35201	0.75	2.3E-01	AF156038.1	NT	235 RNA (Lactococcus casearius, Genbank, 2866 nt)
7201	20254	35449	4.62	2.3E-01	AF178148.1	EST_HUMAN	nc76712.X1 Barlstedt series HPLR80 Homo sapiens cDNA clone IMAGE-2318449 3' similar to gpX13239
7201	20254	35458	4.62	2.3E-01	AF178148.1	EST_HUMAN	nc76712.X1 Barlstedt series HPLR80 Homo sapiens cDNA clone IMAGE-2318449 3' similar to gpX13239
7697	20751	35898	0.76	2.3E-01	AF100222.1	NT	nc76712.X1 Barlstedt series HPLR80 Homo sapiens cDNA clone IMAGE-2318449 3' similar to gpX13239
7616	20945	34530	0.71	2.3E-01	AF175589.1	NT	nc76712.X1 Barlstedt series HPLR80 Homo sapiens cDNA clone IMAGE-2318449 3' similar to gpX13239
7616	20945	34530	0.71	2.3E-01	AF175589.1	NT	nc76712.X1 Barlstedt series HPLR80 Homo sapiens cDNA clone IMAGE-2318449 3' similar to gpX13239
7619	20748	34632	2.15	2.3E-01	AF176981.1	EST_HUMAN	Oxyphagus cynophylax cytochrome oxidase subunit 1a (cox1a2) mRNA, complete cds nuclear gene for mitochondrial product
7619	20748	34633	2.15	2.3E-01	AF176981.1	EST_HUMAN	Oxyphagus cynophylax cytochrome oxidase subunit 1a (cox1a2) mRNA, complete cds nuclear gene for mitochondrial product
8052	20676	34507	3.54	2.3E-01	AF176981.1	EST_HUMAN	nc76712.X1 Barlstedt series HPLR80 Homo sapiens cDNA clone IMAGE-2318449 3' similar to gpX13239
8057	20676	34296	1.55	2.3E-01	BE048071.1	EST_HUMAN	nc76712.X1 Barlstedt series HPLR80 Homo sapiens cDNA clone IMAGE-2318449 3' similar to gpX13239
8219	21124	34509	2.68	2.3E-01	N80633.1	EST_HUMAN	nc76712.X1 Barlstedt series HPLR80 Homo sapiens cDNA clone IMAGE-2318449 3' similar to gpX13239
8297	21172	34509	0.64	2.3E-01	N80633.1	EST_HUMAN	nc76712.X1 Barlstedt series HPLR80 Homo sapiens cDNA clone IMAGE-2318449 3' similar to gpX13239
9257	21172	34507	0.64	2.3E-01	N80633.1	EST_HUMAN	nc76712.X1 Barlstedt series HPLR80 Homo sapiens cDNA clone IMAGE-2318449 3' similar to gpX13239
8410	21913	34645	0.55	2.3E-01	AF177845.1	NT	Homo sapiens proboscoider alpha cluster (LOC93590), mRNA
8410	21913	34645	0.55	2.3E-01	AF177845.1	NT	Homo sapiens proboscoider alpha cluster (LOC93590), mRNA
8424	21936	34706	0.72	2.3E-01	AF161558.2	NT	Streptomyces coelicolor A3(2) phosphoenolpyruvate carboxylase (ppc) gene, complete cds
8424	21936	34706	0.72	2.3E-01	AF161558.2	NT	Streptomyces coelicolor A3(2) phosphoenolpyruvate carboxylase (ppc) gene, complete cds
9573	21948	34848	1.85	2.3E-01	MB0631.1	NT	Arabidopsis thaliana chromosome 4, contig fragment No. 98
9573	21948	34848	1.85	2.3E-01	MB0631.1	NT	Arabidopsis thaliana chromosome 4, contig fragment No. 98
9532	22260	36924	0.27	2.3E-01	AF163454.1	EST_HUMAN	Oxyphagus cynophylax cytochrome oxidase subunit 1a (cox1a2) mRNA, complete cds
9446	22591	36738	0.69	2.3E-01	AF163454.1	EST_HUMAN	nc76712.X1 Barlstedt series HPLR80 Homo sapiens cDNA clone IMAGE-2318449 3' similar to gpX13239
9583	22659	35982	0.53	2.3E-01	AF1472164.1	EST_HUMAN	ESTB04001 Rhadinovirus/Homo sapiens cDNA 5' end similar to D1 homolog (BB-3503586)

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Table 4

Single Exon Probe Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Exon Signal	Mean Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6483	22369	35983	0.53	2.3E-01	AJ372184.1	EST_HUMAN	EST14961 (Rund domain) Homo sapiens cDNA 8' end, similar to DNA topoisomerase (DB 263538)
10110	23071	36237	0.74	2.3E-01	6379218	EST_HUMAN	Mouse protein phosphatase 3A3 3' UTR, similar to human protein phosphatase 3A3 (P3A3) mRNA
10245	23146	36516	0.61	2.3E-01	SE277893.1	EST_HUMAN	6011971041 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:268730 9'
10301	2318	36852	0.84	2.3E-01	AF024466.1	EST_HUMAN	EST170533 MAGE-10 Homo sapiens cDNA clone IMAGE:268730 9'
10347	23236	36954	1.53	2.3E-01	X62124.1	NT	Homo sapiens influenzae genes for viral replicase-modification system (viral) methyltransferase (EG 211.123) and hemagglutinin (EG 3.3.1.21.4)
10390	23269	36961	0.86	2.3E-01	AF136453.1	EST_HUMAN	FM2-DT00358-281265-207.64 170559 Homo sapiens cDNA
10443	23332	36749	3.13	2.3E-01	BE170260.1	EST_HUMAN	MRQ-H70559-240400-014-011 H70559 Homo sapiens cDNA
10458	23362	36798	2.6	2.3E-01	AJ203291.1	NT	Rizobium leguminosarum p341 genomic DNA for acetylacetylase biosynthesis genes
10623	23883	37236	0.85	2.3E-01	AF201629.1	EST_HUMAN	Marine hepatitis virus strain 2, complete genome
10933	23816	37818	6.03	2.3E-01	BF193577.1	EST_HUMAN	6015401552 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:410262 3'
11453	24359	37819	1.7	2.3E-01	AF004833.1	NT	Mouse muscle tissue factor pathway/inhibitor (TFPI) mRNA, complete cds
11634	24540	39012	2.07	2.3E-01	AJ250186.1	NT	Mouse muscle tissue factor pathway/inhibitor (TFPI) mRNA, complete cds
11634	24540	39013	2.07	2.3E-01	AJ250189.1	NT	Mouse muscle tissue factor pathway/inhibitor (TFPI) mRNA, complete cds
11634	24540	39013	2.07	2.3E-01	AJ250189.1	NT	Mouse muscle tissue factor pathway/inhibitor (TFPI) mRNA, complete cds
11700	24712	38203	3.1	2.3E-01	AJ5002167.2	NT	Chlamydomonas reinhardtii rbcL gene, section 4 of 5 of the complete genome
12008	25041		1.05	2.3E-01	AF176738.1	EST_HUMAN	AV1769736 ADIC-Homo sapiens cDNA clone ADIC/CH01 5'
12250	25148		3.85	2.3E-01	U45026.1	NT	Borrelia burgdorferi 23-03 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
12346	25164		42.5	2.3E-01	T21291.1	EST_HUMAN	HCOE5714 H72916 Homo sapiens cDNA clone HOE44 5'
12516	25615	31474	3.16	2.3E-01	AF130523.1	EST_HUMAN	XG21407.x1 Soares_NFL_T_OBG_51 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR-OIG2175
12562	25616	31370	9.03	2.3E-01	BE64244.1	EST_HUMAN	OIG2175 LY51L OXIDASE-RELATED PROTEIN 2, contains PTRs b2 TAR1 repetitive element
12697	25983		1.91	2.3E-01	BF053319.1	EST_HUMAN	6017029031 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:390989 5'
12645	25321		1.6	2.3E-01	AJ000519.1	NT	6024445091 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4377715 5'
12736	25321		1.6	2.3E-01	AJ000519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12688	25533		1.91	2.3E-01	BF47661.1	EST_HUMAN	Rattus norvegicus mRNA for acid gated ion channel
92	13255	28118	0.78	2.2E-01	AF052100.1	EST_HUMAN	nuc83h12.x1 Luciferase, nerve Homo sapiens cDNA clone IMAGE:398950 3' similar to contains element MEF2B repetitive element
1585	14616	21579	2.48	2.2E-01	AF167600.1	EST_HUMAN	ccr140101 Soares_NFL_T_OBG_51 Homo sapiens cDNA clone IMAGE:1615500 3' similar to TR-OIG2175
2107	13115	28120	2.24	2.2E-01	AF167600.1	EST_HUMAN	TR-OIG2175 LY51L OXIDASE-RELATED PROTEIN 2, contains PTRs b2 TAR1 repetitive element
2428	14928	28430	0.5	2.2E-01	BF077338.1	EST_HUMAN	Homo sapiens PPAR- γ cDNA, contains promoter region
2627	15625	28518	1.34	2.2E-01	BE176238.1	EST_HUMAN	6023690361 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:434966 5'
						EST_HUMAN	6014629261 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:393180 5'

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Probe SEQ ID No.	Exon SEQ ID No.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2027	16026	26019	1.92	2.2E-01	BE10238.1	EST_HUMAN	6014620507.1 NX2_67 Homo sapiens cDNA clone IMAGE:3806190.9
2024	15977	26075	5.51	2.2E-01	BE15926.1	EST_HUMAN	PM2-110352-291259-003-02 HT0353 Homo sapiens cDNA
2024	15977	26076	5.01	2.2E-01	BE15926.1	EST_HUMAN	PM2-110352-291259-003-02 HT0353 Homo sapiens cDNA
2053	16015		2.07	2.2E-01	AF02003.1	NT	Homo sapiens FRAX3 common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 6
3451	16462		3.7	2.2E-01	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 92
3616	16466	20731	0.86	2.2E-01	AL163265.2	NT	Homo sapiens chromosome 21 segment HS21Q05
3654	16513		1.11	2.2E-01	AF165726.1	NT	Xiphophorus maculatus truncated Rax1 retrotransposon reverse transcriptase (RT) pseudogene
4306	17322		1.03	2.2E-01	AF119102.1	NT	Crocephalus melanoscelus UNC-119 (UNC-119) gene, complete cds
4316	17320	30194	6.07	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlx3) and two pore domain (Kcnk9) genes, complete cds
4393	17377	30240	2.5	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase Kinase 1 (MeK1) mRNA, complete cds
4393	17377	30241	2.5	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase Kinase 1 (MeK1) mRNA, complete cds
4465	17476	30334	1.18	2.2E-01	U01307.1	NT	Human scRNA (BC020000) beta pseudogene
4465	17476	30335	1.18	2.2E-01	U01307.1	NT	Human scRNA (BC020000) beta pseudogene
4639	17846		1.00	2.2E-01	U50604.1	NT	Human beta-cytoplasmic actin (ACTBP2) pseudogene
4645	17844	30602	1.72	2.2E-01	AA211216.1	EST_HUMAN	2957036.71 Stragene INT neuron (HS7235) Homo sapiens cDNA clone IMAGE:448958.9
5048	18055	30536	1.05	2.2E-01	U69524.1	NT	Human dystrophin gene
6172	18185		1.2	2.2E-01	U13259.1	NT	Mus musculus insulin gene, exon 3
5283	18269	31117	1.16	2.2E-01	H05048.1	EST_HUMAN	gc2H09.71 Soares fetal liver spleen cDNA clone IMAGE:390001.9 similar to
5402	18354	31224	1.95	2.2E-01	5805974	NT	gc2H14119.1_m01 C060 GLYCOPROTEIN RECURSOR (HUMAN);
5409	18385	31225	1.32	2.2E-01	AL163500.2	NT	Vicia faba protein mitochondrion, complete genome
5591	18018	32138	1.79	2.2E-01	8803002	NT	Homo sapiens chromosome 21 segment HS21C100
5952	18029		3.45	2.2E-01	764000.1	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DAPH2), transcript with nt 166, mRNA
6031	18268	32443	0.76	2.2E-01	U07057.1	NT	Synchocystis sp. PCC2805 complete genome, 1627, 2892720-283869
6231	18285	32444	0.76	2.2E-01	U07057.1	NT	Callus gallus 1-bbox containing protein (Ch-Tex) mRNA, complete cds
7003	20330	33251	0.59	2.2E-01	U503483.1	NT	Homo sapiens gene for lumen, complete cds
7103	20331	33252	0.45	2.2E-01	U503483.1	EST_HUMAN	8002533.31 Osteopontin fetal rat brain 807202 Homo sapiens cDNA clone IMAGE:585666.3
7103	20331	33253	0.45	2.2E-01	U503483.1	EST_HUMAN	8002533.31 Osteopontin fetal rat brain 807202 Homo sapiens cDNA clone IMAGE:585666.3
7372	20336	33563	2.35	2.2E-01	AT176238.1	EST_HUMAN	AF176238.BM1 Homo sapiens cDNA clone BM1A1C08.9
7486	20429	33706	1.36	2.2E-01	AF062798.1	NT	Synchocystis proteomes phosphotriphosphatase synthase (ppsk) and ABC transporter ATP-binding protein (ppsk) genes, complete cds, and unknown genes

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10929	23492	37277	0.86	2.2E-01	AE001803.1	NT
10929	23492	37278	0.89	2.2E-01	AE001803.1	NT
11822	24558	39028	1.48	2.2E-01	AB023053.1	NT
11844	24704	39168	5.40	2.2E-01	U01918.1	NT
11853	25053	37432	3.04	2.2E-01	U01918.1	NT
12253	25104		2.11	2.2E-01	BE070683.1	EST_HUMAN
12352	25025		4.39	2.2E-01	U32071.2	NT
12458	26274	31362	3.01	2.2E-01	AF168845.1	NT
12657	19429	31362	3.01	2.2E-01	AF168845.1	NT
12818	26309	31819	1.36	2.2E-01	U1428873	NT
13042	26301		2.36	2.2E-01	AF054601.1	EST_HUMAN
507	14047	26961	1.36	2.1E-01	AA556289.1	EST_HUMAN
1000	14049	26963	1.18	2.1E-01	AF161804.2	NT
1151	14182		2.88	2.1E-01	AE00214.2	NT
11251	14283	27205	1.16	2.1E-01	6754299	NT
1228	14288	27205	1.18	2.1E-01	6754299	NT
1531	14591	27621	1.32	2.1E-01	AJ248985.1	NT
1830	14681	27627	1.71	2.1E-01	AJ006824.1	EST_HUMAN
2170	15182	29188	2.31	2.1E-01	BF060703.1	EST_HUMAN
2503	15926	29505	1.01	2.1E-01	HT3098.1	EST_HUMAN
2503	15926	29506	1.01	2.1E-01	HT3098.1	EST_HUMAN
2568	15594	29578	0.86	2.1E-01	AF023814.1	NT
2607	18016	28816	2.34	2.1E-01	6812445	NT
2874	19803		7.46	2.1E-01	6813301	NT
4133	17130	30336	1.04	2.1E-01	F11675	SWISSPROT
4138	17130	30337	1.04	2.1E-01	F11675	SWISSPROT
4438	17132		1.11	2.1E-01	AF03304.1	NT
4438	17132		1.11	2.1E-01	AF03304.1	NT
4691	17368	30862	2.34	2.1E-01	AB010273.1	NT

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12230	25524		2.08	2.1E-01	X07524.1	NT	Oncopurin nucleoside transferase DNA, repeat region
12713	13394		1.48	2.1E-01	Z27480.1	NT	180 nucleoside transferase (F58) gene, exons 8, 9 and partial cds
12838	13577		1.27	2.1E-01	BC52740.1	EST_HUMAN	180 nucleoside transferase (F58) gene, exons 8, 9 and partial cds
12839	13577		1.27	2.1E-01	BC52740.1	EST_HUMAN	180 nucleoside transferase (F58) gene, exons 8, 9 and partial cds
1291	13222	31728	1.50	2.0E-01	AB071437.1	EST_HUMAN	180 nucleoside transferase (F58) gene, exons 8, 9 and partial cds
567	18266	26220	1.50	2.0E-01	AB071437.1	EST_HUMAN	180 nucleoside transferase (F58) gene, exons 8, 9 and partial cds
723	13761	28703	2.94	2.0E-01	M77085.1	NT	Human sapiens C53A-18 protein (L1031008) mRNA
836	13851	26828	0.96	2.0E-01	M77085.1	NT	O carboxylate peroxide lyase heavy chain (L1031008) mRNA
836	13851	26828	1.07	2.0E-01	AF070658.1	NT	Mus musculus Major Histocompatibility Locus class II region
1050	14065	27024	0.76	2.0E-01	D92005.1	NT	Synuclein, tp. PC05803 complete genome. T27, 76146-220615
1162	14169	27131	2.90	2.0E-01	AL169213.2	NT	Synuclein, tp. PC05803 complete genome. T27, 76146-220615
1267	14315	27264	1.46	2.0E-01	AJ132665.8	NT	Human sapiens chromosome 21 sequence H8210013
1334	14388	27318	1.46	2.0E-01	AJ132665.8	NT	Human sapiens chromosome 21 sequence H8210013
1470	14810		1.16	2.0E-01	AJ243037.1	EST_HUMAN	Human sapiens ract1 gene
1505	14536	27469	9.31	2.0E-01	4593408	NT	PM1-H1942-291288-402-036 H19422 Homo sapiens cDNA
1574	14604	27604	1.95	2.0E-01	AB007674.1	NT	Human sapiens chromosome 1 specific transcript KIAA0555
1574	14604	27604	1.95	2.0E-01	AF200700.1	NT	Human sapiens chromosome 1 specific transcript KIAA0555
1723	14751	27719	1.33	2.0E-01	U22340.1	NT	Human sapiens chromosome 1 specific transcript KIAA0555
1723	14751	27719	1.33	2.0E-01	U22340.1	NT	Human sapiens chromosome 1 specific transcript KIAA0555
1746	14751		1.65	2.0E-01	AF111170.3	NT	Human brainykinin B1 receptor (brainykinin) gene, complete cds
1782	14808		2.00	2.0E-01	U67625.1	NT	Human sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
2370	15578		1.59	2.0E-01	X67625.1	NT	Human sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
2032	15956		1.05	2.0E-01	AF074690.1	NT	Human sapiens full length insert cDNA THS5A11
3548	16594	29489	0.89	2.0E-01	P46907	SWISSPROT	Human sapiens full length insert cDNA THS5A11
3628	16694		1.15	2.0E-01	AW28005.1	EST_HUMAN	HOMEOBOX PROTEIN GLBP2A3 (HOMEOBOX-LEUCINE ZIPPER PROTEIN) AT18-10 (HD-2IP
3770	16902	29689	0.84	2.0E-01	P34941	EST_HUMAN	PROTEIN AT18-10
4038	17085	29555	0.86	2.0E-01	P34941	EST_HUMAN	PROTEIN AT18-10
4114	17137	30011	0.85	2.0E-01	X63697.1	NT	MEF21 repeat element
4535	17547	30409	0.86	2.0E-01	AJ243491.1	NT	SWISSPROT
4881	17680		0.86	2.0E-01	BC526195.1	EST_HUMAN	SWISSPROT
5154	18147	30602	0.81	2.0E-01	AJ087524.1	EST_HUMAN	SWISSPROT
5154	18147	30602	0.81	2.0E-01	AJ087524.1	EST_HUMAN	SWISSPROT
6170	18162	31010	6.00	2.0E-01	862200	NT	Human sapiens hypodermal protein ASH1 (ASH1) mRNA

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Probe SEQ ID NC.	Exon SEQ ID NC.	ORF SEQ ID NO.	Expression Signal	Mean Similar (Top) HIT ELASTE Value	Top HIT Accession No.	Top HIT Database Source	Top HIT Descriptor
12213	25047		1.44	2.0E-01	P24673	SWISSPROT	NADPH-KINONE OXIDOREDUCTASE CHAIN B
12223	25057	36566	45.86	2.0E-01	A455913.1	EST_HUMAN	HB81241 IQG COMP P4, Homo sapiens cDNA clone IMAGE:104846 similar to gb181105 MYOSIN HEAVY CHAIN, NONMUSCLE TYPE 1 (HUMAN)
12601	26348		1.50	2.0E-01	AF20273.2	NT	Phospholipase liver glucose 6-phosphate-2, dihydrogenase mRNA, partial cds
12672	26773		1.80	2.0E-01	AF20273.1	NT	Homo sapiens ribin-Lm baxem (ribin) mRNA, complete cds
12695	26704	31001	2.96	2.0E-01	AW075297.1	EST_HUMAN	EST1397405 MAGE mesencephalon, MAGN Homo sapiens cDNA
12920	26590	31748	3.46	2.0E-01	A023602.1	EST_HUMAN	ov0810.31 Soares, testis, NHT Homo sapiens cDNA clone IMAGE: 164810.3
12941	26608		15.88	2.0E-01	AF070164.2	NT	Homo sapiens Kufs-binding protein (KUBP) mRNA, partial cds
114	13222		5.83	1.0E-01	7646748	NT	Reticular nervous system hyaluronan receptor nuclear translocator 1 (Atrn), mRNA
372	13406	26374	6.6	1.0E-01	AF004583.1	NT	Homo sapiens p60 cat (ep) gene, wild type allele, 3' region, partial cds
678	13741	20055	1.19	1.0E-01	U52361.2	NT	Homo sapiens lamellipodium protein kinase C-interacting protein mRNA, complete cds
679	13741	20659	1.16	1.0E-01	U52361.2	NT	Homo sapiens lamellipodium protein kinase C-interacting protein mRNA, complete cds
686	13748	22603	4.65	1.0E-01	BE070801.1	EST_HUMAN	RC3-B10502-281100-011-011 B10502 Homo sapiens cDNA
687	13748	28663	6.30	1.0E-01	BE070801.1	EST_HUMAN	RC3-B10502-281100-011-011 B10502 Homo sapiens cDNA
1073	14052		3.84	1.0E-01	7325180	NT	Mus musculus interluciferin 2 receptor, gamma chain (IL29), mRNA
1131	14173	27111	6.97	1.0E-01	AA358813.1	EST_HUMAN	EST167784 fetal lung II Homo sapiens cDNA 8 end
1327	14428	27362	1.72	1.0E-01	AF091262.1	NT	Sorghum bicolor 22 kDa kufin cluster
1455	14487		3.97	1.0E-01	AF164263.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rp-2) gene, complete cds
2404	18405	28412	6.5	1.0E-01	B322833	NT	Homo sapiens hypothetical protein FL10587 (FL10587), mRNA
2865	18071	28514	4.92	1.0E-01	U06066.1	NT	Sigmodon hesperus p53 gene, partial cds
2980	18031		8.17	1.0E-01	J00922.1	NT	Gallus gallus ovalbumin (O) gene, complete cds
3045	18097	28100	0.97	1.0E-01	U25148.1	NT	Rattus norvegicus brush border myosin (BBM) mRNA, partial cds
3441	18462	28080	0.82	1.0E-01	6903005	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
3455	18485	25400	6.50	1.0E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3593	18577	25481	6.96	1.0E-01	R16467.1	EST_HUMAN	Y270711 Soares testis liver spleen INTLS Homo sapiens cDNA clone IMAGE:12847.6
3572	18591	26784	0.76	1.0E-01	AF128407.1	NT	Rattus norvegicus tyrosine-specific deacylase gene, complete cds
4078	17104	25883	4.80	1.0E-01	A030768.1	NT	Schistosoma mansoni paramyosin DNA for cytoplasmic domain heavy chain, complete cds
4171	17102	30064	2.05	1.0E-01	AF124100.1	EST_HUMAN	CAGC103715-27115-04-011 C103715 Homo sapiens cDNA
4231	17247		0.98	1.0E-01	A0301912.1	NT	Minicolumn subunit K1, locus 40 of 220 of the complete chromosome 1
4537	17345	35210	1.72	1.0E-01	BE334563.1	EST_HUMAN	MR1-FN010-320705-05-04-011 FN010 Homo sapiens cDNA
4581	17389	37450	0.76	1.0E-01	AF161463.2	NT	Neurospora crassa DNA transposon 4, coding fragment No. 5
4582	17389	37450	0.81	1.0E-01	AF161463.2	NT	Neurospora crassa DNA transposon 4, coding fragment No. 5
5134	18130		1.22	1.0E-01	AF228642.1	NT	Rattus norvegicus chondroitin receptor, CDR6 mRNA, complete cds

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5768	18970		4.11	1.0E-01 AW139149.1	EST_HUMAN	EST_HUMAN	cdg97.41 NGL CGAP, liver Homo sapiens cDNA clone IMAGE:2619444.3 similar to gb:U73779.1 (NGL)
5841	18972	32028	6.51	1.0E-01 AF12733.1	NT	EST_HUMAN	ACID RECEPTOR, ALDH4.1 (ALDH4)
6033	19115	32441	0.50	1.0E-01 AF19124.1	NT	EST_HUMAN	Homo sapiens DNA polymerase gamma 1 (polg1) gene, exon 1a
6103	19193		2.76	1.0E-01 AL133118.1	EST_HUMAN	EST_HUMAN	Mus musculus Wnt4, protein coding, complete cds
6197	19244		0.34	1.0E-01 AE001296.1	NT	EST_HUMAN	Alu133118.1 NP2824 Homo sapiens cDNA clone NT2824001328.5
6594	19255	32609	0.54	1.0E-01 AF12394.1	EST_HUMAN	EST_HUMAN	Chlamydia trachomatis, section 26 of 87 of the complete genome
6651	19260	32693	0.98	1.0E-01 AW149422.1	EST_HUMAN	EST_HUMAN	cdg98.41 NGL CGAP, liver Homo sapiens cDNA clone IMAGE:2580659.3
7311	19179	31302	1.77	1.0E-01 R43212.1	EST_HUMAN	EST_HUMAN	SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN); y69a12.1 Source: infant brain 1 NB Homo sapiens cDNA clone IMAGE:31003.3 similar to gb:203359.1 ATP repetitive element;
7315	19493	31307	0.57	1.0E-01 X68216.1	NT	EST_HUMAN	P. sativum PS-1A416.5 gene
7341	20337	33902	0.83	1.0E-01 AF034526.1	NT	EST_HUMAN	Homo sapiens tubby like protein 1 (TULP1) gene, exons 6-11
7341	20337	33903	0.83	1.0E-01 AF034526.1	NT	EST_HUMAN	Homo sapiens tubby like protein 1 (TULP1) gene, exons 6-11
7553	20559	33953	0.59	1.0E-01 U73846.1	NT	EST_HUMAN	Drosophila melanogaster testis-specific RNA-binding protein (tsr) mRNA, complete cds
7688	20814	34120	0.54	1.0E-01 U69588.1	NT	EST_HUMAN	Staphylococcus aureus toxic shock syndrome toxin-1 (tsst), enterotoxin (ent), and integrase (int) genes, complete cds
7913	20387	34140	1.13	1.0E-01 U80922.1	NT	EST_HUMAN	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPBP1) gene, complete cds
7998	20988	34166	2.71	1.0E-01 AF07274.1	NT	EST_HUMAN	Zea mays starch branching enzyme 1 (sbe1) gene, complete cds
8595	21469	34538	1.72	1.0E-01 AL161557.2	NT	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 87
9244	22172	35529	13.90	1.0E-01 AB033924.1	NT	EST_HUMAN	Homo sapiens mRNA for NKA1188 protein, partial cds
9500	23458	35790	1.86	1.0E-01 M14588.1	NT	EST_HUMAN	Neurapal cat beta-globin gene mRNA, partial cds
9500	23458	35791	1.86	1.0E-01 M14588.1	NT	EST_HUMAN	Neurapal cat beta-globin gene mRNA, partial cds
10397	23276	36697	0.83	1.0E-01 AA912466.1	EST_HUMAN	EST_HUMAN	cdg910.41 NGL CGAP, PMS1 Homo sapiens cDNA clone IMAGE:1597596.3 similar to contains ALU repetitive element;
10736	23622	37053	0.97	1.0E-01 BE830563.1	EST_HUMAN	EST_HUMAN	ROSE10052-06070-025-402 ET10692 Homo sapiens cDNA
10736	23622	37054	0.97	1.0E-01 BE830563.1	EST_HUMAN	EST_HUMAN	ROSE10052-06070-025-402 ET10692 Homo sapiens cDNA
11088	24020	37461	2	1.0E-01 AL161503.2	NT	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
11088	24020	37462	2	1.0E-01 AL161503.2	NT	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
11105	24121	37597	2.89	1.0E-01 AF223861.1	NT	EST_HUMAN	Homo sapiens calcium channel alpha1 subunit (CACNA1C) gene, exons 7, 48, and partial cds, alternatively spliced
11538	25790	38273	1.35	1.0E-01 AF122233.1	NT	EST_HUMAN	Homo sapiens arabinoside channel 1 mRNA, complete cds
12147	26392	39058	2.14	1.0E-01 AC24241.1	NT	EST_HUMAN	Homo sapiens perlecan (E-H1) complex gene, exons 3 to 5
12169	26593	39300	1.39	1.0E-01 J07344.1	NT	EST_HUMAN	Influenza A/Guangdong/2/97/2 nucleoprotein (seg 3) gene, 5 and

Table 4

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12912	26495		20.38	1.7E-01	R24094.1	EST_HUMAN	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:133027 5'
12911	26514		2.71	1.7E-01	Y11141.1	NT	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
389	13068	26568	2.03	1.7E-01	U53676.1	EST_HUMAN	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
831	13856	26824	2.18	1.7E-01	U53676.1	EST_HUMAN	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
1426	14120	27068	0.92	1.7E-01	A23616.0	SWISSPROT	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
1035	14129	27067	0.92	1.7E-01	A23616.0	SWISSPROT	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
1839	14852	27844	0.92	1.7E-01	A161573.2	NT	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
1998	19916		2.77	1.7E-01	AF250561.1	NT	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
2902	19598	29855	2.06	1.7E-01	AF000716.1	NT	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
2502	19599	29859	2.06	1.7E-01	AF000716.1	NT	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
2909	19021	29919	1.83	1.7E-01	A433805.1	EST_HUMAN	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
3040	19032	29994	1.2	1.7E-01	AJ238736.1	NT	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
3040	19032	29995	1.2	1.7E-01	AJ238736.1	NT	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
3152	19202	29993	2.18	1.7E-01	AJ238736.1	NT	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
3422	19483	29970	0.78	1.7E-01	NS5703.1	EST_HUMAN	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
3907	19645	29445	2.08	1.7E-01	AJ269095.1	NT	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
3972	19705	29697	1.11	1.7E-01	AJ224877.1	NT	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
3992	19725		1.11	1.7E-01	AJ224877.1	NT	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
4015	17042	29632	6.06	1.7E-01	AJ253377.1	NT	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
4675	17050		1.86	1.7E-01	X53336.1	NT	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
4933	17661	30869	1.75	1.7E-01	A024788.1	EST_HUMAN	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
5298	18282	31132	1.57	1.7E-01	X17021.1	NT	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
5298	18282	31133	1.57	1.7E-01	X17021.1	NT	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
5313	18297	31150	0.7	1.7E-01	B030010.1	EST_HUMAN	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'
5503	18999	31547	1.8	1.7E-01	A447698.1	EST_HUMAN	Human liver Nucleic Acid Phosphate (NAP) Homo sapiens cDNA clone IMAGE:351579 5'

Table 4
Single Exon Probes Expressed in Adult Liver

Probe Seq ID NO.	Exon Seq ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5503	18699	31948	1.9	1.7E-01	AA47069.1	EST_HUMAN	pc3ac2.1 NCI C639. C639 Homo sapiens cDNA clone IMAGE:681096.3 similar to gp.M1786.5US
5787	18699	31957	0.75	1.7E-01	AF16599.1	NT	ACD10. RHO-SMALL PROTEIN P1 (HUMAN)
6886	19027	32610	15.24	1.7E-01	HP2118.1	EST_HUMAN	Birds a pathogen interstitial cilia protein, SPK3 (Gp33) gene, complete cds
9015	19059	32891	0.46	1.7E-01	AJ253270.1	NT	yo2y6.1 T. Soares fetal liver cDNA N175 Homo sapiens cDNA clone IMAGE:213658.3
6660	19689	32891	0.69	1.7E-01	AJ370970.1	EST_HUMAN	Rickettsia prowazekii strain Madrid E. complete genomic sequence segment 114
6660	19689	32892	0.69	1.7E-01	AJ370970.1	EST_HUMAN	b23n1.1 T. Soares fetal liver N1419W Homo sapiens cDNA clone IMAGE:2045492.3
7172	18444	31513	0.91	1.7E-01	BC202563.1	EST_HUMAN	b23n1.1 T. Soares fetal liver N1419W Homo sapiens cDNA clone IMAGE:2045492.3
7206	20206		2.1	1.7E-01	AF266502.3	NT	80094-06711 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960248.3
7944	20340		0.63	1.7E-01	202310.1	NT	Mesocricetus auratus viduolus precursor (OV1) gene, complete cds
7869	20525	33514	1.49	1.7E-01	AP004022.1	NT	Homo sapiens HFE gene
7877	20611	33510	10.98	1.7E-01	BE374179.1	EST_HUMAN	Echerichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7900	20826	34130	1.25	1.7E-01	PI1774	SWISSPROT	01569022F NIH_MGC_21 Homo sapiens cDNA clone IMAGE:334394.5
7918	25679	34144	0.68	1.7E-01	201095	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN 11.65 (HPLF PROTEIN)
6341	21240	34380	0.41	1.7E-01	BF528962.1	EST_HUMAN	COLLAGEN ALPHA 3(V) CHAIN PRECURSOR
6341	21246	34381	0.41	1.7E-01	BF528962.1	EST_HUMAN	O12-BN047-020600-384-d08 BN047 Homo sapiens cDNA
6367	21271	34605	0.44	1.7E-01	AL114856.1	NT	O12-BN047-020600-384-d08 BN047 Homo sapiens cDNA
6445	21375	34715	1.47	1.7E-01	AF000573.1	NT	Bodycic cDNA strain T4 cDNA library under conditions of nitrogen deprivation
6541	21472	34813	0.64	1.7E-01	AF165099.1	NT	Homo sapiens hemoglobin 1,2-dioxygenase gene, complete cds
6853	21783	35130	0.01	1.7E-01	77047429	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (lccD) gene, complete cds
9256	22163	35559	0.54	1.7E-01	AW002873.1	EST_HUMAN	Homo sapiens cleavage and polyadenylation specificity factor 3, 735D subunit (CPSF3), mRNA
9287	22215	35573	2.31	1.7E-01	DD0384.1	NT	RQ2-BN0032-120200-011-g10 BN0032 Homo sapiens cDNA
9403	22531	35693	1	1.7E-01	AF17413.1	NT	Har (SHR strain) SV1 gene
9403	22531	35694	1	1.7E-01	AF17413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
9540	22476	35654	0.98	1.7E-01	RT7002.1	EST_HUMAN	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
10116	23009	36003	10.51	1.7E-01	AF001505.1	NT	yo2y6.1 T. Soares placenta N107P Homo sapiens cDNA clone IMAGE:142422.5
10220	23111	36512	0.54	1.7E-01	AW07455.1	EST_HUMAN	Radial hirsuties genomic DNA, section 214
10220	23111	36513	0.54	1.7E-01	AW07455.1	EST_HUMAN	Radial hirsuties genomic DNA, section 214
10237	23728	36531	2.58	1.7E-01	U10268.1	NT	EST138504 IMAGE mesopneustes, MANGO Homo sapiens cDNA
10324	23213	36625	0.92	1.7E-01	AJ251749.1	NT	Human class IV alcohol dehydrogenase (ADH4) gene, exon 3
10728	23614		2.47	1.7E-01	AL103264.2	NT	Drosophila melanogaster mRNA for active protease inhibitor (serpin-4), (sp-8 gene)
10880	23766	37190	1.28	1.7E-01	11427203	NT	Homo sapiens chromosome 21 segment RS21C08+
							Homo sapiens solan calvar family 7 (calcine arthric acid transporter, y4 system), member 2 (SLC7A2), mRNA

Single Exon Probes Expressed in Adult Liver
Table 4

Probe SEQ ID NO:	Exon SEQ ID NO:	ORT SEQ ID NO:	Expression Signal	Most Similar (Top) HA BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10891	22766	37161	1.66	1.7E-01	AA220724	EST_HUMAN	h99047.1 NCL CGAP. Cdc Homo sapiens cDNA clone IMAGE:142922 2' similar to gbL20801
11123	24053	37160	7.93	1.7E-01	BE250943.1	EST_HUMAN	TRANSFORMING PROTEIN RHOA (HUMAN);
11124	24108	37161	2.43	1.7E-01	AA314671	EST_HUMAN	9712855.DT NH M22: 41 Homo sapiens cDNA clone IMAGE:351358 5'
11503	24461	37924	6.17	1.7E-01	AA314671	EST_HUMAN	475043.1 NCL CGAP. CDS1 Homo sapiens cDNA clone IMAGE:142924 3'
11533	24461	37925	9.7	1.7E-01	7033000	NT	Max intracellular adenomatous polyposis coli binding protein Ect (Ect) mRNA
11836	24842	38016	2.35	1.7E-01	Y05391.1	EST_HUMAN	Max intracellular adenomatous polyposis coli binding protein Ect (Ect) mRNA
11814	24735	38228	2.11	1.7E-01	AA485378.1	EST_HUMAN	S pombe pcd1+ gene
12134	24075		1.42	1.7E-01	P16272	SWISSPROT	AMP NUCLEOSIDASE
12196	25002	38503	1.49	1.7E-01	P39389	SWISSPROT	AMP NUCLEOSIDASE
12196	25002	38504	1.49	1.7E-01	P65989	SWISSPROT	IGG RECEPTOR FORN LARGE SUBUNIT P51 PRECURSOR (FCRN) (NEONATAL FC RECEPTOR)
12235	25004	39566	3.57	1.7E-01	11419157	NT	IGG RECEPTOR FORN LARGE SUBUNIT P51 PRECURSOR (FCRN) (NEONATAL FC RECEPTOR)
12897	25737	31783	1.47	1.7E-01	AB24404.1	EST_HUMAN	IGG RECEPTOR FORN LARGE SUBUNIT P51 PRECURSOR (FCRN) (NEONATAL FC RECEPTOR)
12898	25477	31783	8.17	1.7E-01	U01317.1	NT	Homo sapiens cDNA clone IMAGE:19509 5'
13007	29550		1.48	1.7E-01	AJ017763.1	NT	h99047.1 NCL CGAP. Cdc1 Homo sapiens cDNA clone IMAGE:1014839 3'
130	13234	28151	1.48	1.6E-01	AF217832.1	NT	h99047.1 NCL CGAP. Cdc1 Homo sapiens cDNA clone IMAGE:1014839 3'
703	10340	29576	1.14	1.6E-01	FA1467.1	EST_HUMAN	h99047.1 NCL CGAP. Cdc1 Homo sapiens cDNA clone IMAGE:1014839 3'
1623	14554	27516	1.52	1.6E-01	AA45893.1	EST_HUMAN	Homo sapiens hominoid protein OTD2 gene, complete cds
1544	14574	27534	3.28	1.6E-01	AF295117.1	NT	h99047.1 NCL CGAP. Cdc1 Homo sapiens cDNA clone IMAGE:1014839 3'
1639	14980	27838	1.56	1.6E-01	P22093	SWISSPROT	ACXN14 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2001	15019		1.11	1.6E-01	U10334.1	NT	h99047.1 NCL CGAP. Cdc1 Homo sapiens cDNA clone IMAGE:1014839 3'
2408	15023	29416	1.13	1.6E-01	XA4232.1	NT	h99047.1 NCL CGAP. Cdc1 Homo sapiens cDNA clone IMAGE:1014839 3'
2510	15017	29521	1.85	1.6E-01	AB357759.1	NT	h99047.1 NCL CGAP. Cdc1 Homo sapiens cDNA clone IMAGE:1014839 3'
2534	15067	29890	10.48	1.6E-01	AF185086.1	NT	h99047.1 NCL CGAP. Cdc1 Homo sapiens cDNA clone IMAGE:1014839 3'
2934	15387	29587	10.48	1.6E-01	AF185086.1	NT	h99047.1 NCL CGAP. Cdc1 Homo sapiens cDNA clone IMAGE:1014839 3'
3408	16440	28537	0.98	1.6E-01	AF165049.1	NT	h99047.1 NCL CGAP. Cdc1 Homo sapiens cDNA clone IMAGE:1014839 3'
3657	15316		1.22	1.6E-01	U10334.1	NT	h99047.1 NCL CGAP. Cdc1 Homo sapiens cDNA clone IMAGE:1014839 3'
3700	16732	29322	1.11	1.6E-01	AJ003165.1	NT	h99047.1 NCL CGAP. Cdc1 Homo sapiens cDNA clone IMAGE:1014839 3'
3700	16732	29323	1.11	1.6E-01	AJ003165.1	NT	h99047.1 NCL CGAP. Cdc1 Homo sapiens cDNA clone IMAGE:1014839 3'
3940	16859	28763	1.18	1.6E-01	AE003663.1	NT	h99047.1 NCL CGAP. Cdc1 Homo sapiens cDNA clone IMAGE:1014839 3'
4086	17111		2.88	1.2E-01	AE004143.1	NT	h99047.1 NCL CGAP. Cdc1 Homo sapiens cDNA clone IMAGE:1014839 3'

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4117	17140	30013	0.98	1.05-01	AF044693.1	NT	C-Hindes fasciculus tyrosine oxidase (hnt) gene, complete cds
4396	17408		1.11	1.05-01	U02771.1	NT	Lymnaea stagnalis octopamine receptor type 1 (ym o1) mRNA, complete cds
4396	17447	30037	15.13	1.05-01	AF179880.1	NT	Homo sapiens apelin gene, complete cds
4697	17475		3.52	1.05-01	AY06301.1	EST_HUMAN	EST130077 IMAGE resources, MGC Homo sapiens cDNA
4675	17683		5.22	1.05-01	0753319	NT	Mus musculus clasperin, subunit 3 (gamma) (C25), mRNA
4616	17617	30084	0.74	1.05-01	AF100154.1	NT	Rattus norvegicus lysine aminotransferase/glycylalanine transaminase K (kat) gene, complete cds
4616	17617	30685	0.74	1.05-01	AF100154.1	NT	Rattus norvegicus lysine aminotransferase/glycylalanine transaminase K (kat) gene, complete cds
5035	18032	30893	0.74	1.05-01	PA0651	SWISSPROT	MICROGLULAR LINKER HISTONE POLYPROTEIN (VIC H) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA, AND GAMMA]
5099	18008	30908	1.08	1.05-01	AA086438.1	EST_HUMAN	284kbp at Sitragene cdon (687204) Homo sapiens cDNA clone IMAGE:518391 3' similar to TR221865
5099	18003	30933	1.39	1.05-01	A.000356.1	NT	E22165 38,855 BP SEGMENT OF CHROMOSOME XIV :
5099	18003	30934	1.39	1.05-01	A.000356.1	NT	Lycopodium esculentum Root fragment 2, satellite region
5161	18154	31001	0.85	1.05-01	BE016707.1	EST_HUMAN	3553108.1 NH1_MGC_10 Homo sapiens cDNA clone IMAGE:3040028 8' similar to gi4561716
5162	18184	31027	1.02	1.05-01	AI017141.1	EST_HUMAN	TRYPTOPHANYL-TRNA SYNTHETASE (HUMAN); gp59957 Mus musculus (MOUSE);
5572	18550	31529	0.86	1.05-01	L40603.1	NT	orf4205.x1 Scores: Jaccard, NHT Homo sapiens cDNA clone IMAGE:1593208 3'
5712	18785	31715	2.52	1.05-01	AW197498.1	EST_HUMAN	Plasmidom (sequencing strain C25) variant-specific surface protein (var-1) gene, complete cds
5712	18785	31716	2.52	1.05-01	AW197498.1	EST_HUMAN	YHPOTHEICAL, 127.6 KD PROTEIN :
5724	18785	31716	2.52	1.05-01	AW197498.1	EST_HUMAN	YHPOTHEICAL, 127.6 KD PROTEIN :
5724	18787	31888	2.17	1.05-01	AF034716.1	NT	Rattus norvegicus COAT1 enhancer binding protein apelin (ebpap) gene, complete cds
5201	19372	32477	0.86	1.05-01	BE028003.1	EST_HUMAN	RC3-BN0034-310800-113-H01 BN0034 Homo sapiens cDNA
6505	19549	32726	0.85	1.05-01	BF183564.1	EST_HUMAN	69180972RT NH1_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'
6505	19549	32726	0.85	1.05-01	BF183564.1	EST_HUMAN	69180972RT NH1_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'
6598	19732	32832	1.77	1.05-01	AI167089.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6598	19732	32833	1.77	1.05-01	AI167089.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7050	20293	33505	0.57	1.05-01	AB438047.1	EST_HUMAN	250804.1 Source: Jaccard, NHT Homo sapiens cDNA clone IMAGE:726511 5
7110	20314	33577	0.77	1.05-01	AB438047.1	EST_HUMAN	Homo sapiens mRNA for TMA150 protein, partial cds
7162	20289		0.51	1.05-01	AF065600.1	EST_HUMAN	69213652RT NH1_MGC_45 Homo sapiens cDNA clone IMAGE:4301041 5
7300	19489	31291	4.28	1.05-01	AY125215.1	EST_HUMAN	U1H-B2-agp-b0-01.1 NCL COOP-3000 Homo sapiens cDNA clone IMAGE:2724118 3'
7680	23514	33513	0.57	1.05-01	Z49632.1	NT	S. cerevisiae Chromosome X reeling factor ORF130w

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NC:	Exon SEQ ID NC:	ORF SEQ ID NC:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description	
8260	21155	34469	1.28	1.6E-01	AW240593.1	EST_HUMAN	2822248 Spine NIH_MGC_7 Homo sapiens cDNA clone IMAGE282248.8	
8266	21220	34596	0.95	1.6E-01	075327	NT	Mus musculus Cdc42-dependent activator protein for secretion (cdap3), mRNA	
8311	21215	34518	0.48	1.6E-01	AU195325.1	EST_HUMAN	AU195325 PLACE1 Homo sapiens cDNA clone PLACE101468.9	
8450	21382	34724	1.86	1.6E-01	463494.1	NT	Goat gamma interferon receptor gamma, partial exon	
8603	21834		0.75	1.6E-01	BE244087.1	EST_HUMAN	TCSAP0007 Pediatric plexus sci cells, parathyroid carcinoma cDNA clone TCSAP0007	
8906	21627	34671	0.75	1.6E-01	U38243.1	NT	Bacteroides vulgatus beta-lactamase (cblA), gene, complete cds and mobilization protein (mobA), gene, complete cds	
9191	22319	35075	1.12	1.6E-01	2502118.1	NT	Bacillus subtilis complete genome (section 16 of 21), from 269771 to 3213413	
9305	22313	35075	1.03	1.6E-01	R13073.1	EST_HUMAN	y69608.1 Sources Infant brain IN18 Homo sapiens cDNA clone IMAGE23875.8	
9488	22416		0.78	1.6E-01	136961.1	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds	
9528	22450	35813	2.14	1.6E-01	246501.1	NT	S cerevisiae chromosome X reading frame ORF Y.R0011w	
9555	22581		0.77	1.6E-01	AF111167.2	NT	Homo sapiens jmn demethylase protein gene, partial cds; cda gene, complete cds; and unknown gene	
10177	22098		2.24	1.6E-01	BF373771.1	EST_HUMAN	RC3-ST10200-041199-0111 NOT ST10200 Homo sapiens cDNA	
10179	22070	35469	2.25	1.6E-01	245601.1	NT	S cerevisiae chromosome X reading frame ORF Y.R0011w	
10213	23104		1.17	1.6E-01	BE155054.1	EST_HUMAN	PM2-210353-270100-004-11 HT0353 Homo sapiens cDNA	
11100	24031	37476	3.05	1.6E-01	AW850583.1	EST_HUMAN	IL3-OT0220-111689-028-001 OT0220 Homo sapiens cDNA	
11434	24350	37769	8.89	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)	
11439	24355	37767	8.89	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)	
11439	24355	37813	1.52	1.6E-01	BE756548.1	EST_HUMAN	0071407507 NIH_MGC_18 Homo sapiens cDNA clone IMAGE319103.9	
11555	24454		3.85	1.6E-01	AF100064.1	NT	Pseudomonas aeruginosa calcium-dependent protein kinase-3 (cdpk3) gene, complete cds	
11847	24697	38168	8.05	1.6E-01	6971652	NT	Mus musculus aspartyl-methylated protein complex ATP-1, beta 1 subunit (Atp1b1), mRNA	
12086	24627	39431	2.17	1.6E-01	N07471.1	NT	Human small polypeptide circular DNA (Hspc64)	
12130	24971		39432	2.17	1.6E-01	BT82727.1	EST_HUMAN	692039466F NC1 GCAP_Braf67 Homo sapiens cDNA clone IMAGE4177073.9
12355	25145	38169	5.34	1.6E-01	AY176565.1	EST_HUMAN	AY176565 GCG Homo sapiens cDNA clone GCG50407.5	
12654	25315	38169	1.98	1.6E-01	L14603.1	NT	Rat convertase PLCB mRNA, 5' end	
12691	25332		1.07	1.6E-01	AW850771.1	EST_HUMAN	RC-H110074-120260-01-2001-1 L110074 Homo sapiens cDNA	
12754	25718		9.25	1.6E-01	AB94510.1	NT	Osmotic stressor K3 mRNA for cell haemoglobin synthesis, complete cds	
13003	25490		2.43	1.6E-01	AQ024981.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds	
13884	25543		4.75	1.6E-01	AF287344.1	NT	Fudanovir variant Q19426 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product	
13900	25552	31756	2.07	1.6E-01	9505622	NT	Rattus norvegicus chondroblastin sulfite proteoglycan 5 (nucrespi5) (Cnsp5), mRNA	

Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
297	13302	29277	1.36	1.5E-01	BE710392.1	EST_HUMAN	U3-H10519-040700-197506 H10519 Homo sapiens cDNA
298	13302	29278	1.36	1.5E-01	BE710392.1	EST_HUMAN	U3-H10519-040700-197506 H10519 Homo sapiens cDNA
299	13305	29279	2.26	1.5E-01	AV171692.1	EST_HUMAN	AV171692 DCA Homo sapiens cDNA clone DCA4490.5
300	13305	29280	1.13	1.5E-01	AL163294.2	NT	Homo sapiens chromosome 21 segment HSF103B4
301	14101	27059	2.41	1.5E-01	AJ009724.1	NT	Cytidine cardo mRNA for EGGS32 myosin heavy chain, 3U7R
1124	14101	27103	1.33	1.5E-01	AJ009724.1	NT	Homo sapiens cardiac SLC22A2 gene for organic cation transporter (OCT2), exon 1
1140	14162	17103	1.54	1.5E-01	136125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5 and
1244	14290	27222	0.86	1.5E-01	AW166518.1	EST_HUMAN	w3&11x1 NCI CGAP N811 Homo sapiens cDNA clone IMAGE:269005 3
1322	14335	27251	2.86	1.5E-01	1226533.1	NT	Human gene for dihydrodipicolimide succinylamylsuccinate, complete cds (exon 1-15)
1302	14335	27262	2.86	1.5E-01	1226533.1	NT	Human gene for dihydrodipicolimide succinylamylsuccinate, complete cds (exon 1-15)
1500	14831	27466	1.54	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mak31) mRNA, complete cds
2656	16008		1.21	1.5E-01	AW672516.1	EST_HUMAN	w56402.22 NCI CGAP P401 Homo sapiens cDNA clone IMAGE:2831078 3 similar to gb.X56072_m1
3032	16103	29029	4.76	1.5E-01	NM11441.1	NT	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);
3100	16151	29047	0.83	1.5E-01	U78957	SWISSPROT	Box taurine factor V variant 2 (factor V) (HUMAN), complete cds
3401	16443	29050	5.96	1.5E-01	AA833046.1	EST_HUMAN	NADH:UBIQUINONE OXIDOREDUCTASE CHAIN 4
3426	16467	29076	0.79	1.5E-01	122104.1	NT	RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN);
3426	16467	29076	0.79	1.5E-01	122104.1	NT	L. taguensis mRNA for G protein-coupled receptor
3485	16527	29426	1.01	1.5E-01	AW612237.1	EST_HUMAN	h29002.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2690059 3 similar to contains element
3819	16849	29733	2.52	1.5E-01	U05964.1	NT	MEF10 repetitive element
3835	16864	29747	0.77	1.5E-01	71048358	NT	Mus musculus CR/Swires glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3935	16903	29846	2.77	1.5E-01	AW056933.1	EST_HUMAN	Homo sapiens pyruvate dehydrogenase E1alpha, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
4134	17155	30943	0.95	1.5E-01	AW056933.1	EST_HUMAN	h10063.x1 Swainc_NF1_7_G0C_S1 Homo sapiens cDNA clone IMAGE:2641411 3
4196	17208	30073	0.72	1.5E-01	212526.1	NT	RC211014b-2110105a-012-c09 H10140 Homo sapiens cDNA
4273	17283	30159	12.39	1.5E-01	AL163264.2	NT	6 alpha mitochondrial DNA for ORF105
4338	17350	30700	1.6	1.5E-01	AF083765.1	EST_HUMAN	Homo sapiens chromosome 21 segment HSF103B4
4524	19152	28746	2.4	1.5E-01	196391.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:269222 6
4633	19362	30770	1.13	1.5E-01	196391.1	EST_HUMAN	020523256F NH11055 31 Homo sapiens cDNA clone IMAGE:234763 5
4633	19362	30770	1.13	1.5E-01	196391.1	EST_HUMAN	C96-H10505-260200-245-H10 H10505 Homo sapiens cDNA
4633	19362	30770	1.13	1.5E-01	196391.1	EST_HUMAN	C96-H10505-260200-245-H10 H10505 Homo sapiens cDNA
5120	18117	30656	2.4	1.5E-01	AL161590.2	NT	Ch4c-11T555c-260200-245-H10 H10505 Homo sapiens cDNA
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20

Table 4

Single Exon Probes Expressed in Adult Liver

Probs SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) HT BLAST E Value	Top HT Accession	Top HT Database Source	Top HT Description
5457	18519	31244	2.14	1.5E-01	P07099	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5458	18548	31388	0.72	1.5E-01	AF259582.1	NT	Canine crocoiditis MHO does ill beta chain (nollid) gene, complete cds
5511	18580		5.58	1.5E-01	P16199	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX 3 STEROID-BINDING PROTEIN) (ABP)
5728	18891	31884	4.9	1.5E-01	AF195079.1	EST_HUMAN	U3-CT219-160200-004-P04 CT219 Homo sapiens cDNA
5771	18944	31946	6.98	1.5E-01	U06018.1	NT	Ms musculus Transforming growth factor alpha (TGFa) mRNA, complete cds
5771	18944	31947	6.98	1.5E-01	U06018.1	NT	Ms musculus Transforming growth factor alpha (TGFa) mRNA, complete cds
6127	19198	32321	0.57	1.5E-01	4602810	NT	Human sperin sodium channel, voltage-gated, type IV, alpha polypeptide (SCNA) mRNA
6287	19291	32450	1.08	1.5E-01	07750559	NT	Ms musculus DNA methyltransferase 2 (Dnmt2) mRNA
6337	19291	32451	1.08	1.5E-01	07750559	NT	Ms musculus DNA methyltransferase 2 (Dnmt2) mRNA
6738	19320	32495	2.15	1.5E-01	U276055.1	EST_HUMAN	Ms musculus genomic fragment 1, 279 kb, chromosome 7
6836	19483	32658	3.03	1.5E-01	BE72756.1	EST_HUMAN	NT 584322P1 NH1 DKC2_20 Homo sapiens cDNA clone IMAGE:383381 5'
9406			2.09	1.6E-01	4603300	NT	Homo sapiens RAD4 (S cerevisiae) like (RAD54) mRNA
9801	18642	32624	1.74	1.5E-01	AF14907.1	NT	Influenza B virus (Nanchang/4809/94) NB protein, gene, complete cds; and neuraminidase gene, partial cds
9785	20554	33024	1.77	1.5E-01	RE01036.1	NT	Archaeoglobus fulgidus strain 03 of 172 of the complete genome
9810	19448	33033	5.41	1.5E-01	11417298	NT	Homo sapiens chromosome 1 open reading frame 3 (CDKLR3) mRNA
8621	18854	33046	1.87	1.5E-01	P48568	SWISSPROT	GLUTAMATE-AMINO ACID TRANSFERASE (GLUTAMATE-AMINO ACID TRANSFERASE)
9832	19502	33177	2.03	1.5E-01	U238452	SWISSPROT	AMINOGLUCONAMIN OXIDASE (AMINOGLUCONAMIN OXIDASE)
9851	20065	33258	1.80	1.5E-01	AF14760.1	EST_HUMAN	Human CYP19C1 CYP19C1 Homo sapiens cDNA clone IMAGE:1241871 5'
9851	20067	33270	1.80	1.5E-01	AF14760.1	EST_HUMAN	Human CYP19C1 CYP19C1 Homo sapiens cDNA clone IMAGE:1241871 5'
7316	19487	31310	6.54	1.5E-01	AF049268.1	EST_HUMAN	Human CYP19C1 CYP19C1 Homo sapiens cDNA clone IMAGE:3077409 5'
7383	20590		0.71	1.5E-01	AA811546.1	EST_HUMAN	Human CYP19C1 CYP19C1 Homo sapiens cDNA clone IMAGE:3077409 5'
7693	20519		0.21	1.5E-01	AF210942.1	EST_HUMAN	Human CYP19C1 CYP19C1 Homo sapiens cDNA clone IMAGE:3077409 5'
7748	20519		0.21	1.5E-01	AF210942.1	EST_HUMAN	Human CYP19C1 CYP19C1 Homo sapiens cDNA clone IMAGE:3077409 5'
7748	20519		0.21	1.5E-01	AF210942.1	EST_HUMAN	Human CYP19C1 CYP19C1 Homo sapiens cDNA clone IMAGE:3077409 5'
8030	20548	34283	1	1.5E-01	AF090073.1	NT	Human CYP19C1 CYP19C1 Homo sapiens cDNA clone IMAGE:3077409 5'
8030	20548	34283	1	1.5E-01	AF090073.1	NT	Human CYP19C1 CYP19C1 Homo sapiens cDNA clone IMAGE:3077409 5'
8042	20590	34270	1.48	1.5E-01	AF090081.1	EST_HUMAN	Human CYP19C1 CYP19C1 Homo sapiens cDNA clone IMAGE:3077409 5'
8042	20590	34271	1.48	1.5E-01	AF090081.1	EST_HUMAN	Human CYP19C1 CYP19C1 Homo sapiens cDNA clone IMAGE:3077409 5'
8205	21157	34442	0.64	1.5E-01	U46601.1	EST_HUMAN	Human CYP19C1 CYP19C1 Homo sapiens cDNA clone IMAGE:3077409 5'
8530	21557	34604	0.41	1.5E-01	P21993	SWISSPROT	MEIOCYTOS RECEPTOR (MEIOCYTOS RECEPTOR) (66 KD PROTECTIVE TUMOR SURFACE ANTIGEN)

Table 4

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) HI BLAST E Value	Top HI Accession No.	Top HI Database Source	Top HI Description
8708	21728	35077	1.24	1.5E-011	AA005317.1	EST - HUMAN	0050512.1 NCI_QGAP_K410 Homo sapiens cDNA clone IMAGE:173030 3' similar to gb:M20002
8887	21817		0.57	1.5E-011	R3834769.1	EST - HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
8670	21600	10.05	1.5E-011	1.0E-004	U10800.1	EST - HUMAN	RG1105(25)P127 Homo sapiens cDNA clone IMAGE:3912604 5'
9002	21631	35287	1.78	1.5E-011	U27835.1	NT	C18080 Oncoferritin human acute phase cDNA clone IMAGE:2200 5'
9185	22083	35441	1.73	1.5E-011	U28476.1	NT	Pyruvatekinase oligos growth hormone (GH) mRNA, complete cds
9174	22052	35587	1.02	1.5E-011	U24348	SWISSPROT	WNT-10A PROTEIN PRECURSOR
9359	22324	35957	1.52	1.5E-011	405197.12	EST - HUMAN	Homo sapiens adenylylated protein complex 1, beta 1 subunit (ADP1B7), mRNA
8549	22476	35946	2.57	1.5E-011	N74288.1	EST - HUMAN	z159d06.6 1 Scores field liver spleen NFIL3 Homo sapiens cDNA clone IMAGE:206886 3' similar to
9755	22850	36043	1.22	1.5E-011	R78595468.1	EST - HUMAN	PIR-S34443.3 R44443 R4023 protein homolog - human;
9742	22868		2.43	1.5E-011	X754916.1	EST - HUMAN	GY3000433 Human F-Postate Differentia Oligonucleotide Homo sapiens cDNA
9369	23133	34678	7.35	1.5E-011	U00456.1	NT	AP247519 TP Homo sapiens cDNA clone IMAGE:17418 5'
10332	23221	36656	0.70	1.5E-011	M77144.1	NT	Aspergillus terreus 18S rRNA, partial cds
10422	23321	36738	7.83	1.5E-011	X5007070.1	NT	Human type 11.3-like hydroxyacid dehydrogenase 1, delta-1, 4-delta isomerase gene, complete cds
10432	23321	36739	7.83	1.5E-011	X5007070.1	NT	Aspergillus californicus embryonary phase D rRNA, complete cds
10432	23321	36739	7.83	1.5E-011	X5007070.1	NT	Aspergillus californicus embryonary phase D rRNA, complete cds
10569	23565	37014	2.51	1.5E-011	S38952.1	NT	P. luteolus rRNA for mitchr beta subunit
10708	23584	37113	3.32	1.5E-011	A1814046.1	EST - HUMAN	w45312.x1 NCI_QGAP_P422 Homo sapiens cDNA clone IMAGE:2419173 3' similar to gb:M26508 BETA
10708	23584	37114	3.32	1.5E-011	A1814046.1	EST - HUMAN	GALACTOGLUCOSE-RELATED PROTEIN PRECURSOR (HUMAN);
10375	23761	37188	1.32	1.5E-011	U00493.1	EST - HUMAN	w45312.x1 NCI_QGAP_P422 Homo sapiens cDNA clone IMAGE:2419173 3' similar to gb:M26508 BETA
11018	23902	37340	1.49	1.5E-011	A0111984.1	NT	GALACTOGLUCOSE-RELATED PROTEIN PRECURSOR (HUMAN);
11018	23902	37341	1.49	1.5E-011	A0111984.1	NT	Diemo terio transcription factor Paeve (Paeo) mRNA, complete cds
11139	24008	37513	1.84	1.5E-011	BE084862.1	EST - HUMAN	Chloroplast purpurea psb1 gene
11139	24008	37514	1.84	1.5E-011	BE084862.1	EST - HUMAN	Chloroplast purpurea psb1 gene
11263	24198	37654	6.36	1.5E-011	AL163260.2	NT	CM2-BT0668.2 03030-122-411 BT0668 Homo sapiens cDNA
11263	24198	37655	6.36	1.5E-011	AL163260.2	NT	CM2-BT0668.2 03030-122-411 BT0668 Homo sapiens cDNA
11615	24425	37883	1.48	1.5E-011	AW191916.1	EST - HUMAN	CM2-BT0668.2 03030-122-411 BT0668 Homo sapiens cDNA
11615	24425	37883	1.48	1.5E-011	AW191916.1	EST - HUMAN	CM2-BT0668.2 03030-122-411 BT0668 Homo sapiens cDNA
11907	24521	34020	1.57	1.5E-011	N67319.1	EST - HUMAN	W453035.3 NCI_QGAP_P422 Homo sapiens cDNA clone IMAGE:2401310 3'
12039	24891		1.57	1.5E-011	N67319.1	EST - HUMAN	W453035.3 NCI_QGAP_P422 Homo sapiens cDNA clone IMAGE:2401310 3'
12039	24891		1.57	1.5E-011	N67319.1	EST - HUMAN	W453035.3 NCI_QGAP_P422 Homo sapiens cDNA clone IMAGE:2401310 3'
12039	24891		1.57	1.5E-011	N67319.1	EST - HUMAN	W453035.3 NCI_QGAP_P422 Homo sapiens cDNA clone IMAGE:2401310 3'

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
12500	26331		2.95	1.4E-01	AF003598.2	NT	Ratios polyketide chain oxidase CYP3C mRNA, complete cds
12702	26367		1.97	1.5E-01	AB026988.1	NT	Human sapiens cDNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
12721	26793		3.33	1.9E-01	BA00761.1	EST_HUMAN	Human sapiens cDNA, feline liver spleen (INF.S) Homo sapiens cDNA, clone IMAGE:194430.5
12801	26803		3.37	1.9E-01	AY741772.1	EST_HUMAN	AY741772 CG Homo sapiens cDNA, clone C8DA0204.5
12902	26722	31697	7.70	1.9E-01	AL130742.2	NT	Centromeric repeat NCTG111168 complete genome, segment 1/8
13092	26803	31752	6.97	1.4E-01	U27943.1	NT	Simi scRNA for sodium sulfate symporter
3169	13411		1.38	1.4E-01	AF005653.1	NT	Human sapiens cDNA, cell receptor beta beta
605	13697		9.3	1.4E-01	D73638.1	EST_HUMAN	Xenopus laevis mRNA for DNA (Oxytrich-5)-methyltransferase, complete cds
12806	14319		1.33	1.4E-01	T91664.1	EST_HUMAN	Y54C01.1 Scores fetal liver spleen (INF.S) Homo sapiens cDNA, clone IMAGE:118332.3
1778	14800		1.35	1.4E-01	68076800	NT	Mus musculus growth differentiation factor 5 (GDF5), mRNA
1778	14802	27770	1.31	1.4E-01	AE001770.1	NT	Thermoplasma maritimum section 22 of 136 of the complete genome
1923	16044		1.06	1.4E-01	AW135741.1	EST_HUMAN	ULH81.1 act4-030JL1 NCI CGAP S263 Homo sapiens cDNA, clone IMAGE:2714007.3
2002	16020		11.07	1.4E-01	AA720516.1	EST_HUMAN	NY72807.1 NCI CGAP GC61 Homo sapiens cDNA, clone IMAGE:1281821.3
2409	15498	28489	1.35	1.4E-01	AF00706	SWISSPROT	GLYCOL-3-PHOSPHATE ADP-TRANSFERRASE PRECURSOR (GPA)
2840	19036	28489	3.90	1.4E-01	AB033496.1	EST_HUMAN	W174091.1 NCI CGAP L12 Homo sapiens cDNA, clone IMAGE:2441695.3
3169	19395	29260	1.03	1.4E-01	R63396.1	EST_HUMAN	Y574010.1 Scores infant brain (HIB) Homo sapiens cDNA, clone IMAGE:40048.5
3068	19596	29890	1.25	1.4E-01	R6232.1	EST_HUMAN	Y57403.1 Scores infant brain (HIB) Homo sapiens cDNA, clone IMAGE:41407.5
3068	19696	29891	1.25	1.4E-01	R6232.1	EST_HUMAN	Y57403.1 Scores infant brain (HIB) Homo sapiens cDNA, clone IMAGE:41407.5
4269	17295	30152	10.37	1.4E-01	AI090941.1	EST_HUMAN	B59C02.1 NCI CGAP L242 Homo sapiens cDNA, clone IMAGE:2273570.3
4269	17295	30152	10.37	1.4E-01	AI090941.1	EST_HUMAN	B59C02.1 NCI CGAP L242 Homo sapiens cDNA, clone IMAGE:2273570.3
4337	17351	30214	4.49	1.4E-01	AE001770.1	NT	Thermoplasma maritimum section 22 of 136 of the complete genome
4518	17627		0.89	1.4E-01	AA772687.1	EST_HUMAN	g5001.01 Scores fetal liver spleen (INF.S) S1 Homo sapiens cDNA, clone IMAGE:43973.3 similar to g5001.057 NCI INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN) contains Au repetitive element
4680	17978	30836	0.88	1.4E-01	AI088959.1	EST_HUMAN	AV088959 GRC Homo sapiens cDNA, clone GRC03059.5
5480	18559	31410	4.18	1.4E-01	U00771.1	EST_HUMAN	ye151.1.1 Stragene Link (3637210) Homo sapiens cDNA, clone IMAGE:177612.3
5572	18591	31435	4.32	1.4E-01	AB000595.1	NT	Canada tropical DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5572	18591	31435	4.32	1.4E-01	AB000595.1	NT	Canada tropical DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6552	19354	32782	3.04	1.4E-01	BE32861.1	EST_HUMAN	W0702421 NCI CGAP J08T1 Homo sapiens cDNA, clone IMAGE:310358.3
6757	19791	33004	4.13	1.4E-01	AE011747.1	EST_HUMAN	AE011747 HEBRA1 Homo sapiens cDNA, clone HEBR100708.5
6757	19791	33005	4.13	1.4E-01	AE011747.1	EST_HUMAN	AE011747 HEBRA1 Homo sapiens cDNA, clone HEBR100708.5
6863	19865	33059	4.04	1.4E-01	AI082766.1	EST_HUMAN	AB1762421 Scores fetal liver spleen (INF.S) CGC S1 Homo sapiens cDNA, clone IMAGE:259151.3
6907	19959		1.10	1.4E-01	BE260336.1	EST_HUMAN	BE1765221 NCI JMC-7 Homo sapiens cDNA, clone IMAGE:339159.1

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6801	10921	33186	2.17	1.4E-01 BF576533.1	EST_HUMAN	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
7182	20426		1.13	1.4E-01 AF116255.1	EST_HUMAN	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
7182	20711		1.13	1.4E-01 AF116255.1	EST_HUMAN	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
7810	20739	34242	0.02	1.4E-01 F02746.1	EST_HUMAN	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
7896	20793		0.68	1.4E-01 AF126237.1	EST_HUMAN	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
7899	20796	34099	0.43	1.4E-01 T33770.1	EST_HUMAN	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
8009	20882	34560	1.21	1.4E-01 AF16845.1	NT	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
8220	21125	34457	0.69	1.4E-01 AG05162.1	EST_HUMAN	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
8553	21484	34520	0.85	1.4E-01 BF10256.1	EST_HUMAN	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
9044	21673		1.55	1.4E-01 AF155947.1	EST_HUMAN	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
9843	22271		0.57	1.4E-01 AA93053.1	EST_HUMAN	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
9470	22336	35781	0.31	1.4E-01 AA307073.1	EST_HUMAN	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
9545	22472	35530	0.78	1.4E-01 AF002363.1	EST_HUMAN	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
9557	22593	35957	1.2	1.4E-01 R02746.1	EST_HUMAN	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
9607	22853	35958	1.2	1.4E-01 R02746.1	EST_HUMAN	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
9728	22853	36036	8.78	1.4E-01 BF510955.1	EST_HUMAN	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
9815	22721	36104	1.39	1.4E-01 W83411.1	EST_HUMAN	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
9885	22800	36180	0.51	1.4E-01 X72403.1	NT	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
9885	22800	36187	0.51	1.4E-01 X72403.1	NT	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
9896	22811	36201	1.26	1.4E-01 Y0166.1	NT	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
9896	22811	36201	1.26	1.4E-01 Y0166.1	NT	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
9892	21340	34276	1.68	1.4E-01 AF121361.1	NT	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
10321	23210	36922	0.74	1.4E-01 AF03060.1	NT	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
10495	23381	36794	1.11	1.4E-01 AF02381.1	NT	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
10580	23479	36903	0.73	1.4E-01 AF021806.1	EST_HUMAN	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
10580	23479	36904	0.73	1.4E-01 AF021808.1	EST_HUMAN	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
10750	23836	37068	0.7	1.4E-01 BF02326.1	EST_HUMAN	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to
10750	23836	37068	0.7	1.4E-01 BF02326.1	EST_HUMAN	U14340.1	Human sapiens cDNA clone IMAGE:2126111 3' similar to

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Table 4

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
11551	24080		1.78	1.4E-01	AA81480.1	EST_HUMAN	cd36c3.1 NCI CGAP GDB1 Homo sapiens cDNA clone IMAGE32084.3'
12602	24222	37954	3.28	1.4E-01	FS5303.1	EST_HUMAN	WPC16.11 Source: human 284648 Homo sapiens cDNA clone IMAGE15108.8'
11469	24352	37954	1.82	1.4E-01	AW104862.1	EST_HUMAN	WPC16.11 Source: NIEHS, GBC, S1 Homo sapiens cDNA clone IMAGE268374.3'
11537	24447	37958	1.91	1.4E-01	TS6102.1	EST_HUMAN	pe7210.1 Source: fetal liver, spleen, NIEHS Homo sapiens cDNA clone IMAGE32280.8'
11537	24447	37958	1.91	1.4E-01	TS6102.1	EST_HUMAN	pe7210.1 Source: fetal liver, spleen, NIEHS Homo sapiens cDNA clone IMAGE32280.8'
11539	24449	37912	1.5	1.4E-01	P08948	SWISSPROT	INTERGRIN ALPHA-5 PRECURSOR (FRRONECTIN RECEPTOR ALPHA SUBUNIT) (INTERGRIN ALPHA-5) (VLA-5) (CD46)
11738	24640	38120	1.77	1.4E-01	X60922.1	NT	Cp197898a ORF for putative membrane transport protein
11773	26711		1.65	1.4E-01	AW016373.1	EST_HUMAN	U1H-B10-5a1-c-26-3.1 NCI CGAP S1a1 Homo sapiens cDNA clone IMAGE2710258.3'
11801	24001	37440	2.05	1.4E-01	U28792.1	NT	Bonella burgdorferi: phosphatidylethanolamine 3-phosphatase, dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), phosphoenolpyruvate isomerase (TPI) genes, complete cds
11957	24802		1.44	1.4E-01	X62102.1	NT	M. macleodae p18K gene for 16 kDa protein
12160	24888	35058	1.51	1.4E-01	AF148793.2	NT	Mus musculus neuromedin U precursor (Nau) gene, partial cds; iPhLp (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pht27) gene, complete cds; and HBAR (H-bar) gene, complete cds
12602	25288	31613	4.54	1.4E-01	X74773.1	NT	P. sativa psallid gene seq
12614	25305		2.27	1.4E-01	11958117	NT	Rattus norvegicus desmin (Des), mRNA
12856	25845		2.04	1.4E-01	BE151902.1	EST_HUMAN	BC131055B1 NIH JGCG.3 Homo sapiens cDNA clone IMAGE354328.8'
12747	25885		8.48	1.4E-01	AF043221.1	NT	Fugu tubripes putative neurotransmitter receptors, YOR140w homolog, and glycylamide ribonucleoside transferase (GART) genes, complete cds
12825	25891		5.22	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
13019	25784		3.23	1.4E-01	D03583.1	NT	Mus musculus mRNA for prolactin, complete cds
13106	25622		3.39	1.4E-01	U01037.1	NT	Human Ssr1 like protein kinase (A-Raf-1) gene, complete cds
342	13432	26246	2.17	1.3E-01	4759467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
342	13432	26247	2.17	1.3E-01	4759467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
652	13621	26256	1.88	1.3E-01	AB013193.1	NT	Homo sapiens gene for NBS1, complete cds
659	13721	26232	1.24	1.3E-01	AJ277068.1	NT	Human calcitriol HUNLVG618980UK RNA for capsid protein (ORF2), strain HUNLVG618980UK
659	13721	26233	1.24	1.3E-01	AJ277068.1	NT	Human calcitriol HUNLVG618980UK RNA for capsid protein (ORF2), strain HUNLVG618980UK
659	13822	26268	0.94	1.3E-01	XJ03330.1	NT	P. damelli Histone gene cluster for core histones H2A, H2B, H3 and H4
919	13971	26219	1.57	1.3E-01	AF135916.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1313	14071	27159	1.24	1.3E-01	AF111015.1	NT	Isolated cDNA from rat cDNA library under conditions of nitrogen deprivation
1354	14055		2.23	1.3E-01	AF110853.1	NT	Berberis amurensis stem 14 cDNA library under conditions of nitrogen deprivation

Table 4

[illegible]

Probe NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1243	14279	27221	1.32	1.3E-01	AV1712467.1	EST_HUMAN	AV1712467 DCA Homo sapiens cDNA clone DCAAT109.5'
1482	14463	27857	0.95	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMO mRNA, complete cds
1862	14603	27857	1.16	1.3E-01	6980657	NT	Mus musculus procollagen, type XI, alpha 1 (Col1a1), mRNA
1973	14961	27974	2.21	1.3E-01	AL111078.1	NT	Bovine epsilon chain T4 cDNA library under conditions of nitrogen deprivation
2183	15194		0.03	1.3E-01	AJ433978.1	EST	Rhodospirillum rubrum scdA gene, complete cds
2305	15317		1.15	1.3E-01	AF193104.1	NT	Homo sapiens transcription factor (GCM) enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, complete cds
2403	15408		2.79	1.3E-01	AF001016.1	NT	Archaeoglobus fulgidus section 81 of 172 of the complete genome
2626	15623	29816	2.66	1.3E-01	AE003918.1	NT	Cereus auratus leratin type IRINA, complete cds
3410	16462	29398	0.96	1.3E-01	AF169797.1	NT	Homo sapiens T-type calcium channel alpha-1C, complete cds
3512	16593	29490	1.1	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
3768	16917	29735	0.78	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii O15 genes DNA, 1281000 nt, position (17)
3819	16917	29735	0.78	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii O15 genes DNA, 1281000 nt, position (17)
3870	16936	29752	0.97	1.3E-01	AF079840.1	NT	Salmonella enterica serovar Gallinarum phage phi6, complete cds
4074	17103		1.57	1.3E-01	AL161581.2	NT	Arctodaphnia italica DNA, chromosome 5, contig fragment No. 77
4135	18321	26932	0.77	1.3E-01	AJ277006.1	NT	Human calcitriol HUN1.V333100165UK RNA for capid protein (ORF2), strain HUN1.V333100165UK
4195	17321	29335	0.77	1.3E-01	AJ277003.1	NT	Human calcitriol HUN1.V333100165UK RNA for capid protein (ORF2), strain HUN1.V333100165UK
4256	17279	30123	1.13	1.3E-01	AF007718.1	NT	Bacteriophage SPB2 complete genome
4256	17279	30123	4.13	1.3E-01	AF063431.1	EST	UV3411016101200436-403 D1018 Homo sapiens cDNA
4263	17279	30148	2.18	1.3E-01	AF026905.1	EST	Schistosoma mansoni tubulin biophosphate adduct cDNA, complete cds
4262	17299	30162	26.86	1.3E-01	AW127174.1	EST	SC3R10.1.2 Soares, NHL, T, GBC S.1 Homo sapiens cDNA clone IMAGE:2813595.3'
4367	17491	30296	1.06	1.3E-01	AF152778.1	EST	AV175277 NPD Homo sapiens cDNA clone NPDA2502.5'
4397	17491	30270	1.79	1.3E-01	AF152778.1	EST	AV175277 NPD Homo sapiens cDNA clone NPDA2502.5'
4418	17430		1.93	1.3E-01	AL163390.2	NT	Homo sapiens chromosome 21 segment HS21C060
4362	17670	30457	0.86	1.3E-01	AJ13762.1	EST	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
4650	17659	30522	2.2	1.3E-01	BE127300.1	EST	601120065F1 NH1 MG6, J9 Homo sapiens cDNA clone IMAGE:2990069.5'
5099	19009		0.71	1.3E-01	AF136819.1	EST	RA136819 PLACET1 Homo sapiens cDNA clone IMAGE:1004693.5'
5152	19143		1.04	1.3E-01	AF091891.1	EST	RA136819 PLACET1 Homo sapiens cDNA clone IMAGE:1004693.5'
5265	19241	31003	1.32	1.3E-01	AJ426331.1	EST	RA136819 PLACET1 Homo sapiens cDNA clone IMAGE:1004693.5'
5268	19234	31103	0.66	1.3E-01	AF176979.1	EST	Homo sapiens cDNA clone IMAGE:2720562.3'
5268	19234	31103	0.66	1.3E-01	AF176979.1	EST	Schistosoma mansoni HMG-CoA reductase (hmg1) 1, gene, complete cds

Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11078	24010		2.71	1.3E-01	BF330560.1	EST_HUMAN	MF4-E110394-130700-010-N03-B10363 Homo sapiens cDNA
11301	24220	37680	1.92	1.3E-01	AF16831.1	EST_HUMAN	932607T1 Sarcos planicus N227P1 Homo sapiens cDNA clone IMAGE:150418 5'
11340	24340	37675	1.98	1.3E-01	AF10117.1	NT	Human placenta degenerate (N227P1) (S100A3) gene, complete cds
11524	24531		1.98	1.3E-01	BF022703.1	EST_HUMAN	MF4-L110132-22500-022-003 (S100A3) 12 Homo sapiens cDNA
11531	24531		1.98	1.3E-01	BF022703.1	EST_HUMAN	MF4-L110132-22500-022-003 (S100A3) 12 Homo sapiens cDNA
11776	24576	38163	1.44	1.3E-01	BF577328.1	EST_HUMAN	903070A6F1 NIH MGC 33 Homo sapiens cDNA clone IMAGE:4251348 5'
11776	24576	38164	1.44	1.3E-01	BF577328.1	EST_HUMAN	903070A6F1 NIH MGC 33 Homo sapiens cDNA clone IMAGE:4251348 5'
12025	24697	38560	3.34	1.3E-01	BF572446.1	EST_HUMAN	01176905F1 NIH MGC 31 Homo sapiens cDNA clone IMAGE:350454 5'
12146	24698	38466	3.48	1.3E-01	BE119364.1	EST_HUMAN	01176905F1 NIH MGC 31 Homo sapiens cDNA clone IMAGE:350454 5'
12146	25208	31952	1.75	1.3E-01	BE119345.1	EST_HUMAN	0114827A1F1 NIH MGC 38 Homo sapiens cDNA clone IMAGE:3976208 5'
12387	25285		3.48	1.3E-01	AJ242780.1	NT	Gallus gallus sox11 gene for lymphoblast, exon 1-3
12957	25518		1.70	1.3E-01	AW001114.1	EST_HUMAN	wb2405-11 Soares, Decoyagale, colon, NHQD Homo sapiens cDNA clone IMAGE:2553077 5' similar to TR-090287 090287 KIA0639 PROTEIN, ;
404	13517	25438	8.68	1.2E-01	AJ42744.1	EST_HUMAN	939002-1 NCI, OGAP, Brn23 Homo sapiens cDNA clone IMAGE:2088539 3' similar to gbL1057500 .rat1 ANNEKIN V (HUMAN);
447	13114		1.08	1.2E-01	U05912.1	NT	Diposaurus discolorum ORF DG 015 gene, partial cds
550	13837		2.5	1.2E-01	AF930442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1403	14434	27380	2.23	1.2E-01	AU149146.1	EST_HUMAN	AU148148 NT29M4 Homo sapiens cDNA clone NT29M4001691 3'
1403	14434	27380	2.23	1.2E-01	AU149146.1	EST_HUMAN	AU148148 NT29M4 Homo sapiens cDNA clone NT29M4001691 3'
1410	14441		2.04	1.2E-01	AV735246.1	EST_HUMAN	AV735246 ccd4 Homo sapiens cDNA clone ccdAJB11 5'
1526	14557		1.23	1.2E-01	AA897474.1	EST_HUMAN	445494-11 Soares, NF1_L_C9C_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TRQ16971 C10071 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR, ;
1655	14685	27548	1.2	1.2E-01	Q14604	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOSOLIC 4, (T CELL TRANSCRIPTION FACTOR
1677	14707	27570	3.09	1.2E-01	AJ28542.1	EST_HUMAN	939002-1 NCI, OGAP, E2a2 Homo sapiens cDNA clone IMAGE:190055 3'
1793	14819		14.19	1.2E-01	X09211.1	NT	H-sapiens DNA for endogenous retroviral like element
2198	15207	28211	1.22	1.2E-01	BF5245400.1	EST_HUMAN	901821607F1 NIH MGC 32 Homo sapiens cDNA clone IMAGE:4040294 5'
2305	15313	28517	0.68	1.2E-01	AL183213.2	NT	Homo sapiens chromosome 21 segment HS21013
2030	15628	28921	1.98	1.2E-01	AV169556.1	EST_HUMAN	QV348006-225000-720-110 BN0506 Homo sapiens cDNA
2716	15767	28742	1.09	1.2E-01	M02368.1	EST_HUMAN	1s19g7.1 N1 OGAP-Pant Homo sapiens cDNA clone IMAGE:2229888 3' similar to TRQ14048 Q14048 COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN, [1] contains element PTR5 repetitive element, ;
2858	15842	28544	1.24	1.2E-01	U16018.1	NT	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds

Table 4

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most S'milar (Top) HT BLAST E Value	Top HT Accession	Top HT Database Source	Top HT Descriptor
2946	15908	28841	5.32	1.2E-01	AF220770.1	EST_HUMAN	esRR000.x1 Barleaved cdc1a HPLB7 Homo sapiens cDNA clone IMAGE:2345024 3' attilar to cdc1L06093
2977	16720	29041	5.04	1.2E-01	AF10394.1	NT	69S RIBOSOMAL PROTEIN L30 (HUMAN);
3048	16000	29003	0.87	1.2E-01	X6082.1	NT	Human cytosolic kinase-B mRNA, comp site cds
3277	16325	29221	0.87	1.2E-01	X6082.1	EST_HUMAN	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3404	16348		1.05	1.2E-01	AF10068.1	EST_HUMAN	OV-10/2656-20/109-021-cds BT0250 Homo sapiens cDNA
3302	16344	28394	1.03	1.2E-01	AF10068.1	EST_HUMAN	MuHomo sapiens juncosH1 section 142 of 160 of the complete genome
3536	16576		0.65	1.2E-01	AF100337.1	EST_HUMAN	UHF-BNO-46w-a-10-CU-11 NIH_MGC_30 Homo sapiens cDNA clone IMAGE:3074247 5'
3582	16571	28572	0.65	1.2E-01	X26118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 276131 to 3013940
3682	16619	28523	0.93	1.2E-01	X00682.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3699	16576		1.17	1.2E-01	X26118.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3883	16882		1.19	1.2E-01	BF12265.1	EST_HUMAN	Bacillus subtilis complete genome (section 15 of 21); from 276131 to 3013940
3883	16882		1.19	1.2E-01	BF12265.1	EST_HUMAN	001010708RT NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4038588 5'
4278	17282	30167	2.81	1.2E-01	X24281.1	NT	P. dactylis mRNA; repeat region (ID 20R17)
4278	17282	30168	2.81	1.2E-01	X24283.1	NT	P. dactylis mRNA; repeat region (ID 20R17)
4417	17428	30253	0.74	1.2E-01	AF13551.1	NT	Cricetus meani calcitonin receptor molecule (N-CAM) gene, exon 19
4834	17833	30706	1.1	1.2E-01	X26118.1	NT	L. taenioides mRNA for glycoprotein-1
4897	17889		0.73	1.2E-01	X26118.1	NT	L. taenioides mRNA for glycoprotein-1
4938	17888	30846	1.03	1.2E-01	BF110194.1	EST_HUMAN	001807456T NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4774004 5'
5034	18041	30871	0.87	1.2E-01	AF10044.1	EST_HUMAN	SALMONELLA THURMUTHERIA mRNA, complete cds
5231	18237		1.02	1.2E-01	AF103272.2	SWISSPROT	HOMOXYNIN PRECURSOR
5251	18237	31087	1.02	1.2E-01	AF103272.2	NT	Homo sapiens chromosome 21, segment H87C027
5251	18237	31088	1.02	1.2E-01	AF103272.2	NT	Homo sapiens chromosome 21, segment H87C027
5415	18336	31233	0.85	1.2E-01	X13160.1	EST_HUMAN	Musca domestica vitamin K dependent protein S (PROS) mRNA, complete cds
5431	18336	31236	0.87	1.2E-01	AF143393.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-8, and partial cds, alternatively spliced
5493	18594	31408	0.89	1.2E-01	AF23391.1	NT	cd080421.1 Source: pathogenic; Tumor NACP-Homo sapiens cDNA clone IMAGE:321650 5'
5493	18593	31418	2.48	1.2E-01	X03303.1	EST_HUMAN	Homo sapiens gene encoding placitophilin (exons 1-13)
5533	18531	31510	2.07	1.2E-01	X26205.1	EST_HUMAN	M. domestica Borth, Granary Smilt adn mRNA for alcohol dehydrogenase
5595	18768	31603	0.92	1.2E-01	X26204.1	NT	001405618T NIH_MGC_70 Homo sapiens cDNA clone IMAGE:385903 5'
6441	19487	32594	0.91	1.2E-01	BE020945.1	SWISSPROT	MATING-TYPE-13-P-3C-HFIC POLYPEPTIDE PI
6495	19540	32717	0.73	1.2E-01	AF10842	SWISSPROT	LD-C710651-22/099-113-cDNA CT0031 Homo sapiens cDNA
6533	19733	32793	2.24	1.2E-01	AF10842/5.1	EST_HUMAN	Musca domestica glycolytic phosphatase mRNA, complete cds
6523	19733	32848	1.56	1.2E-01	AF10842/5.1	EST_HUMAN	005601.1 NCI, CGAP, CG81 Homo sapiens cDNA clone IMAGE:1269024 3'
6536	19735	32927	0.65	1.2E-01	AF107455.1	NT	

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Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6339	19098	33191	1.18	1.2E-01	B547985.1	EST_HUMAN	0023211.NCI_CGAP_Bio67 Homo sapiens cDNA clone IMAGE:418946 F
7107	20312	33179	0.93	1.2E-01	B25024.1	EST_HUMAN	IG vna src gene, V92, V93, V94, V95, large T, origin, and small T, origin, genes, complete cds
7338	20333	33222	0.71	1.2E-01	A17796.1	EST_HUMAN	g63004.T Swiss fetal liver spleen, INHLS Homo sapiens cDNA clone IMAGE:193769 5'
7359	20333	33223	0.71	1.2E-01	A17796.1	EST_HUMAN	g63004.T Swiss fetal liver spleen, INHLS Homo sapiens cDNA clone IMAGE:193769 5'
8030	20953	34298	0.64	1.2E-01	AJ27174.1	NT	Homo sapiens partial ILF3 gene for interleukin enhancer binding factor 3 (alternative transcript dhs970)
8036	21210	34548	0.65	1.2E-01	D67488.1	NT	dhs970 gamma, dhs970 alpha and ILF3
8036	21210	34547	0.65	1.2E-01	D67488.1	NT	Human mRNA for KIAA0282 gene, partial cds
8472	21403		1.62	1.2E-01	BC021072.1	EST_HUMAN	Human mRNA for KIAA0282 gene, partial cds
8540	21471	34812	3.35	1.2E-01	A018733.1	EST_HUMAN	PM3 B01037-50300-002-000 B01037 Homo sapiens cDNA
8566	21577	34861	0.66	1.2E-01	A020269	SWISSPROT	w69693.x1 NCI_CGAP_C38 Homo sapiens cDNA clone IMAGE:232880 3' similar to SWGST2_HUMAN
8864	21874	35165	0.74	1.2E-01	A020881.1	EST_HUMAN	Q99735 MICROSOFT GLUTATHIONE S-TRANSFERASE II ;
							NADH-HUBQUINONE OXIDOREDUCTASE B22 SUBUNIT (C-B22)
8907	21897		10.92	1.2E-01	AV089552.1	EST_HUMAN	4071610.X1 Barasol cDNA clone IMAGE:237439 3'
							pc4b07.X1 NCI_CGAP_Exc0 Homo sapiens cDNA clone IMAGE:236767 3' similar to gb-M13432 LAMIN A (HUMAN);
8987	21916		4.31	1.2E-01	A058772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sh (ein) gene, partial cds and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
9023	21952	35308	1.07	1.2E-01	A03953.1	NT	Mrassa vectorial ATPase 57Kd subunit (vma-2) gene, complete cds
9023	21952	35309	1.07	1.2E-01	A03953.1	NT	Mrassa vectorial ATPase 57Kd subunit (vma-2) gene, complete cds
9103	22091		0.62	1.2E-01	AJ27178.1	NT	Homo sapiens Xq pseudocentromeric region, segment 22
9247	22175		1.72	1.2E-01	U32741.1	NT	Hemophilus influenzae Rd section 20 of 103 of the complete genome
9282	22210		0.85	1.2E-01	X16191.1	NT	Mrussinus DNA fragment of Apocrypton 8 gene
10100	22949	35339	2.16	1.2E-01	XZ7061.1	NT	S cerevisiae HXT5 gene
10810	23397	36809	1.47	1.2E-01	AV170867.1	EST_HUMAN	AV170867.C0 Homo sapiens cDNA clone CAJAK508 5'
11323	24242		2.68	1.2E-01	D20184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
11504	24474		1.63	1.2E-01	B53252.2	EST_HUMAN	807653787.NH1.MGC_181 Homo sapiens cDNA clone IMAGE:394026 3'
11597	24499		1.53	1.2E-01	B531483.1	EST_HUMAN	807653787.NH1.MGC_181 Homo sapiens cDNA clone IMAGE:394026 3'
11702	24604	36779	2.03	1.2E-01	AF040463.1	NT	Human cDNA fragment of human DNMT1 (DNMT1) gene, exon 10
12126	24659	36713	1.76	1.2E-01	U30246.1	EST_HUMAN	pm0025.1 Swiss human brain, INHLS Homo sapiens cDNA clone IMAGE:29880 3'
11845	24695	38185	1.43	1.2E-01	6964174.1	NT	Homo sapiens UTP-Glutathione S-transferase, polypeptide 4 (B-CAL T4) mRNA
11840	24784		1.41	1.2E-01	B551093.1	NT	Human cDNA fragment of human phosphatase regulatory subunit 1 (R01) mRNA, complete cds
12221	25053	38554	1.51	1.2E-01	B5368765.1	EST_HUMAN	CHAE11001018-310550-296-011 E17016 Homo sapiens cDNA

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4294	17222	30387	1.03	1.1E-01	AW189412.1	EST_HUMAN	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
4210	17227		0.95	1.1E-01	AF030091.1	NT	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
4331	17335		1.107	1.1E-01	AF150931.1	NT	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
4334	17336	30366	0.99	1.1E-01	AW182036.1	EST_HUMAN	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
4692	17639	30555	0.8	1.1E-01	AF094954.2	NT	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
4646	17045	30603	1.36	1.1E-01	Y07656.1	NT	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
5143	18138		0.95	1.1E-01	AW1026847.1	EST_HUMAN	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
5148	17227		0.92	1.1E-01	AF030091.1	NT	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
8241	18228	31076	0.76	1.1E-01	AW189412.1	EST_HUMAN	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
8241	18228	31077	0.76	1.1E-01	AW189412.1	EST_HUMAN	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
5303	18287	31140	1.02	1.1E-01	P70291	SWISSPROT	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
5957	18939		1.93	1.1E-01	AAT474716.1	EST_HUMAN	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
5942	19039	32129	1.36	1.1E-01	AF020827.1	NT	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
5952	19047	32171	0.81	1.1E-01	AL110665.1	NT	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
8017	19076	32204	0.76	1.1E-01	BF336519.1	EST_HUMAN	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
8017	19076	32205	0.76	1.1E-01	BF336519.1	EST_HUMAN	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
8046	19111	32240	1.96	1.1E-01	X68851.1	NT	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
8096	19147	32262	4.55	1.1E-01	M85533.1	NT	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
8296	19310	32474	1.59	1.1E-01	AJ007673.1	NT	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
8291	19332	32468	1.8	1.1E-01	BE769152.1	EST_HUMAN	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
8301	19352	32521	8.23	1.1E-01	AW539699.1	EST_HUMAN	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
8992	19728	32929	0.81	1.1E-01	AL163062.2	NT	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
8700	19738	32938	1.45	1.1E-01	AF030746.1	EST_HUMAN	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
8746	19780	32953	0.81	1.1E-01	AF163067.1	EST_HUMAN	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
8854	19824	33138	4.03	1.1E-01	Q96035	SWISSPROT	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
7001	20028		3.2	1.1E-01	AF032622.1	NT	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
7103	20309	33970	2.17	1.1E-01	11452372	NT	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA
7400	20359	33333	0.81	1.1E-01	AE000758.1	NT	MF3-ST026-290100-025-g07 ST0260 Homo sapiens cDNA

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7400	20099	33334	0.61	1.1E-01	AE007156.1	NT	Unspliced liver/liver section 56 of 59 of the complete genome
7551	25591		0.89	1.1E-01	BF36793.1	EST_HUMAN	2010165047 NH1.MGC.361 Homo sapiens cDNA clone IMAGE:455363 5'
7693	26974	33619	0.98	1.1E-01	AF000000.1	NT	Pyrodicta brevis/O15 gnotob DMC1.116031 F1438031.1 part 1 (87)
7693	26985	34165	8.05	1.1E-01	BF362628.1	EST_HUMAN	2010165047 NH1.MGC.361 Homo sapiens cDNA clone IMAGE:455363 5'
7693	26985	34166	8.05	1.1E-01	BF362628.1	EST_HUMAN	2010165047 NH1.MGC.361 Homo sapiens cDNA clone IMAGE:455363 5'
8023	26339	34254	0.52	1.1E-01	AB356308.1	EST_HUMAN	2010165047 NH1.MGC.361 Homo sapiens cDNA clone IMAGE:455363 5'
8104	21013	34543	1.37	1.1E-01	FA1037	SWISSPROT	104320.01 Scores: NF_L1_GBC_S1 Homo sapiens cDNA clone IMAGE:1626172 3'
8149	21059		0.72	1.1E-01	214585.1	NT	TRAB PROTEIN (NF_L1_GBC_S1 Homo sapiens cDNA clone IMAGE:1626172 3')
8150	21059	34590	3.36	1.1E-01	AA788784.1	EST_HUMAN	3451368.01 Scores: pncatylase, kinase, NADPH Homo sapiens cDNA clone 1240493 3' similar to gb:J09483
8327	21223	34667	0.83	1.1E-01	BE762203.1	EST_HUMAN	CHROMOGRANIN A PRECURSOR (HUMAN)
8549	21471	34610	0.6	1.1E-01	U57492.1	NT	2010165047 NH1.MGC.361 Homo sapiens cDNA clone IMAGE:387226 5'
8789	21716	35053	1.94	1.1E-01	AA483574.1	EST_HUMAN	Medulloblastoma cerebellar section 34 of 150 of the complete genome
8789	21716	35053	1.94	1.1E-01	AA483574.1	EST_HUMAN	9024910.01 NCI CGAP Thyl1 Homo sapiens cDNA clone IMAGE:049382
8890	21760	35166	1.42	1.1E-01	X91283.1	NT	Hs49410.01 NCI CGAP Thyl1 Homo sapiens cDNA clone IMAGE:346332
8890	21760	35166	1.42	1.1E-01	X91283.1	NT	Hs49410.01 NCI CGAP Thyl1 Homo sapiens cDNA clone IMAGE:346332
8870	21800		1.1	1.1E-01	AN6167918.1	EST_HUMAN	PAH-310270-00020-001-409 S10270 Homo sapiens cDNA
8625	21825	35211	1.96	1.1E-01	AL134346.1	EST_HUMAN	DKFZ547P184.11 547 (synonym: Hs171) Homo sapiens cDNA clone DKFZ547P184.5'
9377	22335	35609	1.95	1.1E-01	U02482.1	NT	Peridonec acidified H placental PSMB74 peptidom (pap) gene cluster papA, papB, papC and papD genes, complete cds
9499	22367	35760	1.28	1.1E-01	AB07474.1	EST_HUMAN	Yf48001.01 Scores: NF_L1_GBC_S1 Homo sapiens cDNA clone IMAGE:2358619 3' similar to gb:J09483 repetitive element
9500	22467	35848	0.61	1.1E-01	AF050081.1	NT	Homo sapiens C16orf33 large protein mRNA, complete cds
9505	22521	35844	2.84	1.1E-01	AA162183.1	EST_HUMAN	200312.121 Stragemo muscle 697200 Homo sapiens cDNA clone IMAGE:397743 5'
9505	22521	35845	2.84	1.1E-01	AA162183.1	EST_HUMAN	200312.121 Stragemo muscle 697200 Homo sapiens cDNA clone IMAGE:397743 5'
9678	22634	35977	0.82	1.1E-01	Y12727.1	NT	P. mirus pelid dips gene and age gene
9708	22643	36013	4.43	1.1E-01	Y127075.1	EST_HUMAN	Yf48003.01 Scores: fetal liver spleen TNE1.3 Homo sapiens cDNA clone IMAGE:108726 3' similar to
9708	22643	36013	4.43	1.1E-01	Y127075.1	EST_HUMAN	Yf48003.01 Scores: fetal liver spleen TNE1.3 Homo sapiens cDNA clone IMAGE:108726 3' similar to
9695	22681		0.76	1.1E-01	BE142005.1	EST_HUMAN	6041369727 NH1.MGC.72 Homo sapiens cDNA clone IMAGE:392048 5'
10029	23029		2.47	1.1E-01	BF065146.1	EST_HUMAN	CMT110416.271091-025-1110142 Homo sapiens cDNA
10421	23310		0.64	1.1E-01	AL161643.2	NT	MR22-200272-04900-005-408 G0027 Homo sapiens cDNA
10622	23688		1.48	1.1E-01	R60300.1	EST_HUMAN	MR22-200272-04900-005-408 G0027 Homo sapiens cDNA
10825	23711	37138	1.14	1.1E-01	U06539.1	NT	Aradipoda tritarsa DNA chromosome 4, coding fragment No. 43
11244	10191	29027	2.09	1.1E-01	U03263.1	EST_HUMAN	Aradipoda tritarsa DNA chromosome 4, coding fragment No. 43
							Cerealis capillaris yolk vitellinogen (papA, papB and papC) gene cluster, complete cds
							HSC74P022 normalized fibroblast cDNA Homo sapiens cDNA clone c-11023 3'

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8300	21106		2.05	1.0E-01	Y12488.1	NT	Musculus atm gene
8324	21229	34563	0.51	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for p17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
8324	21229	34564	0.51	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for p17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
8420	21123	34560	0.11	1.0E-01	BF12524.1	EST_HUMAN	60187048RT NH MGCC 46 Homo sapiens cDNA clone IMAGE:4053494.3
8512	21443	34785	0.86	1.0E-01	AA307091.1	EST_HUMAN	4532991.1 Soares, Indira, NHT Homo sapiens cDNA clone IMAGE:407569.3 similar to ghM5182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);
8744	21974		0.6	1.0E-01	4158265	NT	Homo sapiens fibroblast growth factor 13 (FGF13) mRNA
9061	21900		1.26	1.0E-01	AW18297.1	EST_HUMAN	AD5401.x1 NCL COAP, UM Homo sapiens cDNA clone IMAGE:2975880.3 similar to g52X17206 40S
9727	22652	36035	1.23	1.0E-01	AF102552.2	NT	RIBOSOMAL PROTEIN S4 (HUMAN); contains TARI.18 TAR1, negative element;
10028	22926	36516	0.37	1.0E-01	MT4693.1	EST_HUMAN	y533904.x1 Soares infant brain 1N1S Homo sapiens cDNA clone IMAGE:34540.9
10038	22936		2.14	1.0E-01	MT6726.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
10079	22982		2.71	1.0E-01	AE001507.1	NT	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
10093	22943	35831	0.77	1.0E-01	W01695.1	EST_HUMAN	z556510.01 Soares, Indira, Jcst1_Jcst1-H1919 Homo sapiens cDNA clone IMAGE:327282.3
10336	23225	39540	2.03	1.0E-01	BF240154.1	EST_HUMAN	60180650RT NH MGCC 64 Homo sapiens cDNA clone IMAGE:4133487.6
10444	23333	39750	0.70	1.0E-01	AB046796.1	NT	Homo sapiens mRNA for KIAA1679 protein, partial cds
10444	23333	39751	9.76	1.0E-01	AB046796.1	NT	Homo sapiens mRNA for KIAA1679 protein, partial cds
10941	23927		1.21	1.0E-01	AW155745.1	EST_HUMAN	EST386015.1 Stargeno field spleen (697205) Homo sapiens cDNA clone IMAGE:72552.3 similar to contains Alu repetitive element
10946	23532	38664	0.86	1.0E-01	TF1062.1	EST_HUMAN	60169604RT NH MGCC 7 Homo sapiens cDNA clone IMAGE:3093009.6
109520	23796	37133	1.27	1.0E-01	BF02769.1	EST_HUMAN	AU195227 THYROT NH MGCC 55 Homo sapiens cDNA clone IMAGE:4100969.5
11101	24032		1.06	1.0E-01	AU199727.1	EST_HUMAN	60187700RT NH MGCC 55 Homo sapiens cDNA clone IMAGE:4100969.5
11472	24385	37834	2.34	1.0E-01	BF242546.1	EST_HUMAN	60187700RT NH MGCC 55 Homo sapiens cDNA clone IMAGE:4100969.5
11472	24385	37835	2.34	1.0E-01	BF242546.1	EST_HUMAN	60187700RT NH MGCC 55 Homo sapiens cDNA clone IMAGE:4100969.5
11837	24688	38177	4.8	1.0E-01	BF067463.1	EST_HUMAN	60185659RT NH MGCC 7 Homo sapiens cDNA clone IMAGE:3359724.5
12430	25005		3	1.0E-01	BF371719.1	EST_HUMAN	60165504RT NH MGCC 10 Homo sapiens cDNA clone IMAGE:3481933.5
12698	25330		1.86	1.0E-01	X03654.1	NT	Drosophila melanogaster 12 gene
12699	25336		4	1.0E-01	U52671.1	NT	Consensus polyoma positive type 1 serine/threonine phosphatase (PP1) mRNA, complete cds
12697	25305		2.82	1.0E-01	BE33719.1	EST_HUMAN	60165504RT NH MGCC 10 Homo sapiens cDNA clone IMAGE:3481933.5
12698	25334		30.18	1.0E-01	U52671.1	NT	Consensus polyoma positive type 1 serine/threonine phosphatase (PP1) mRNA, complete cds
13045	25576		8.15	1.0E-01	AF001507.1	NT	Basillus thuringiensis gamma DNA, section 171
2829	18189	28413	1.39	9.9E-02	AF174008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pkc-2II) mRNA, complete cds
2835	18324	28520	1.39	9.9E-02	BE155561.1	EST_HUMAN	601070210RT NH MGCC 12 Homo sapiens cDNA clone IMAGE:345493.5

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2835	18204	28261	1.20	9.9E-02	BE54454.1	EST_HUMAN	80107219T NH_MJC_12 Homo sapiens cDNA clone IMAGE:3456385 6'
3111	19828	29250	4.21	9.9E-02	AF00849.1	EST_HUMAN	Homo sapiens scapone II cDNA clone, partial cds
4332	17059	29048	0.19	9.9E-02	AF21637.1	EST_HUMAN	246583.45 Swine erythrocyte YH401 Homo sapiens cDNA clone IMAGE:749932 3'
7185	20195	31426	0.46	9.9E-02	BE51498.1	EST_HUMAN	60150426P1 NH_MJC_71 Homo sapiens cDNA clone IMAGE:3506914 6'
7309	19477	31265	8.22	9.9E-02	DA3730.1	NT	Acetabularia lemane BSO_mRNA 1c1 Biallelic 3' UTR/3' UTR, complete cds
8404	21425	34765	0.32	9.9E-02	AW103088.1	EST_HUMAN	464070.11 UCL_OGAP_O23 Homo sapiens cDNA clone IMAGE:2666828 3' similar to contains Alu repetitive element/contains element MIR repeat element
8404	21425	34766	0.32	9.9E-02	AW103088.1	EST_HUMAN	464070.11 UCL_OGAP_O23 Homo sapiens cDNA clone IMAGE:2666828 3' similar to contains Alu repetitive element/contains element MIR repeat element
9799	22763	36148	1.86	9.9E-02	675511.1	NT	Mus musculus phospholipid transfer protein (PLTP), mRNA
589	19063		1.16	9.9E-02	X55338.1	NT	O. sativa RAmYcO gene for alpha-amylase
3168	18237	29131	4.99	9.9E-02	AF184274.1	NT	Caenorhabditis elegans unc-52, complete cds
4323	17337	30201	9.42	9.9E-02	AF257320.1	NT	Lepidoptera maculata beta-tubulin mRNA, complete cds
4323	17337	30202	9.42	9.9E-02	AF257320.1	NT	Lepidoptera maculata beta-tubulin mRNA, complete cds
7902	20927		0.50	9.9E-02	AF54193.1	NT	Human HP-1 delta mRNA for protein tyrosine phosphatase delta
9795	22760		1.08	9.9E-02	M01943.1	NT	Human lamin B1 chain gene, exon 26
11862	23802	37431	2.03	9.9E-02	BF037421.1	EST_HUMAN	80146070P1 NH_MJC_66 Homo sapiens cDNA clone IMAGE:3864287 6'
12452	28174		1.7	9.9E-02	6383761	NT	Rattus norvegicus microtubule-associated protein Ix (Map1), mRNA
1376	14411	27366	1.33	9.7E-02	AE008606.1	NT	Alce aborescens mRNA for INAP-male, complete cds
1908	14336		0.86	9.7E-02	4033710	NT	Homo sapiens fibroblast growth factor receptor 3 (leukodystrophy, fibroblastic dwarfism) (FGFR3), mRNA
2278	15287	28265	2.33	9.7E-02	BE10890.1	EST_HUMAN	OV1-H70516-070300-005-404 HT0516 Homo sapiens cDNA
4098	17094		4.76	9.7E-02	Q67975	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (LYCOPROTEIN A33)
5529	18508	31456	0.80	9.7E-02	AF095189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III (dnaC) genes, complete cds
5529	18508	31457	0.80	9.7E-02	AF095189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III (dnaC) genes, complete cds
5247	18300	33460	1.38	9.7E-02	AF064476.1	EST_HUMAN	EST1306540 IMAGE resequencer, IMAGE Homo sapiens cDNA
7679	20703	33912	3.3	9.7E-02	Z59118.1	NT	Bovine satellite complete genome (section 10 of 21), from 2887777 to 3213410
8602	21463	34685	1.02	9.7E-02	NZ2788.1	EST_HUMAN	yw16033.31 Human Olfactory Epithelium-Homo sapiens cDNA clone IMAGE:251788 3'
8602	21463	34686	1.02	9.7E-02	NZ2788.1	EST_HUMAN	yw16033.31 Human Olfactory Epithelium-Homo sapiens cDNA clone IMAGE:251788 3'
9408	22336	38700	1.36	9.7E-02	AF039384.1	EST_HUMAN	RP27D1A_FROLYA_CIS-TRANS ISOMERASE A (HUMAN)
11642	24548		2.11	9.7E-02	U56837.1	NT	Mus musculus Ighn1 (Lgh1) mRNA, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2026	15046	28041	1.01	9.0E-02 (A)30721.1	EST_HUMAN	EST_HUMAN	0527411 x1 Scores, NIH/BL, S1 Homo sapiens cDNA clone IMAGE:467468 3
2026	15046	28042	1.01	9.0E-02 (A)30721.1	EST_HUMAN	EST_HUMAN	0527411 x1 Scores, NIH/BL, S1 Homo sapiens cDNA clone IMAGE:467468 3
4454	17464	33231	8.84	9.0E-02 (Z)29562.2	NT	NT	Protein matrix, limited protease, strain IM4320
5122	18118	30960	1.47	9.0E-02 (A)093290.1	EST_HUMAN	EST_HUMAN	ES178303 IMAGE:459094, MAGI Homo sapiens cDNA
5206	18291	31131	0.74	9.0E-02 (B)017229.1	EST_HUMAN	EST_HUMAN	RC547025-021099-011-023 BT0254 Homo sapiens cDNA
6343	18393	31131	2.9	9.0E-02 (B)010393.1	EST_HUMAN	EST_HUMAN	01490090F1 NH MKC, 70 Homo sapiens cDNA clone IMAGE:3500165 5'
8402	21305		0.46	9.0E-02 (B)078753	NT	NT	Mus musculus lymphocyte antigen 7B (L7B) mRNA
8947	21877		0.18	9.0E-02 (A)137084.1	EST_HUMAN	EST_HUMAN	AU137084 PLACE1 Homo sapiens cDNA clone PLAC1005740 5'
10073	22608	36383	2.68	9.0E-02 (A)087988.1	EST_HUMAN	EST_HUMAN	AV687808 GXC Homo sapiens cDNA clone GKX4402 5'
10384	23273	35948	1.71	9.0E-02 (B)04986.1	EST_HUMAN	EST_HUMAN	801434080F1 NH MKC, 72 Homo sapiens cDNA clone IMAGE:3910363 5'
10542	23428	35948	1.99	9.0E-02 (A)24321.1	NT	NT	Homo sapiens DMB11 candidate tumour suppressor gene, exons 1 to 35
10542	23428	35949	1.80	9.0E-02 (A)24321.1	NT	NT	Homo sapiens DMB11 candidate tumour suppressor gene, exons 1 to 35
10620	23505	35940	0.94	9.0E-02 (B)67270.1	EST_HUMAN	EST_HUMAN	802086759F1 NH MKC, 83 Homo sapiens cDNA clone IMAGE:4250669 5'
10849	23834	36966	2	9.0E-02 (A)01988.1	NT	NT	Anthrithum majus transcript Tarr3 pseudogene for transcriptase (in 5.4 copy)
10849	23834	36967	2	9.0E-02 (A)01988.1	NT	NT	Anthrithum majus transcript Tarr3 pseudogene for transcriptase (in 5.4 copy)
10751	23937	37070	4.05	9.0E-02 (Z)79702.1	SWISSPROT	SWISSPROT	COMPLEMENT DECA-YACCEIRATING FACTOR PRECURSOR (CD55)
11883	24121	37656	6.87	9.0E-02 (A)626755.1	EST_HUMAN	EST_HUMAN	Myocardium tuberculos 167Rv complete genome, segment 102182
12414	24681	38481	1.43	9.0E-02 (H)4589.1	EST_HUMAN	EST_HUMAN	zif1901 x1 Scores, testis, NIH Homo sapiens cDNA clone IMAGE:745382 3'
12074	25638		1.63	9.0E-02 (H)4589.1	EST_HUMAN	EST_HUMAN	zif1901 x1 Scores, testis, NIH Homo sapiens cDNA clone IMAGE:745382 3'
13103	25918		3.86	9.0E-02 (A)200187.1	NT	NT	Xenopus laevis mRNA for dclap2-2 (dcl2 gene)
4182	17212	30079	2.37	9.0E-02 (A)062355.1	EST_HUMAN	EST_HUMAN	CM2-9A023-00200-057412 BN0023 Homo sapiens cDNA
5952	18633	32452	0.86	9.0E-02 (P)1854	SWISSPROT	SWISSPROT	TRANSEKTOLE 2 (TK 2) (TRANSEKTOLE RELATED PROTEIN)
7694	20518	33918	4.96	9.0E-02 (A)003473.1	NT	NT	Trimeric protein, limited protease, strain IM4320
8001	20919	34296	7.96	9.0E-02 (A)161532.1	NT	NT	Antidopsis thaliana DNA chromosome 4, contig fragment No. 38
8152	18933	35052	0.86	9.0E-02 (P)1854	SWISSPROT	SWISSPROT	TRANSEKTOLE 2 (TK 2) (TRANSEKTOLE RELATED PROTEIN)
8190	21391	34732	2.46	9.0E-02 (B)035861.1	EST_HUMAN	EST_HUMAN	801435602F1 NH MKC, 68 Homo sapiens cDNA clone IMAGE:3897243 5'
8190	21391	34733	2.46	9.0E-02 (B)035861.1	EST_HUMAN	EST_HUMAN	801435602F1 NH MKC, 68 Homo sapiens cDNA clone IMAGE:3897243 5'
11122	24052	37497	2.80	9.0E-02 (B)035861.1	EST_HUMAN	EST_HUMAN	801435602F1 NH MKC, 68 Homo sapiens cDNA clone IMAGE:3897243 5'
11122	24052	37498	2.80	9.0E-02 (B)035861.1	EST_HUMAN	EST_HUMAN	801435602F1 NH MKC, 68 Homo sapiens cDNA clone IMAGE:3897243 5'
12278	26930	38958	1.83	9.0E-02 (A)70701.1	NT	NT	Human transforming growth factor beta type II receptor (TGF-beta RI), promoter region
13031	25570		1.75	9.0E-02 (A)72732.1	NT	NT	Antidopsis thaliana putative transcription factor (AT72732.1), complete cds
18527	14879	21859	3.42	9.0E-02 (B)071053.1	EST_HUMAN	EST_HUMAN	802100032F1 NH MKC, 91 Homo sapiens cDNA clone IMAGE:4261871 5'
3948	16977	26831	6.78	9.0E-02 (Z)35303.1	NT	NT	Mus musculus coding region filament-binding protein (Cobp), mRNA
5162	18174	31019	0.11	9.0E-02 (Z)35303.1	EST_HUMAN	EST_HUMAN	Mus musculus coding region filament-binding protein (Cobp), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3351	16337	22397	1.11	9.2E-02	AI350354.1	EST_HUMAN	173621.1 NCL CGAR_C03 Homo sapiens cDNA clone IMAGE:926158.5'
3947	16983		1.21	9.2E-02	U92048.1	NT	Homo sapiens fetal cytotrophoblastic antigen (Pctg), mRNA
4338	17332		0.75	8.2E-02	U92048.1	NT	Homo sapiens fetal cytotrophoblastic antigen (Pctg), mRNA
4132	17452		0.37	9.2E-02	BE42722.1	EST_HUMAN	60904.03057 NIH MG63.T71 Homo sapiens cDNA clone IMAGE:236176.5'
4735	17735	30515	1.87	9.2E-02	X64042.1	NT	Gallus gallus ggc gene
8557	21518	34862	2.03	9.2E-02	T46920.1	EST_HUMAN	p65503.1 Stratagene plasmids (p657223) Homo sapiens cDNA clone IMAGE:ns006.9' similar to p65500.9 GUANINE NUCLEOTIDE-BINDING PROTEIN (G), ALPHA SUBUNIT (HUMAN)
13045	26926	35228	2.03	9.2E-02	X65206.1	NT	Hulaire callose isomerase gene
8795	21885		1.57	9.2E-02	1143872	NT	Podocara anserina mitochondrion, complete genome
446	13113	26000	3	9.1E-02	X77065.1	NT	O. cuniculata K12 keratin gene
19054	23846	37274	0.88	9.1E-02	PT6895	SWISSPROT	8-PHOSPHORYLUTOKINASE (PHOSPHORYLUTOKINASE)
2440	16444	28444	1.27	9.1E-02	AI372569.1	EST_HUMAN	PA2-BT10345-161289-001-002.BT0349 Homo sapiens cDNA
3737	16769		1.41	9.1E-02	AI372569.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
4608	17805	36463	2.1	9.1E-02	AI161564.2	NT	Homo sapiens MS555 gene, partial cds; and CUC1, DD4H, G59, G56, G58, G64, G66, G67, BAT5, G8b, CS928, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, COT LST-1, LTB, TNF, and LTA genes, complete cds
5932	18909	32119	1.05	9.1E-02	AF129765.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
7690	22982		0.45	9.1E-02	AF028003.1	EST_HUMAN	sa17405.Y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968.5'
7783	20712	34014	11.62	9.1E-02	AF06058.1	NT	Acropora perisperm genomic DNA, section 4/7
8128	21038	34957	0.87	9.1E-02	AF060001.1	NT	Mus musculus Tyrosinophyll zeta mRNA, complete cds
8186	21076	34006	0.79	9.1E-02	U38973.1	NT	Widely distributed protein p24 gene for phytochrome
8372	21276	34608	0.42	9.1E-02	AJ289357.1	NT	Homo sapiens gamma actin gene, exon 9
8480	22408	35769	1.08	9.1E-02	Y14578.1	NT	FB16F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB16F10.3cnd
10310	23735		1.58	9.1E-02	T03844.1	EST_HUMAN	T6F16F10Y1 adin (T6F16F10Y1) testis, embryos, Genomic 3275 nt
10398	23821	37248	0.93	9.1E-02	ST4059.1	NT	Human RH1, TCT, G11687.5, G14887.6, and PRL1 genes
10504	23846	37274	0.88	9.1E-02	Y11187.1	NT	Rena calceolaria dihydropyridine receptor mRNA, complete cds
11605	24517	37887	3.26	9.1E-02	AF037025.1	NT	Reus non-viral cell cycle protein p53/22 gene, complete cds
12525	25246		2.31	9.1E-02	AF050565.1	NT	Homo sapiens protein MUC3B gene for MUC3B mRNA, exon 1-11
12958	26757		10.85	9.1E-02	AJ291906.1	NT	FOLATE RECEPTOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV16) (KB CELLS FBP)
768	13825	26756	2.06	9.0E-02	AF16328	SWISSPROT	Prosp10.1 NCL CGAR_C03 Homo sapiens cDNA clone IMAGE:3178642.3' similar to contains AU repetitive element
1682	14690	27850	5.44	9.0E-02	BE220462.1	EST_HUMAN	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12900	25208		1.59	8.9E-02	AF091614.1	NT	Hinducible p/CAF, clone 560, section 76 of 132 of the complete genome
1400	14401	27865	0.26	8.9E-02	CG21724	SWISSPROT	PROBABLE DNA LIGASE (POL) V(D)J RECOMBINATION LEUCINE SYNTHASE (A7P)
3975	17003	22960	1.24	8.9E-02	AA29528.1	EST_HUMAN	EST111695 Uterus Homo sapiens cDNA 5' end
4418	17441		0.33	8.9E-02	Q00238	SWISSPROT	TRANSCRIPTION INITIATION FACTOR, FRID 635 KOA SUBUNIT (TAFL135) (TAFL135) (TAFL135)
4405	17417		0.78	8.9E-02	4592433	NT	Homo sapiens paired box gene 6 (arid3a, variabilis) (PA33), isoform b, mRNA
7074	20955		0.7	8.9E-02	D17530.1	NT	Sheep mRNA for angiotensinogen, complete cds
9559	22468	35827	2.38	8.9E-02	AA15887.1	EST_HUMAN	z59605 at SRR14988 cdbn (#93705) Homo sapiens cDNA clone IMAGE555289 3'
11658	24467	37631	2.78	8.9E-02	BE234465.1	EST_HUMAN	901-91707F NH1 MGC 7 Homo sapiens cDNA clone IMAGE3355248 3'
11658	24467	37632	2.78	8.9E-02	BE234465.1	EST_HUMAN	901-91707F NH1 MGC 7 Homo sapiens cDNA clone IMAGE3355248 5'
11709	24611	39088	6.42	8.9E-02	AL040126.1	EST_HUMAN	DKFZ434D1313.11 434 (synonym: Hn33) Homo sapiens cDNA clone DKFZ434D1313 5'
3789	19701	22681	4.71	8.7E-02	U62695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed Xq28TS protein (XQ28ORF), and biglycan (BGN) genes, complete cds, and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3789	10791	22682	4.71	8.7E-02	U62695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed Xq28TS protein (XQ28ORF), and biglycan (BGN) genes, complete cds, and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4820	17821	30090	1.35	8.7E-02	AF178024.1	NT	Max musculus ANK interacting protein-3a (Iip3) mRNA, complete cds
5155	18148	30994	0.80	8.7E-02	AF18639.1	EST_HUMAN	W62262-21 NCI CCAP-LT88 Homo sapiens cDNA clone IMAGE2422823 3'
5497	18576	31423	5.51	8.7E-02	AA263976.1	EST_HUMAN	z55608 at NCI CCAP-CCB1 Homo sapiens cDNA clone IMAGE791488 3'
5497	18576	31423	5.51	8.7E-02	AA263976.1	EST_HUMAN	z55608 at NCI CCAP-CCB1 Homo sapiens cDNA clone IMAGE791488 3'
7161	20258	33524	0.7	8.7E-02	A271985.2	NT	Max musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7161	20258	33525	0.7	8.7E-02	A271985.2	NT	Max musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7994	20093	33527	0.89	8.7E-02	AF281942.1	NT	Oncophanes myotis TAT-shifting protein 1 mRNA, partial cds
9091	22010	35596	0.71	8.7E-02	AE004757.1	NT	Pseudomoc aneurysms PA01, section 348 of 926 of the complete genome
9091	22010	35597	0.71	8.7E-02	AE004757.1	NT	Pseudomoc aneurysms PA01, section 348 of 926 of the complete genome
11194	23083		2.5	8.7E-02	D07768.1	NT	Oryctolagus cuniculus cyclinoma P-439 (CYP43A) gene, 5' end
11708	24567	38140	2.04	8.7E-02	AJ007763.1	NT	Chondrocyte cyclinoma P-439 and P-439-like genes
12497	25230		2.04	8.7E-02	AF171161.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12497	25230		2.04	8.7E-02	AF171161.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12675	25350		2.97	8.7E-02		6000057	Max musculus mitogen 2 (M2), mRNA
12675	25350		2.97	8.7E-02		6000057	Max musculus mitogen 2 (M2), mRNA
1280	14313	27362	4.95	8.9E-02	AL271733.1	NT	Max musculus ANK interacting protein-3a (Iip3) mRNA, segment 22
2259	16258	28215	2.25	8.9E-02	BE406367.1	EST_HUMAN	901-90401F NH1 MGC 21 Homo sapiens cDNA clone IMAGE308849 5'
3251	16278	28219	3.01	8.9E-02	BE406367.1	EST_HUMAN	Max musculus myosin beta (Myb) gene, complete cds
3713	16745		3.92	8.9E-02	AT153362.1	NT	Disphidinium alveolatum phenyl glyoxalase (hcg) gene, complete cds

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Probe ID SEQ ID NO.	Exon SEQ ID NO.	QRT SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6308	18260	3143	1.8	8.0E-02	AF060714.1	NT	Rattus norvegicus synaptic vesicle protein 2C (SV2C) mRNA, complete cds
6331	10391	3149	4.2	8.0E-02	Y03625.1	NT	Homo sapiens CDNA clone 1200, complete cds
5831	10391	3260	1.50	8.0E-02	U03625.1	NT	Mouse gamma globin gene, D region, D-seg, mu switch region (part 5)
5924	10398	3260	1.50	8.0E-02	U03625.1	NT	Mouse gamma globin gene, D region, D-seg, mu switch region (part 5)
8917	20433	34251	1.34	8.0E-02	P14616	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN (IGF1R) (IGF1R-RELATED RECEPTOR)
8659	21440	34761	1.23	8.0E-02	U70066	NT	Homo sapiens Smf2-related GTP activator protein (SRGAP) mRNA
8659	21440	34761	1.23	8.0E-02	U70066	NT	Homo sapiens Smf2-related GTP activator protein (SRGAP) mRNA
8648	21579	34616	0.99	8.0E-02	U01088.1	NT	Dichotylidium discoideum proteasome subunit C2 homology (PDC) gene, complete cds
8708	21559	34556	0.96	8.0E-02	U01088.1	NT	Homo sapiens 14q32.3 mapped gene, complete cds, and unknown gene
10297	23147	36556	1.3	8.0E-02	AF111703	NT	Homo sapiens 14q32.3 mapped gene, complete cds, and unknown gene
10292	23182	36556	0.67	8.0E-02	AF111703	EST_HUMAN	Homo sapiens 14q32.3 mapped gene, complete cds, and unknown gene
10650	23536	36590	0.71	8.0E-02	AF102604.1	NT	Rattus norvegicus SPA-1 like protein p128A mRNA, complete cds
11385	24301	37747	1.39	8.0E-02	AF208551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds, mitochondrial gene for mitochondrial product
11385	24301	37749	1.89	8.0E-02	AF208551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds, mitochondrial gene for mitochondrial product
11696	24597	38074	2.74	8.0E-02	BF300606.1	EST_HUMAN	001893437F1 NIH JMRC_17 Homo sapiens cDNA clone IMAGE:4136219 5'
11696	24597	38076	2.74	8.0E-02	BF300606.1	EST_HUMAN	001893437F1 NIH JMRC_17 Homo sapiens cDNA clone IMAGE:4136219 5'
11872	23972	37409	0.04	8.0E-02	AED01073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
12007	24946	38346	1.83	8.0E-02	AF230660.1	NT	Bacillus stearothermophilus Barfi methylase (Bfm) and Barfi restriction endonuclease (Bfr) genes, complete cds
2419	15423	29424	3.2	8.0E-02	AED00652.1	NT	Helicobacter pylori 26695 strain 130 2/134 of the complete genome
5996	18937	32556	0.7	8.0E-02	AA095491.1	EST_HUMAN	0018907 at NCBI CGAP_K68 Homo sapiens cDNA clone IMAGE162977 3' similar to gb-X01144.HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN)
5907	18937	32556	1.89	8.0E-02	P01089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
9244	10298	32456	5.41	8.0E-02	AF238985.1	NT	Mac musculus phosphoprotein C-like protein mRNA, partial cds
9167	22098	35454	2.4	8.0E-02	U794779	NT	Mac musculus myosin XV (Myo15), mRNA
10351	23240	39559	3.24	8.0E-02	BE835054.1	EST_HUMAN	RC4-070037-260700-014-408 OT0037 Homo sapiens cDNA
10351	23240	39560	3.24	8.0E-02	BE835054.1	EST_HUMAN	RC4-070037-260700-014-408 OT0037 Homo sapiens cDNA
10949	23736	37168	0.57	8.0E-02	XY6791.1	NT	V. anguillar gene for anguillar protein C
10953	23847	37273	0.99	8.0E-02	AF155101.1	NT	Homo sapiens cDNA clone 22 open reading frame 5 (C22ORF5), mRNA
11386	24532	37890	10.13	8.0E-02	AF155101.1	NT	Homo sapiens insulin-like growth factor, mRNA, complete cds
10114	24532	37890	3.02	8.0E-02	AF001662.1	NT	Shigella flexneri mutants gene for glucose-6-phosphate uridylyltransferase, complete cds
12883	25713		2.03	8.0E-02	U03665.1	NT	Adenovirus major mRNA for 110-residue transcription factor

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7370	20364	33033	2.05	8.2E-02	AF300556.1	NT	For human connective tissue growth factor precursor (CTGF) gene, complete cds
8195	21163		0.32	8.2E-02	AY143411.1	EST_HUMAN	AY143411 CD-Hom sapiens cDNA clone CHLNF07.6
8296	22184		0.35	8.2E-02	U03937.1	NT	Human integrin alpha 5 gene (ITPA5) gene, 5' flanking region
8331	22529	35023	3.97	8.2E-02	AW079128.1	EST_HUMAN	BCSP-1000939-471-00010001 Homo sapiens cDNA
8336	22529	35023	3.97	8.2E-02	AW079128.1	EST_HUMAN	BCSP-1000939-471-00010001 Homo sapiens cDNA
8336	22529	35023	3.97	8.2E-02	BE255161.1	EST_HUMAN	BCSP-1000939-471-00010001 Homo sapiens cDNA
10286	24176	39365	2.27	8.2E-02	BE255161.1	EST_HUMAN	BCSP-1000939-471-00010001 Homo sapiens cDNA
11648	24554	39234	1.63	8.2E-02	BS964298	EST_HUMAN	Rattus norvegicus E-cadherin gene, cDNA clone IMAGE:2355506.5
12607	25241	31665	4.43	8.2E-02	AE002245.2	NT	Chlamydomonas reinhardtii A1303, section 73 of the complete genome
12711	25363	31796	1.49	8.2E-02	AW565156.1	EST_HUMAN	O14-CT0361-021295-03-001 CT0361 Homo sapiens cDNA
12882	25703		3.91	8.2E-02	AF275931.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
1513	14614	27508	1.22	8.1E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcI, and mdcJ genes), complete cds
5951	16028	32149	1.02	8.1E-02	AE004008.1	NT	Xylella fastidiosa, section 162 of 228 of the complete genome
6840	19679	32590	0.87	8.1E-02	U11532.1	EST_HUMAN	A118487 Heart Homo sapiens cDNA clone A1484
7951	20498		0.8	8.1E-02	AL103279.2	NT	Homo sapiens chromosome 21 segment HS210379
8018	20934		1.45	8.1E-02	AI692981.1	EST_HUMAN	w89608.X1 NC1 CGAP LUG2 Homo sapiens cDNA clone IMAGE:2358503.9
8914	21844	35197	0.69	8.1E-02	U1426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060) mRNA
8914	21844	35198	0.69	8.1E-02	U1426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060) mRNA
10429	233.2		1.76	8.1E-02	AY050150.1	NT	Homo sapiens extracellular glycoprotein keratin precursor, gene, complete cds
11629	24774	34272	1.67	8.1E-02	AL103262.2	NT	Homo sapiens chromosome 21 segment HS210302
663	15884	28095	4.67	8.0E-02	U00316.1	EST_HUMAN	EST306723 MAGC resequences, MAGC Homo sapiens cDNA
963	140.3	28095	1.67	8.0E-02	U00316.1	EST_HUMAN	Melancon cartilage virus subtypes 1, complete genome
1725	15908	27721	10.65	8.0E-02	D26935.1	NT	Human gene for dihydropyrimidine dehydrogenase, complete cds (exon 1-15)
1725	15908	27721	10.65	8.0E-02	D26935.1	NT	Human gene for dihydropyrimidine dehydrogenase, complete cds (exon 1-15)
1821	14942	27519	2.05	8.0E-02	BE007218.1	EST_HUMAN	PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA
2163	15495		3.37	8.0E-02	BF246744.1	EST_HUMAN	001650548F1 NH1 MGCC 37 Homo sapiens cDNA clone IMAGE:4075618.5
2868	14160	27008	2.15	8.0E-02	U025149.1	NT	Dicystidium acidobium optic nucleotide phosphodiesterase gene, complete cds
2944	15896	28697	0.79	8.0E-02	AL450697.1	NT	Thermoplasma acidophilum complete genome; segment 515
3887	10916	29794	0.05	8.0E-02	AW590118.1	EST_HUMAN	EST191891 MAGC resequences, MAGC Homo sapiens cDNA
4119	17789		0.69	8.0E-02	490039	NT	Homo sapiens cAMP responsive element binding protein-beta 2 (CREB2) mRNA
4298	17927		7.91	8.0E-02	X72704.1	NT	M. musculus gene for glutathione S
5944	140.3	28095	9.44	8.0E-02	U00316.1	NT	Melancon cartilage virus subtypes 1, complete genome
5945	15912	32131	0.49	8.0E-02	AW591338.1	EST_HUMAN	EST196320 MAGC resequences, MAGC Homo sapiens cDNA

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Single men: 1000 and 10000	
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Probe SEQ ID NC:	Exon SEQ ID NC:	ORF SEQ ID NC:	Expression Signal	Most Similar (To) HT BLAST E Value	Top HT Accession No.	Top HT Database Source	Top HT Descriptor
7431	20129	33371	1.19	7.8E-02/UC695.2	NT		Homo sapiens zinc finger protein 12 (ZFP12), expressed-3cdNSTs protein (X0280RF), and jagurin (EGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8437	22365	35725	0.67	7.8E-02/X7344.1	NT		S. cerevisiae CYS15 gene, complete cds
8905	22531	35596	0.84	7.8E-02/AF23437.1	NT		Homo sapiens FIVE domain-containing dual specificity protein phosphatase FIVE-DSP1b mRNA, complete cds
8905	22531	35599	0.84	7.8E-02/AF23437.1	NT		Homo sapiens FIVE domain-containing dual specificity protein phosphatase FIVE-DSP1b mRNA, complete cds
8909	22887	36271	1.13	7.8E-02/AA69284.1	EST_HUMAN		nc8908.t1 NCI CGAP_P41 Homo sapiens cDNA clone IMAGE:717131
10318	23207	39678	0.61	7.8E-02/259124.1	NT		Bacillus subtilis complete genome (section 21 of 21); from 3600281 to 4214874
11108	24039	37483	1.92	7.8E-02/U32325.1	NT		Human intercalin-11 receptor alpha chain gene, complete cds
12883	25479	31764	1.89	7.8E-02/U72847.1	NT		Homo sapiens emopikotin (EVP1) gene, exons 15 through 18
3646	16384	31764	2.13	7.7E-02/AJ238935.1	NT		Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
6734	18807	31801	0.43	7.7E-02/AF02036.1	NT		Gallus gallus collagen type XII alpha-1 (COL12A1) gene, promoter region and partial cds
8413	21815	34847	0.61	7.7E-02/BC674475.1	EST_HUMAN		7c40d03.x1 NCI CGAP_Luc21 Homo sapiens cDNA clone IMAGE:3281501 3' similar to TR-06416 06416 18 PROTEIN. ;
8488	21419	34760	4.99	7.7E-02/AA02946.1	EST_HUMAN		TR-G1175004 G1175005 SPLICEDSOME ASSOCIATED PROTEIN. ;
10330	22328	36668	5.01	7.7E-02/P36360	SWISSPROT		PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
10630	22516	38549	1.09	7.7E-02/A316982.1	EST_HUMAN		nc8908.t1 NCI CGAP_H5C2 Homo sapiens cDNA clone IMAGE:2003369 3' similar to glc-238976 603
10630	22516	38590	1.09	7.7E-02/A316982.1	EST_HUMAN		nc8908.t1 NCI CGAP_H5C2 Homo sapiens cDNA clone IMAGE:2003369 3' similar to glc-238976 603
11449	24365	37814	5.97	7.7E-02/11427797	NT		Homo sapiens KIA0038 gene product (KIA0038), mRNA
12724	25760	37814	1.81	7.7E-02/11427797	NT		Homo sapiens KIA0038 gene product (KIA0038), mRNA
3446	16787	29584	3.15	7.7E-02/BC114432.1	EST_HUMAN		Homo sapiens intercalin regulatory factor 7 (IRF7), mRNA
6334	16384	32552	1.18	7.7E-02/AQ30471.1	EST_HUMAN		EST1122141 Camelsat11 Homo sapiens cDNA 3' and similar to similar to proteodactin 43
8314	19355	32552	0.7	7.7E-02/AQ30471.1	EST_HUMAN		nc8902.24 Homo sapiens cDNA 3' and similar to similar to proteodactin 43
9909	22887	36284	0.80	7.7E-02/BC13628.1	EST_HUMAN		nc8902.24 Homo sapiens cDNA 3' and similar to similar to proteodactin 43
9909	22887	36284	1.49	7.7E-02/AJ131016.1	NT		Homo sapiens SVI1 gene, complete cds
9909	22887	36284	1.49	7.7E-02/AJ131016.1	NT		Homo sapiens SVI1 gene, complete cds
10716	23378	37028	0.58	7.7E-02/BC17003.2	EST_HUMAN		nc8902.24 Homo sapiens cDNA 3' and similar to similar to proteodactin 43
10830	20722	37028	0.58	7.7E-02/BC17003.2	EST_HUMAN		nc8902.24 Homo sapiens cDNA 3' and similar to similar to proteodactin 43
11069	23644	37330	0.98	7.7E-02/BC26555.1	NT		nc8902.24 Homo sapiens cDNA 3' and similar to similar to proteodactin 43

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
110500_23844	37391		0.96	7.6E-02	X25656.1	NT	Laccludium mRNA for fucose phosphatide transferase
121262_24643	39146		2.23	7.6E-02	AW56046.1	EST_HUMAN	QY3-BN0046-150/00-151-e04 BN0048 Homo sapiens cDNA
8111_13867	28932		1.05	7.5E-02	5902603	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 6 (SLC6A9), mRNA
8111_13867	28933		1.05	7.5E-02	5902603	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 6 (SLC6A9), mRNA
4630_17036	35500	0.84	7.5E-02	ABV15961.1	NT	Homo sapiens L16 gene for interleukin-16, intron 1 and exon 2	
50958_19127	32258		1.45	7.5E-02	AI84741.7	EST_HUMAN	W63602.1 NCL CGAP IG111 Homo sapiens cDNA clone IMAGE:242287.3
8813_21843	35196		1.49	7.5E-02	AI849437.1	EST_HUMAN	W63602.1 NCL CGAP IGm25 Homo sapiens cDNA clone IMAGE:242491.3 similar to g0.M14328 ALPHA ENOLASE (HUMAN)
9074_22033	35337		1.49	7.5E-02	AI116913.1	EST_HUMAN	U110873 HEMBA Homo sapiens cDNA clone HEMBA100/284.5
105355_23421		0.65	7.5E-02	3F227793.1	EST_HUMAN	7691605.1 NCL CGAP IG28 Homo sapiens cDNA clone IMAGE:3378594.3 similar to contains element ME427 regulatory element;	
10971_23856	37252		0.87	7.5E-02	3F260696.1	EST_HUMAN	ME427 regulatory element;
110971_23856	37252		0.87	7.5E-02	3F260696.1	EST_HUMAN	ME427 regulatory element;
9000_13370	25488		1.77	7.4E-02	AV53847.1	NT	Chlamydomonas reinhardtii 16S rDNA
2818_18516		0.68	7.4E-02	87590599	EST_HUMAN	R52110054200000001-H09110354 Homo sapiens cDNA	
38551_19597	29597		1.81	7.4E-02	U76855.1	EST_HUMAN	Mat musculus pancreatic histone/histone transcription factor 1 (F1N1), mRNA
48171_17818	30556		1.15	7.4E-02	U76855.1	EST_HUMAN	W63601.1 NCL CGAP IG282.31 Homo sapiens cDNA clone IMAGE:333368.3
4089_17801	30775		3.04	7.4E-02	6973443.2	NT	Homo sapiens 5S rDNA rPLP carrier protein 1 (L1N1), mRNA
3054_19351	30043		1.05	7.4E-02	6973443.2	NT	Homo sapiens 5S rDNA rPLP carrier protein 1 (L1N1), mRNA
5766_18346	31191		1.05	7.4E-02	U912148.1	EST_HUMAN	Mytilus edulis hemoglobin beta chain (Hemoglobin), mRNA
6771_19376	33116		1.26	7.4E-02	U912148.1	EST_HUMAN	Mytilus edulis hemoglobin beta chain (Hemoglobin), mRNA
9388_23816	34116		0.65	7.4E-02	U900422.1	EST_HUMAN	Caenorhabditis elegans mRNA for DYS-1 protein, protein
9488_23816	34116		0.65	7.4E-02	U900422.1	EST_HUMAN	Caenorhabditis elegans mRNA for DYS-1 protein, protein
2482_21412	34749		1.33	7.4E-02	BE580112.1	EST_HUMAN	U110873 HEMBA Homo sapiens cDNA clone IMAGE:3112586.3
9368_21997	35351		0.63	7.4E-02	U50081.1	NT	Homo periodic histone protein 2 (H1P2) gene, spans 15 to 21, and complete cds
8709_22034	38014		1.1	7.4E-02	AV62906.1	EST_HUMAN	HNF7H11 Y NCL CGAP IG11 Homo sapiens cDNA clone IMAGE:260781.5 similar to SWISCA2_HUMAN
97309_22634	38016		1.1	7.4E-02	AV62906.1	EST_HUMAN	HNF7H11 Y NCL CGAP IG11 Homo sapiens cDNA clone IMAGE:260781.5 similar to SWISCA2_HUMAN
10330_33739	36653		1.02	7.4E-02	U62205.1	NT	O15127 SECRETORY CARRIER ASSOCIATED MEMBRANE PROTEIN 2.
12178_25654	39615		1.49	7.4E-02	U62205.1	NT	O15127 SECRETORY CARRIER ASSOCIATED MEMBRANE PROTEIN 2.
22717_29801	37493.1		3.75	7.4E-02	AV37493.1	EST_HUMAN	Human LIM kinase1 and alternatively spliced LIM-kinase1 (LIMK) gene, complete cds
							Rattus norvegicus ribonucleic protein component 1 (TLPI), complete cds
							CAH-102024-081199-037-d11 H12043 Homo sapiens cDNA

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Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
12854	26464	31761	2.43	7.4E-02	BF055092.1	EST_HUMAN	60145319FT NIH_MGC_86 Homo sapiens cDNA clone IMAGE:2857725 5'
491	13552	25716	1.08	7.3E-02	BE04951.2	EST_HUMAN	60168193RT NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3895009 3'
491	13552	25716	1.08	7.3E-02	BE04951.2	EST_HUMAN	60168193RT NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3895009 3'
708	13767	26583	2.8	7.3E-02	AE001758.1	NT	Uncloned human exon 101 of 133 of the complete genome
1498	16992	27485	4.36	7.3E-02	AL262931.1	EST_HUMAN	U04204R0103500254501104 Homo sapiens cDNA
1498	16992	27485	4.36	7.3E-02	AL262931.1	EST_HUMAN	U04204R0103500254501104 Homo sapiens cDNA
3189	17200	30070	1.02	7.3E-02	AL265341.1	NT	Homo sapiens NCB genes for a complete, section 144
5118	18115		1.84	7.3E-02	U12263.1	NT	Mus musculus transcription factor USF7 (USF7) gene, exon 8-10 and complete, cda
6723	18759	32868	2.08	7.3E-02	AA77697.1	EST_HUMAN	324402.31 Soares, fetal liver, spleen, IVRLS, 51 Homo sapiens cDNA clone IMAGE:461778 3' similar to
7852	20668	34113	3.2	7.3E-02	P08143	SWISSPROT	dbL02428 26S PROTEASE SUBUNIT 4 (HUMAN);
7852	20668	34114	3.2	7.3E-02	P08143	SWISSPROT	dbL02428 26S PROTEASE SUBUNIT 4 (HUMAN);
8293	21197		0.45	7.3E-02	BF110097.1	EST_HUMAN	601808047FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4735615 5'
8746	21670		1.48	7.3E-02	Y10857.2	NT	Homo sapiens KIAA0434 protein (KIA0434), mRNA
8746	21670	35257	0.65	7.3E-02	Y10857.2	NT	Mus musculus cat6 gene, exon 1, partial
9751	22676		1.34	7.3E-02	AB011000.1	NT	Homo sapiens mRNA for KIA0518 protein, partial cda
11665	19759	32865	2.1	7.3E-02	AA77697.1	EST_HUMAN	324402.31 Soares, fetal liver, spleen, IVRLS, 51 Homo sapiens cDNA clone IMAGE:461778 3' similar to
124	13230	26145	2.42	7.3E-02	AE000852.1	NT	dbL02428 26S PROTEASE SUBUNIT 4 (HUMAN);
124	13230	26145	2.42	7.3E-02	AE000852.1	NT	Melanoblastin thermolabile domain from bases 1029155 to 1030234 (section 88 of 146) of the complete
124	13230	26146	2.42	7.3E-02	AE000852.1	NT	gene
1484	14525	27480	2.25	7.3E-02	AL183301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1484	14525	27487	2.25	7.3E-02	AL183301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2581	16580		3.68	7.3E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 28 reverse transcriptase (pol) gene, internal fragment, partial
3954	16982	26805	-0.72	7.3E-02	AI473632.1	EST_HUMAN	code
4455	17465	30325	3.42	7.3E-02	BF12507.1	EST_HUMAN	UHFHW-414-05-015-1 NCL_CGAP_Sus8 Homo sapiens cDNA clone IMAGE:2732646 3'
4908	17897	30673	0.71	7.3E-02	11449569	NT	52077079FT NIH_MGC_32 Homo sapiens cDNA clone IMAGE:4281950 5'
5470	19351	31350	2.77	7.3E-02	U67831.1	NT	Piscocyclops callinectes, complete genome
5471	19352	31354	8.48	7.3E-02	P11120	NT	Melanococcus jamaicensis section 73 of 150 of the complete genome
6595	19405		0.65	7.3E-02	BF21596.1	EST_HUMAN	CALMODULIN
7851	20470	33759	1.26	7.3E-02	BF21096.1	EST_HUMAN	60185350FT NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4665224 5'
7851	20470	33759	1.26	7.3E-02	BF21096.1	EST_HUMAN	60185350FT NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4665224 5'

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Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7549	20487	33776	0.63	7.3E-02	AF221126.1	NT	Staphylococcus pneumoniae putative sequease (sp) (spsR), putative histidine kinase (spsK), and putative phosphatase (spsP) genes, complete cds
7578	20512		1.24	7.3E-02	5884687	NT	Staphylococcus pneumoniae putative sequease (sp) (spsR), putative histidine kinase (spsK), and putative phosphatase (spsP) genes, complete cds
8793	21695	35939	0.69	7.3E-02	P05143	SWISS-PROT	PROLINE-RICH PROTEIN (MR-3)
8793	21695	35940	0.69	7.3E-02	P05143	SWISS-PROT	PROLINE-RICH PROTEIN (MR-3)
9819	22542		0.63	7.3E-02	Y1721.1	NT	Lactococcus lactis capE gene
10104	22665		0.87	7.3E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
10133	23029	36426	2.37	7.3E-02	AF12452.1	EST_HUMAN	AV12452 DCA Homo sapiens cDNA clone DCAUG07.5'
10279	23189	36552	4.17	7.3E-02	L14601.1	NT	801769523F11 NH MGCC 20 Homo sapiens cDNA clone IMAGE:4263438.5'
10425	2331.4	36731	1.35	7.3E-02	BF125936.1	EST_HUMAN	801769523F11 NH MGCC 20 Homo sapiens cDNA clone IMAGE:4263438.5'
10506	23395	36807	2.45	7.3E-02	AF075187.1	EST_HUMAN	ATYPICAL PKC-SPECIFIC BINDING PROTEIN.1
10869	23576	37006	0.62	7.3E-02	AA766224.1	EST_HUMAN	cat2207 at NC1 CGAP GC81 Homo sapiens cDNA clone IMAGE:131884.3'
10839	23725	37146	2.25	7.3E-02	U82665.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28S1 protein (XQ28ORF), and blykcam (BLYCAM) genes, complete cds, and plasma membrane calcium ATPase isoform 3 (PMCA-3) gene, partial cds
10953	23837	37264	4.82	7.3E-02	BC65503.1	EST_HUMAN	801349528F11 NH MGCC 33 Homo sapiens cDNA clone IMAGE:3985951.5'
10978	23860		3.84	7.3E-02	BC65503.1	EST_HUMAN	801069194F11 NH MGCC 33 Homo sapiens cDNA clone IMAGE:3451565.5'
11351	24269	37711	3.84	7.3E-02	AF046874.1	NT	Rattus norvegicus bHLH transcription factor Maf1 (Maf1) gene, complete cds
12397	25165	31872	1.82	7.3E-02	AA776956.1	EST_HUMAN	861404.71 Score: 1198889.51 Homo sapiens cDNA clone IMAGE:1049368.5'
12471	25217		1.81	7.3E-02	AA694495.1	EST_HUMAN	nc02008 at NC1 CGAP Pfaffl Homo sapiens cDNA clone IMAGE:1098933.3'
12526	25290		4.57	7.3E-02	U82638.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
12540	25752		5.88	7.3E-02	AW000662.1	EST_HUMAN	CAH1N0065-205000-116 c11 NN1006 Homo sapiens cDNA
1927	14445	27920	2.31	7.1E-02	U02360.1	NT	Human Immunodeficiency virus type 1 (HIV) proviral structural capsid protein (p24) gene, partial cds
2311	15319	26520	4.11	7.1E-02	BF236802.1	EST_HUMAN	801672821F11 NH MGCC 33 Homo sapiens cDNA clone IMAGE:4692881.5'
6486	21417	34753	1.08	7.1E-02	AF12354.1	EST_HUMAN	864204.025F11 NH MGCC 33 Homo sapiens cDNA clone IMAGE:173362.3'
7260	23804		4.11	7.1E-02	BC34754.1	EST_HUMAN	864204.025F11 NH MGCC 33 Homo sapiens cDNA clone IMAGE:3651824.5'
851	19825	26526	1.22	7.0E-02	U02360.1	SWISS-PROT	COLLAGEN ALPHA-1(XV) CHAIN PROCURSOR
1916	14426		1.22	7.0E-02	U02360.1	NT	Human Maf1 gene, complete cds
1916	14426	27761	1.18	7.0E-02	AA69543.1	EST_HUMAN	861404.71 Score: 1198889.51 Homo sapiens cDNA clone IMAGE:1049368.5'
3079	16726	29025	2.02	7.0E-02	AF139162.1	EST_HUMAN	U14481-seq-57-04.11 NC1 CGAP Suid3 Homo sapiens cDNA clone IMAGE:2716020.3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (To) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3987	16996	29230	1.44	7.0E-02	AA154381	EST_HUMAN	h5x12.1 Source, testis, NIH Homo sapiens cDNA clone 1376678 3' similar to gb:U00002.60S
4126	17165	30026	1.39	7.0E-02	BE070263.1	EST_HUMAN	PHOSPHOLIPASE PROTEIN 32 (HUMAN)
4237	17259	30026	1.39	7.0E-02	AF072092.1	EST_HUMAN	U74470/07/20010406-ct010 B10407 Homo sapiens cDNA
4310	17324	30161	1.21	7.0E-02	AF077823.1	NT	GM12878 Homo sapiens cDNA clone IMAGE:4050071 5'
5641	18334	30984	0.97	7.0E-02	BF381687.1	EST_HUMAN	Genis familiaris inducible ribic code synthase mRNA, complete cds
5692	18840	30984	0.97	7.0E-02	BF381687.1	EST_HUMAN	001816251/1 NIH MG-63 Homo sapiens cDNA clone IMAGE:4050071 5'
7799	20728	34730	0.88	7.0E-02	U09483.2	NT	Lumbricus rubellus mRNA for cytochrome B
8050	20983	34779	0.74	7.0E-02	AV880263.1	EST_HUMAN	AV880263 GKG Homo sapiens cDNA clone GYCCAE08 5'
8943	22566	35940	1.28	7.0E-02	K02501.1	NT	Gallus gallus mRNA for perlecan, accotin, XL spliced variant (acc gene)
10124	23015	36411	1.97	7.0E-02	K02501.1	NT	African swine fever virus, complete genome
10459	23347	36784	0.95	7.0E-02	U27866.1	NT	Rat Ig gamma 1 spliced H-chain gene C-region, 3' and
11811	24732	38228	3.20	7.0E-02	AAT24265.1	EST_HUMAN	Human myosin binding protein H (MYBR-H) gene, complete cds
12040	25840	31760	1.68	7.0E-02	11421838	NT	all04065.01 Source, NPL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:14837
13006	26514	37806	0.97	6.9E-02	AL163210.2	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN)
537	13806	26515	9.27	6.9E-02	AL163210.2	NT	Homo sapiens hypodermal protein FLJ20116 (FLJ20116), mRNA
1391	14392	3857	1.06	6.9E-02	4507998	NT	Homo sapiens chromosome 21 segment H821C010
3857	16886	29770	1.36	6.9E-02	Q08364	SW ISPROT	Homo sapiens regulator of Gs-selective protein signaling (ZSAP1) mRNA, and translated products
3957	16936	29771	1.36	6.9E-02	Q08364	SW ISPROT	26S PROTEASOMAL REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5233	18238	31050	0.93	6.9E-02	AA070269.1	EST_HUMAN	26S PROTEASOMAL REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
6141	19200		0.46	6.9E-02	AF161934.1	NT	all05068.01 Source, testis, NIH MG-63 Homo sapiens cDNA clone IMAGE:1032710 3'
8602	20976		0.55	6.9E-02	AF161934.1	NT	Homo sapiens HSP-101 mRNA, partial cds
8630	21591		0.83	6.9E-02	U12022.1	NT	Human calmodulin (CALM) gene, exons 2,3,4,5 and 6, and complete cds
9116	22044	35400	0.96	6.9E-02	BE597435.1	EST_HUMAN	Human calmodulin (CALM) gene, exons 2,3,4,5 and 6, and complete cds
9116	22044	35401	0.96	6.9E-02	BE597435.1	EST_HUMAN	601340651/1 NIH MG-63 Homo sapiens cDNA clone IMAGE:388300 5'
9604	22960	35983	0.7	6.9E-02	U22687.1	NT	601340651/1 NIH MG-63 Homo sapiens cDNA clone IMAGE:388300 5'
12415	25184		5.82	6.9E-02	U22687.1	NT	Barbara child peroxisome RE1 protein (p26) and three capid protein VP (p9) genes, complete cds
12571	25276		1.33	6.9E-02	P44621	SW ISPROT	Adenovirus 212 mRNA for RNA head protein
12780	25409		5.15	6.9E-02	AF169553.1	NT	PROTEIN TRANSLOCATOR PROTEIN HSP-60 (HSP-60)
1624	14465	27821	4.83	6.9E-02	AF169553.1	NT	Homo sapiens nuclear pore domain protein P (NUP62) gene, complete cds
1896	15314	28504	0.94	6.9E-02	AF169553.1	NT	Homo sapiens nuclear pore domain protein P (NUP62) gene, complete cds
4247	17263	35728	0.97	6.9E-02	BE267611.1	EST_HUMAN	601340651/1 NIH MG-63 Homo sapiens cDNA clone IMAGE:393706 5'
						NT	Male muscular phosphatidase 9A (P4460), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4668	17679		0.76	6.9E-02	BE1410761	EST_HUMAN	NR0110056.071039.001.c05.H10069 Homo sapiens cDNA
4691	16941		0.66	6.9E-02	P219720	SWISSPROT	GELLSUBFACE RECEPTOR DAE-1 PRECURSOR
7728	26137		1.31	6.9E-02	BE0918001	EST_HUMAN	R171.BT0254-003004017400.BT0254 Homo sapiens cDNA
7469	26020	33691	0.98	6.9E-02	AL103268.2	NT	Homo sapiens chromosome 21 segment HS210268
8137	21045	34376	0.74	6.9E-02	U19866.1	NT	Dibacalium discalium myosin heavy chain isoform A (HHC-A) mRNA, complete cds
8866	21795	35147	5.72	6.9E-02	AL348287.1	NT	Proocoeus alysi complete genome segment 581
8895	21795	35148	5.72	6.9E-02	AL348287.1	NT	Proocoeus alysi complete genome segment 581
12244	20226		1.63	6.9E-02	T03214.1	EST_HUMAN	FB443 Fetal brain, Strikawa Homo sapiens cDNA clone FB443 3' end similar to LINE-1
12844	26144		1.7	6.9E-02	AA766011.1	EST_HUMAN	46706.s1 Soames testis, N11 Homo sapiens cDNA clone 1320763 3'
13390	25604		2.09	6.9E-02	8910868	EST_HUMAN	Mus musculus latent TGF beta binding protein (lgb), mRNA
1651	14382		2.6	6.7E-02	AF116934.1	NT	Oncorhynchus mykiss TAF11 protein (OnmyTAF1) mRNA, OnmyTAF101 allele, complete cds
1911	14632	27609	1.47	6.7E-02	AF116934.1	EST_HUMAN	907964.s1 Soames, NHL T1, GBC3 S1 Homo sapiens cDNA clone IMAGE1841408 3'
3781	16812	26983	5.04	6.7E-02	P12728	SWISSPROT	HOMEOBOX PROTEIN HOX-D1 (HOXD1)
4037	17054	26984	0.8	6.7E-02	U57763.1	NT	Oryzias latipes Rapi1b mRNA, complete cds
8433	21369	34704	0.82	6.7E-02	X62906.1	NT	Oryzias latipes Rapi1b mRNA, complete cds
8433	21369	34705	0.82	6.7E-02	X62906.1	NT	Haplotype DNA for cGMP phosphodiesterase (exons 4-22)
10127	23018	36413	0.64	6.7E-02	AW197369.1	EST_HUMAN	Haplotype DNA for cGMP phosphodiesterase (exons 4-22)
10127	23018	36414	0.64	6.7E-02	AW197369.1	EST_HUMAN	U1H-BH1-acc-g-01-011.s1 NC1_OGAP_S3u3 Homo sapiens cDNA clone IMAGE2715433 3'
1377	14409	27353	0.91	6.9E-02	AI79509.1	EST_HUMAN	U1H-BH1-acc-g-01-011.s1 NC1_OGAP_S3u3 Homo sapiens cDNA clone IMAGE2715433 3'
1396	14427	27381	0.96	6.9E-02	AI79509.1	EST_HUMAN	U1H-BH1-acc-g-01-011.s1 NC1_OGAP_S3u3 Homo sapiens cDNA clone IMAGE2715433 3'
2196	15206	29210	2.21	6.9E-02	AI389241.1	NT	SW1.LN1, NYCOO P06648 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG, 1
3826	16063	29467	10.68	6.9E-02	R04061.1	EST_HUMAN	SW1.LN1, NYCOO P06648 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG, 1
3837	16876	29479	9.69	6.9E-02	7106357	NT	Disophila melanogaster cactin mRNA, complete cds
3837	16876	29480	9.69	6.9E-02	7106357	NT	Mus musculus Cap2 gene for capbin 12, exons 1,21, three alternative transcripts
4167	17188	30061	1.93	6.9E-02	AI260235.1	NT	Homo sapiens neofolitin (MSLN), transcript variant 1, mRNA
5100	16937	30013	1.263	6.9E-02	Q17709	SWISSPROT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5100	16937	30044	1.263	6.9E-02	Q17709	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
6869	19998	33114	3.37	6.9E-02	X00411.1	NT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
6901	19931	33146	0.83	6.9E-02	P28199	SWISSPROT	P-vulgaris mRNA for chalcone synthase
6901	19931	33146	0.83	6.9E-02	P28199	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFIN
7108	19931	33146	0.83	6.9E-02	P28199	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFIN
7108	19931	33146	0.83	6.9E-02	P28199	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFIN

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Probes Seq ID NO.	Exon Seq ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) HT BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
5667	10706	32907	0.76	6.4E-02	AF17298.1	EST_HUMAN	we7412.1 Swiss Decipherable cDNA, N1QD Homo sapiens cDNA clone IMAGE:246780.3
7139	23333	33597	4.59	6.4E-02	BE97444.1	EST_HUMAN	6018642R2 NH1.MGC. 35 Homo sapiens cDNA clone IMAGE:359700.3
7605	27032	34095	0.46	6.4E-02	AF16757.2	NT	Nesioeste myoblasts myotube A strain Z949 complete genome segment 87
8611	27041		3.15	6.4E-02	AF763333	NT	Mac musculus duodenal subunit 6 (cds) (Cds6), mRNA
8223	27451	35033	4.96	6.4E-02	AF169305.1	EST_HUMAN	5.118 seq F Human fetal liver Lentiid ZAP Express Homo sapiens cDNA.5
8972	27568	35971	0.75	6.4E-02	AF151053.1	EST_HUMAN	AF151053 Human mRNA from c23+ stem cells Homo sapiens cDNA clone CSDA1A.10
10114	29005		0.01	6.4E-02	BE13368.1	EST_HUMAN	RC1-011085-150502-91+g2 OT10033 Homo sapiens cDNA
10239	29130	36533	1.96	6.4E-02	AF001128.1	NT	Homo sapiens mRNA for MIA0354 protein, partial cds
10754	29840	37073	0.98	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 13, 17, and 18
10754	29840	37074	0.98	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 13, 17, and 18
12131	24972	39475	2.01	6.4E-02	U01328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rickett gene, and sodium phosphate transporter (NPT3) gene, complete cds
12131	24972	39476	2.01	6.4E-02	U01328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rickett gene, and sodium phosphate transporter (NPT3) gene, complete cds
12483	29844		4.18	6.4E-02	AF107860.1	NT	Homo sapiens muscle 98 (MUC98) gene, partial cds
12931	29254	31930	2.41	6.4E-02	AJ27174.1	NT	Drosophila melanogaster mRNA, for mod(mdg)51.4 protein
1780	14906	27776	1.82	0.9E-02	AF106005.1	NT	Mac musculus major histocompatibility locus class III region Hs0701 gene, partial cds; snRNP. G7A, NG28
3006	16700		2.84	0.9E-02	P37002	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
5084	18341	30960	1.00	0.9E-02	AK053769.1	EST_HUMAN	w80910.31 NQ1 CGAP-UT Homo sapiens cDNA clone IMAGE:246700.3
5306	18347	31190	0.89	0.9E-02	D00972.1	NT	Synovial sarcoma 1, PCC05803 complete genome, 10271, 7116642-164241
6376	19425	32591	1.14	0.9E-02	BF120738.1	EST_HUMAN	691812310F NH1.MGC. 541 Homo sapiens cDNA clone IMAGE:4097489.5
7612	20547		0.71	0.9E-02	X67869.1	NT	H sapiens gene encoding La autoantigen
8631	27737	36119	1.1	0.9E-02	AJ439915.1	NT	Drosophila melanogaster Dmrt1a gene, exons 1-3
10571	29404	36616	3.76	0.9E-02	AJ010162.1	NT	Pesabite 5 virus RNA for polyprotein (NS5A region), partial cds; alt:ns: CMR-152
10754	29850		1.14	0.9E-02	AF166870.1	EST_HUMAN	AF166870 GCG Homo sapiens cDNA clone GCGACD1.3
11138	19425	32591	3.33	0.9E-02	BF120738.1	EST_HUMAN	691812310F NH1.MGC. 541 Homo sapiens cDNA clone IMAGE:4097489.5
4369	17355	33227	2.34	0.2E-02	AF161572.2	NT	Katagaplan Rat1a DNA, chromosom 4, coding fragment No. 65
4447	17458		1.05	0.9E-02	AF171236.1	NT	Rattus norvegicus differentiation-associated, Na-dependent L-type phosphate cotransporter (DNPI) mRNA
4448	18413		0.80	0.9E-02	U07584.1	NT	Methanococcus jannaschii section 126 of 150 of the complete genome

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3716	16324	26230	1.13	6.0E-02	AA372376.1	EST_HUMAN	EST14296 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3703	16734	26230	1.23	6.0E-02	BC264443.2	EST_HUMAN	601601519R1 NIH MG-C 68 Homo sapiens cDNA clone IMAGE:3976060 3'
5695	16399	35037	2.43	6.0E-02	261793.2	NT	Streptococcus pyogenes pefC, pefE and transposase genes and ORF DNA
5232	16222	31068	0.79	6.0E-02	AF149768.1	NT	Rattus norvegicus insulin specific protein mRNA, complete cds
5563	16386		1.93	6.0E-02	AA137021.1	EST_HUMAN	RC3-81T023-011189-013-304.B1070233 Homo sapiens cDNA
9460	18205	32980	1.03	8.0E-02	A067937.1	EST_HUMAN	w68H05.41 Soares, NPL, T, GBC_S1 Homo sapiens cDNA clone IMAGE:2360673 3' similar to contains L1 L1 L1 L1 negative element
7328	18498	31271	2.42	8.0E-02	5174868	NT	Homo sapiens stimulated trans-acting factor (60 kDa) (STAF50) mRNA
7328	18498	31272	2.42	8.0E-02	5174868	NT	Homo sapiens stimulated trans-acting factor (60 kDa) (STAF50) mRNA
7552	20489	33778	2.15	8.0E-02	BF32346.1	EST_HUMAN	60181274P2 NIH MG-C 66 Homo sapiens cDNA clone IMAGE:4040228 5'
7970	20804	33502	0.64	6.0E-02	BF110486.1	EST_HUMAN	601874710T1 NIH MG-C 54 Homo sapiens cDNA clone IMAGE:4101074 5'
8133	21043	34273	1.78	6.0E-02	A194276.1	EST_HUMAN	q59808.X1 Soares, Isela, NHT Homo sapiens cDNA clone IMAGE:1784169 3'
9812	22718	36100	0.8	8.0E-02	A023187.1	EST_HUMAN	h78a06.X1 NCI CGAP GC5 Homo sapiens cDNA clone IMAGE:2237352 3'
9812	22718	36101	0.8	8.0E-02	A023187.1	EST_HUMAN	h78a06.X1 NCI CGAP GC5 Homo sapiens cDNA clone IMAGE:2237352 3'
9940	22845	35235	1.91	8.0E-02	AJ245935.1	NT	Adipenser basai partial TGLV gene for immunoglobulin light chain variable region, exon 1-2
9940	22845	35236	1.91	6.0E-02	AJ245935.1	NT	Adipenser basai partial TGLV gene for immunoglobulin light chain variable region, exon 1-2
10416	23305	36725	0.64	6.0E-02	AA450797.1	EST_HUMAN	EST110054 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-1
10416	23305	36724	0.64	6.0E-02	AA450797.1	EST_HUMAN	EST110054 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-1
11178	24677		1.78	6.0E-02	AA126395.1	EST_HUMAN	zr07008.1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:560190 5' similar to gi-X68911.605 RIBOSOMAL PROTEIN L31 (HUMAN)
12893	25448		3.06	6.0E-02	A060273.1	EST_HUMAN	w68H03.41 Soares, NPL, T, GBC_S1 Homo sapiens cDNA clone IMAGE:2360685 3' similar to TH-060298
248	13346	26258	4.63	5.0E-02	AF163471.1	EST_HUMAN	RC3-81T023-020100-012-4r01D10001 Homo sapiens cDNA
3025	19677	29895	2.7	5.0E-02	AF140260.1	NT	Mouse muscle p53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
7220	25955	33467	0.6	5.0E-02	AF145960.1	NT	Drosophila melanogaster L22D107.611g (sing) mRNA, complete cds
9776	27104	35462	2.28	5.0E-02	9362648	NT	Mouse muscular lincos related homebox 5 (Drosophila) (h25), mRNA
9683	21341		0.95	5.0E-02	BF242746.1	EST_HUMAN	60187400P1 NHT MG-C 55 Homo sapiens cDNA clone IMAGE:4103994 5'
11224	24150		3.46	5.0E-02	6818670	NT	Mouse muscular lincos related (L24), mRNA
11459	24374	37822	1.5	5.0E-02	11453358	NT	Mouse muscular lincos related (L24), mRNA
11974	24817		1.7	5.0E-02	BF27283.1	EST_HUMAN	60185656F1 NHT MG-C 82 Homo sapiens cDNA clone IMAGE:424384 5'
11986	24831		1.68	5.0E-02	AF149731.1	NT	Calu-6 cell HCG beta-actin mRNA
351	14671		4.0	3.8E-02	D06101.0	NT	Thymosin immunosuppressant mcrC, mcrA genes and URF-1

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1687	14717	27678	1.07	5.8E-32	Q87768	SWISSPROT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
1688	17934	29690	1.41	5.8E-02	A60107.75.1	NT	Kinesin1a matinsin clone 87, cf 135 of the complete genome
3731	15793	30332	7.89	5.8E-02	A50155.0227.1	EST_HUMAN	w242402.x1 NCI CGAP T4711 Homo sapiens cDNA clone IMAGE:2544578 3'
4464	14745	30333	7.89	5.8E-02	A5051927.1	EST_HUMAN	w242402.x1 NCI CGAP T4711 Homo sapiens cDNA clone IMAGE:2544578 3'
4693	17698	30537	0.93	5.8E-02	A4247905.1	EST_HUMAN	gh0801.x1 Soares_jmd_liver_spleen_INFLS.S1 Homo sapiens cDNA clone IMAGE:1484897 3' similar to
4693	17698	30598	5.93	5.8E-02	A4247905.1	EST_HUMAN	gh5901.x1 Soares_jmd_liver_spleen_INFLS.S1 Homo sapiens cDNA clone IMAGE:1484897 3' similar to
4839	17694	31098	2.83	5.8E-02	A1092924.1	NT	Cells gamma Myosin kinase JUK1 (JAK1) mRNA, complete cds
5852	18246	31098	1.11	5.8E-02	A317768	SWISSPROT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
5772	18258	31109	0.97	5.8E-02	A4753968.1	NT	Male testicular epididymal 9 month foetal receptor (Egr) gene, exons 6 through 28, and complete cds,
5772	18258	31110	0.97	5.8E-02	A4753968.1	NT	Male testicular epididymal growth factor receptor (Egr) gene, exons 6 through 28, and complete cds,
8129	19168	32324	0.93	5.8E-02	A1450094.1	EST_HUMAN	z68411.x1 Stratiopene Hela cell c. 837/216 Homo sapiens cDNA clone IMAGE:527008 3'
8131	21041	34370	2.7	5.8E-02	A591160.1	NT	Human polyomeric microscactin DNA
8131	21041	34371	2.7	5.8E-02	A591160.1	NT	Human polyomeric microscactin DNA
8224	22152	35504	0.54	5.8E-02	A1452393.1	NT	Human sapiens chromosome 21 segment HS21Q083
9226	22152	35504	0.54	5.8E-02	A1452393.1	NT	Drosophila melanogaster male fertility type-A (fru) mRNA, complete cds
12431	25191	25191	4.96	5.8E-02	A1902177.1	EST_HUMAN	nc05611.x1 NCI CGAP T4711 Homo sapiens cDNA clone IMAGE:1172884 3'
12709	25916	25916	4.96	5.8E-02	A1902166.1	EST_HUMAN	nc056105.x1 NCI CGAP B2.2 Homo sapiens cDNA clone IMAGE:1032465 3' similar to WP_C37A2.2
3105	16156	29047	0.88	5.7E-02	A081644.1	EST_HUMAN	CE098111
3167	16170	29095	1.56	5.7E-02	A119117.1	NT	Homo sapiens degenerate transporter (SLC6A3) gene, complete cds
3869	16886	29780	3.21	5.7E-02	A5060797.1	EST_HUMAN	ESTS788655 MAPK kinase sequences, MGI Homo sapiens cDNA
6054	20855	34108	0.95	5.7E-02	A1275948.1	NT	Homo sapiens ABOH (ABCA1) gene, complete cds
7879	20855	34108	0.95	5.7E-02	A1275948.1	EST_HUMAN	0014439371 NIH MGCG-95 Homo sapiens cDNA clone IMAGE:3871985 9'
7879	20855	34108	0.95	5.7E-02	BE071911.1	EST_HUMAN	0014439371 NIH MGCG-95 Homo sapiens cDNA clone IMAGE:3871985 9'
7923	34201	34201	0.78	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
7923	34201	34202	0.78	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
7923	34201	34203	1.95	5.7E-02	A299603.1	NT	Human beta-2-microglobulin (beta-2-microglobulin) gene, complete cds
10394	23253	36870	0.72	5.7E-02	G681280	EST_HUMAN	Male muscle cell oncogene (E-cad), mRNA
1833	24539	38670	3.77	5.7E-02	A72585.1	EST_HUMAN	en-3609.01 Normal Human Tubular Bone Cells: Homo sapiens cDNA clone IMAGE:18620 random

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Ht BLAST E Value	Top Ht Accession No.	Top Ht Database Source	Top Ht Description
11633	24529	38011	3.71	5.7E-02	AF09365.1	EST_HUMAN	en18K09.y1 Normal Human Trabecular Bone Cells; Homo sapiens cDNA clone VHT3C, nt18000 random
11935	24703		1.55	5.7E-02	AF16303.2	NT	Homo sapiens cDNA clone IMAGE:393586, 5' segment H227/C15
12235	25473		5.52	5.7E-02	AF17124.1	NT	Ph.D.M.A. for SP3A2, cDNA clone
12759	26403		5.56	5.7E-02	AF17124.1	NT	Homo sapiens cDNA clone IMAGE:393586, 5' segment H227/C15
12837	26859		3.11	5.7E-02	AF17124.1	NT	Homo sapiens fragile ribD cDNA polymerase (F03) genes, exons 8, 9, and partial cds
12971	26858		5.5	5.7E-02	AF20126.1	NT	Pen tripeptidyl aminopeptidase-E gene, complete cds
1549	14890	27840	1.35	5.6E-02	AF094493.1	NT	Hydroxylase tubulin-like fibrous protein L18 (pH8) gene, intron, chloroplast gene for chloroplast product
4752	17657	30917	1.08	5.6E-02	AB015100.1	NT	Lycopodium obscurum LE-AC36 mRNA for 1-aminocyclohexane-1-carboxylate synthase, complete cds
4809	17810	30575	1.14	5.6E-02	AA32560.1	EST_HUMAN	23415021.41 NCL CGAP, GCB1 Homo sapiens cDNA clone IMAGE:700418.3
6954	19583	33207	4.17	5.6E-02	AF172708.1	EST_HUMAN	KIA0005 PROTEIN, 1
7218	20218	33465	0.76	5.6E-02	AB069162.1	EST_HUMAN	044712.41 NCL CGAP, GCB1 Homo sapiens cDNA clone IMAGE:1371119.3 similar to contains AU
7512	20451	33736	3.36	5.6E-02	BE008007.1	EST_HUMAN	repetitive element/contains element L1 repetitive element
7525	20464	33752	0.86	5.6E-02	AB03788.1	EST_HUMAN	W24495.41 NCL CGAP, Bm38 Homo sapiens cDNA clone IMAGE:335659.3 similar to gb:305409 RAF
8324	21298	34602	0.54	5.6E-02	AF163593.1	EST_HUMAN	PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (HUMAN);
9350	22258	35552	2.4	5.6E-02	BE54203.1	EST_HUMAN	g054g11.1 Scores, testis, NHT Homo sapiens cDNA clone IMAGE:343276.9
9360	22258	35553	2.4	5.6E-02	BE54203.1	EST_HUMAN	6010071987 NIH MG00, 101 Homo sapiens cDNA clone IMAGE:343276.9
10328	23217	36831	1.07	5.6E-02	AA42864.1	EST_HUMAN	H49407.41 NCL CGAP, AM Homo sapiens cDNA clone IMAGE:023248 similar to TR-G706950 G706950
11907	24559		2.43	5.6E-02	AF26223.1	NT	LAMINA ASSOCIATED POLYPEPTIDE 10, 1
2703	19597	28691	7.01	5.6E-02	X97865.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
3251	19359	29574	3.96	5.6E-02	079550.1	NT	H1 sapiens gene encoding L1 subunit
3852	19911		1.54	5.6E-02	BF36859.1	EST_HUMAN	Mus musculus S18 domain protein TB (S18p18), mRNA
4312	17820	30792	1.40	5.6E-02	AF13511.1	NT	Mus musculus S18 domain protein TB (S18p18), mRNA
4944	17883	30541	0.72	5.6E-02	AF101268.1	NT	CalD Topoisomerase mRNA fragment
5558	19527	32544	2.87	5.6E-02	G01174.1	NT	CalD Topoisomerase mRNA fragment
5558	19527	32544	2.87	5.6E-02	G01174.1	NT	TOPOMOSIN ALPHA CHAIN NON MUSCLE
7273	20236	34003	3.91	5.6E-02	G01174.1	NT	TOPOMOSIN ALPHA CHAIN NON MUSCLE
5507	21253	34972	0.74	5.6E-02	AF17081.1	NT	Mus musculus tubulin (TUB1) cDNA
							Homo sapiens sodium-dependent vitamin G transporter 1 (SVCT1) mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) HT BLAST E Value	Top HT Accession No.	Top HT Database Source	Top HT Descriptor
8897	21628	34073	0.74	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
10180	23071	34073	0.85	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
10180	23071	34073	0.81	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
10270	23160	38570	1.27	5.5E-02	U93492.1	NT	Mus musculus second IL1 receptor, alpha chain (IL1R2) gene, exons 1 and 2
11468	24373	37821	7.83	5.5E-02	U05771.1	NT	Chimpanzee fructose 1,6-bisphosphate aldolase B (aldolase B) gene, partial cds, cDNA
13099	25801	31962	1.62	5.5E-02	U144594.1	NT	Human fructose 1,6-bisphosphate aldolase B (aldolase B) gene, partial cds, cDNA
3095	16117		0.88	5.4E-02	AJ277468.1	NT	Oryza sativa ribosomal protein L16 gene, complete cds
3483	18410		8.2	5.4E-02	BC073483.1	EST_HUMAN	Human ribosomal protein L16 gene, complete cds
8702	21833		1.14	5.4E-02	Z69116.1	NT	Bacillus subtilis complete genome (section 18 of 21); from Z68436 to Z69370
11055	24017	37488	1.76	5.4E-02	AL120885.1	EST_HUMAN	Human ribosomal protein L16 gene, complete cds
11142	24071	37517	2.59	5.4E-02	U02790.1	NT	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
12515	25770		2.17	5.4E-02	U144594.1	NT	Rana catesbeiana heart shock protein 30 (HSP30) mRNA, complete cds
1080	14124	27081	1.35	5.3E-02	AW351248.1	EST_HUMAN	QVO-ST0713-02129-002-400 ST0713 Homo sapiens cDNA
1080	14124	27082	1.35	5.3E-02	AW351248.1	EST_HUMAN	QVO-ST0713-02129-002-400 ST0713 Homo sapiens cDNA
1625	14566	27517	10.63	5.3E-02	Ts4769.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN DRP1 ALPHA CHAIN (HUMAN);
2518	15920	28423	3.27	5.3E-02	AJ276408.1	NT	Pseudomonas putida tipS gene
2894	19039	28639	0.88	5.3E-02	M56417.1	NT	Discothelia melanogaster leucine B2 gene, complete cds
2894	19039	28640	0.86	5.3E-02	M56417.1	NT	Discothelia melanogaster leucine B2 gene, complete cds
3195	16249	29188	4.2	5.3E-02	AJ276408.1	NT	Pseudomonas putida tipS gene
4721	17729	30580	1.05	5.3E-02	AJ011048.1	NT	Arabidopsis thaliana ald gene, exons 1-11
6223	18272	31098	9.91	5.3E-02	M60468.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
6523	18891	31423	1.98	5.3E-02	A0000527.1	NT	Helicobacter pylori 26898 strain 5 of 134 of the complete genome
5922	19591	31430	1.98	5.3E-02	A0000527.1	NT	Helicobacter pylori 26898 strain 5 of 134 of the complete genome
6040	19990	32569	1.11	5.3E-02	M62289.1	NT	Human hepatitis delta protein (HSP-22) mRNA, complete cds
7211	20211	33456	4.08	5.3E-02	0995443	NT	Lymphocytic choriomeningitis virus 1, complete genome
7481	20392	33952	1.47	5.3E-02	U93032.1	NT	Human protein tyrosine phosphatase (LAR) gene, complete cds
7762	20882		2.51	5.3E-02	T57622.1	NT	Nuclear protein TIF1 isoform (hTIF1, mTIF1, cTIF1)
8457	21318	34650	0.63	5.3E-02	T57622.1	SWISSPROT	HYPOPHOSPHATASE 1 (HPP1) PROTEIN IN SWISS-PROT INTERGENIC REGION
8876	21903		0.7	5.3E-02	U10308.1	NT	Mus musculus 12S ribosomal protein L16 gene, complete cds
9070	22506	35870	1.58	5.3E-02	M03127.1	NT	Podopore anastasia mitochondrial opsin-ssn cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	QRT-SEQ ID NO:	Expression Signal	Most Similar (Tco) HI BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10331	23517	36581	0.97	5.3E-02	AB222605.1	NT	Homo sapiens NCAM10 mRNA for mRNA (quantitative RT-PCR) for NCAM10, complete cds
10331	23517	36582	0.97	5.3E-02	AB222605.1	NT	Homo sapiens NCAM10 mRNA for mRNA (quantitative RT-PCR) for NCAM10, complete cds
10749	23635		0.98	5.3E-02	U07097.1	NT	Oryz. mRNA for 20-23 POU genes, splice variant (neurite, 9-16 hpf and postembryonic, 20-23 hpf)
10234	23707	37134	1.34	5.3E-02	X69432.1	NT	8.1 kb pGL3 mRNA for transcription factor
2204	16312		1.34	5.3E-02	X69432.1	NT	8.1 kb pGL3 mRNA for transcription factor
3160	16210	29101	2.61	5.2E-02	A177661.1	NT	Homo sapiens mRNA A. Shiga (PABA epoxide hydrolase) (SEPTA) mRNA
3160	16210	29101	2.61	5.2E-02	A177661.1	NT	Homo sapiens partial LMU1 gene for LIM domain only 1 protein, exon 1
4016	17043	29533	0.99	5.2E-02	A629610.1	NT	Homo sapiens partial LMU1 gene for LIM domain only 1 protein, exon 1
4379	17390	30283	3.99	5.2E-02	A629610.1	NT	A. subsp. (H. subsp.) partial LMU1 gene for LIM domain only 1 protein, exon 1
5322	18308	31765	0.72	5.2E-02	AB033201.1	NT	Human steroid hormone receptor Nco1 mRNA, complete cds
6140	19199	32356	0.46	5.2E-02	U17311.1	NT	Rattus norvegicus mRNA for tyrosinase, complete cds
5845	18395		1.19	5.2E-02	AB33065.1	EST HUMAN	Saccharomyces cerevisiae Ock65 (Ock65) gene, complete cds
7650	20854	33851	1.12	5.2E-02	F96322	SWISSPROT	W6044-X1 NC1 COAP_Lyn12 Homo sapiens cDNA clone IMAGE2006160 3' similar to contains MER16.1b
8778	21703		2.68	5.2E-02	AL163204.2	NT	MER16.1b (MER16.1) gene, complete cds
10250	23141	35547	2.08	5.2E-02	D10527.1	NT	DNA POLYMERASE SENSITIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
10250	23141	35548	2.08	5.2E-02	D10527.1	NT	Homo sapiens chromosome 21 segment HS210504
12748	22837		2.04	5.2E-02	Q03030	SWISSPROT	Turnip mosaic virus genomic RNA for Coat protein, complete cds
2387	15392		0.98	5.1E-02	AL134071.1	EST HUMAN	Turnip mosaic virus genomic RNA for Coat protein, complete cds
4008	17005	30775	0.98	5.1E-02	AF065167.1	NT	OVALOACTATE DECARBOXYLASE ALPHA CHAIN
6726	19122		0.98	5.1E-02	A0351740.1	NT	DYKZ044D073.71 547 (genomym: Htt) Homo sapiens cDNA clone DKFZP444D073.5
5181	19179	31018	1.1	5.1E-02	B357425.2	EST HUMAN	Hodgkin's disease receptor-like kinase ARK1A3 gene, partial cds
6899	19897	33225	0.74	5.1E-02	A1280395.1	NT	Homo sapiens PBL gene for salivary prothrombin protein P-B, complete cds
7180	19432	31321	1.45	5.1E-02	B576626.1	EST HUMAN	HU-1 patient 58 from fetal protease (pol) gene, complete cds
8828	21758	35102	1.08	5.1E-02	U26434.1	NT	QVO UM0051: 286900 350-bp UM0051 Homo sapiens cDNA
8828	21758	35103	1.08	5.1E-02	U26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPR1) gene, complete cds
8821	21681	35209	1.08	5.1E-02	A131006.1	NT	Human hypoxanthine phosphoribosyltransferase (HPR1) gene, complete cds
9442	22370	35733	0.84	5.1E-02	P03533	SWISSPROT	Scopocarpa littoralis mRNA for 3-dehydroxydione 3beta-reductase
9442	22370	35734	0.84	5.1E-02	P03533	SWISSPROT	Scopocarpa littoralis mRNA for 3-dehydroxydione 3beta-reductase
10375	23214	36525	8.81	5.1E-02	F41268.1	NT	NERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (CK 14)
10375	23214	36525	8.81	5.1E-02	F41268.1	NT	NERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (CK 14)
10078	23864	36994	2.93	5.1E-02	F41268.1	NT	Canine albumin protein phosphatase (SST) gene, complete cds
11269	24191	37540	2.48	5.1E-02	A133550.1	NT	ANTERIOR-SPECIFIC PROLINE-RICH PROTEIN APOG (PROTEIN CEX)
11269	24191	37540	2.48	5.1E-02	A133550.1	NT	Homo sapiens ES18 mRNA, partial cds

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Probe Seq ID NC:	Exon Seq ID NC:	ORF SEQ ID NC:	Expression Signal	Most Similar (Top) HE BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top HE Descriptor
11269	24191	37841	2.49	5.1E-02 AF593030.1	NT	Homo sapiens ES 19 mRNA, partial cds	
12792	34390		1.78	5.1E-02 AF592487.1	NT	Curculio medialis caducatus pronuclease (MPC3) mRNA, complete cds	
3356	44239	28491	2.23	5.0E-02 AF593004.1	NT	Mus musculus 589 cdk epsilon hydrolase gene, exon 10	
933	43576		7.44	5.0E-02 769104.1	NT	Bacillus subtilis complete genome (section 1 of 231) from 1 to 210369	
1232	14208	27211					
2007	19325	28916	4.36	5.0E-02 PQ2810	SWISSPROT		SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1-PRP-3) (PRP-2-PRP-4) (PRP-5-PRP-6) (PROTEIN APPROPIN C) (CONTAINS PEPTIDE P-C)
2866	14083	27007	1.71	5.0E-02 U77742.1	NT	Oryzopsis ambigua UDP-glucuronosyltransferase (UGT5F3) mRNA, complete cds	
3386	44239		1.67	5.0E-02	7369610	NT	Mus musculus Ubc-5f like kinase 2 (C. elegans) (Ulk2), mRNA
3666	16922		1.15	5.0E-02 U32762.1	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome	
3750	16782	29671	6.07	5.0E-02 P42322	SWISSPROT	Anticarsina pennsylvanica histone H4 containing protein homolog mRNA, complete cds	
4834	17633	30353	0.73	5.0E-02 AF188500.1	NT	CASEIN KINASE II BETA CHAIN (CK II)	
6370	10410	32365	1.02	5.0E-02 AF592641.1	NT	Homo sapiens ubiquitin histone H4 containing protein homolog mRNA, complete cds	
6553	16804		1.09	5.0E-02 AJ245235.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds	
7329	18407	31273	0.22	5.0E-02 P35516	SWISSPROT	Mus musculus Dmp-1 gene, exons 1-3	
7957	20889	34200	10.25	5.0E-02 P36816	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL-L)	
8199	21105		0.49	5.0E-02 AF1062464.1	EST_HUMAN	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL-L)	
10096	23582	37012	1.55	5.0E-02 AF305235.1	NT	MRG-CTD1006-10069-002-gr10 CT10064 Homo sapiens cDNA	
11923	24768	38235	2.4	5.0E-02 U67000.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fas3) mRNA, complete cds	
12312	23807		6.67	5.0E-02 Q04047	SWISSPROT	Methanococcus jannaschii section 142 of 150 of the complete genome	
241	13338		17.96	4.9E-02 M14230.1	NT	NO-ON-TRANSIENT A-PROTEIN	
300	13474	26393	2.19	4.9E-02 AF775948.1	NT	Chicken 28-10a vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds	
380	13474	26394	2.19	4.9E-02 AF775948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds	
2917	16970	28687	0.78	4.9E-02 U33696.1	NT	Xer myxophyce synthase (Y1) gene, complete cds	
3332	16378	29278	1.65	4.9E-02 P54258	SWISSPROT	ATROPHIN1 (DENTATORICULOPALLIDOLYSIN ATROPHY PROTEIN)	
3630	16968		0.72	4.9E-02 AA186040.1	EST_HUMAN	zef48.2.1 Stratiogene INT neuron (9637233) Homo sapiens cDNA clone IMAGE 532226 3' similar to contains Alu repetitive element; contains element M8K1 repetitive element	
3652	16988	29582	0.88	4.9E-02 AA000914.1	EST_HUMAN	zef48.2.1 Stratiogene INT neuron (9637233) Homo sapiens cDNA clone IMAGE 532226 3' similar to contains Alu repetitive element; contains element M8K1 repetitive element	
3652	16988	29583	0.88	4.9E-02 AA000914.1	EST_HUMAN	zef48.2.1 Stratiogene INT neuron (9637233) Homo sapiens cDNA clone IMAGE 532226 3' similar to contains Alu repetitive element; contains element M8K1 repetitive element	
4320	17334	30186	1.06	4.9E-02 AF135438.1	NT	Delta rate of novo DNA methyltransferase 3 (Dnmt3) mRNA, partial cds	
4320	17334	30187	1.06	4.9E-02 AF135438.1	NT	Delta rate of novo DNA methyltransferase 3 (Dnmt3) mRNA, partial cds	
4391	17405		1	4.9E-02 M202281	EST_HUMAN	Disaccharide 6-phosphatase (D6P) gene, complete cds	
4654	17942	30810	1.58	4.9E-02 AF167821.1	EST_HUMAN	95g510.1 VGL COAP UM Homo sapiens cDNA clone IMAGE 292388 3'	
4954	17952	30511	1.33	4.9E-02 AF167821.1	EST_HUMAN	95g510.1 VGL COAP UM Homo sapiens cDNA clone IMAGE 292388 3'	

Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6336	18319	31167	2.64	4.9E-02	7662616	NT	Homo sapiens PRO1848 protein (PRO1848), mRNA
5555	18633	31512	1.76	4.5E-02	1001223.1	NT	Rat elastase II gene, exon 6
5555	18633	31513	1.76	4.5E-02	1001223.1	NT	Rat elastase II gene, exon 6
7602	20447	33724	1.19	4.9E-02	A000965.1	NT	Archaeoglobus fulgidus, section 127 of 172 of the complete genome
9175	21103	33724	1.19	4.9E-02	A000965.1	NT	Archaeoglobus fulgidus, section 127 of 172 of the complete genome
8914	22442	36004	0.65	4.9E-02	AL001850.2	NT	Chlamydia muridarum, section 40 of 65 of the complete genome
17782	23668	37697	0.58	4.9E-02	AF0032	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
11830	24600	38179	3.68	4.9E-02	AF03603.1	NT	TRANSCRIPTION FACTOR E3
12681	25341	38179	3.68	4.9E-02	AF03603.1	NT	Homo sapiens angiotensin II receptor 1, complete cds
12924	26169	38179	1.62	4.9E-02	E022690	NT	Homo sapiens CS box-containing WD protein (LOC35884), mRNA
350	13439	26352	2.06	4.9E-02	M10064.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
351	13439	26352	2.14	4.9E-02	D15471.1	NT	Human mRNA, Xq terminal portion
511	13482	26400	6.29	4.9E-02	AF03100.1	NT	Human mRNA, Xq terminal portion
2292	15300	28305	2.06	4.9E-02	W61983.1	EST_HUMAN	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
3254	16002	25208	1.72	4.9E-02	X17144.1	NT	ze94602.3f Soanes, senescent, fibroblasts, NHISF Homo sapiens cDNA clone IMAGE329511.3 similar to
5276	18294	31114	0.86	4.9E-02	U61914.1	NT	ze94602.3f Soanes, senescent, fibroblasts, NHISF Homo sapiens cDNA clone IMAGE329511.3 similar to
8716	21647	34693	1.33	4.9E-02	AW389497.1	EST_HUMAN	ze94602.3f Soanes, senescent, fibroblasts, NHISF Homo sapiens cDNA clone IMAGE329511.3 similar to
9674	22600	35673	0.84	4.9E-02	AL001196.1	EST_HUMAN	ze94602.3f Soanes, senescent, fibroblasts, NHISF Homo sapiens cDNA clone IMAGE329511.3 similar to
9674	22600	35674	0.84	4.9E-02	AL001196.1	EST_HUMAN	ze94602.3f Soanes, senescent, fibroblasts, NHISF Homo sapiens cDNA clone IMAGE329511.3 similar to
7143	20251	33503	3.42	4.7E-02	M01183.1	EST_HUMAN	ze94602.3f Soanes, senescent, fibroblasts, NHISF Homo sapiens cDNA clone IMAGE329511.3 similar to
7212	20212	33457	0.79	4.7E-02	BF060625.1	EST_HUMAN	ze94602.3f Soanes, senescent, fibroblasts, NHISF Homo sapiens cDNA clone IMAGE329511.3 similar to
7212	20212	33458	0.79	4.7E-02	BF060625.1	EST_HUMAN	ze94602.3f Soanes, senescent, fibroblasts, NHISF Homo sapiens cDNA clone IMAGE329511.3 similar to
7247	20196	33459	1.59	4.7E-02	M62769.1	NT	ze94602.3f Soanes, senescent, fibroblasts, NHISF Homo sapiens cDNA clone IMAGE329511.3 similar to
8151	21088	35100	0.82	4.7E-02	U145188.1	NT	ze94602.3f Soanes, senescent, fibroblasts, NHISF Homo sapiens cDNA clone IMAGE329511.3 similar to
8936	21700	35100	0.96	4.7E-02	X15453.1	NT	ze94602.3f Soanes, senescent, fibroblasts, NHISF Homo sapiens cDNA clone IMAGE329511.3 similar to
8936	22435	35790	1.23	4.7E-02	M62211.1	NT	ze94602.3f Soanes, senescent, fibroblasts, NHISF Homo sapiens cDNA clone IMAGE329511.3 similar to
9227	22181	36073	3.03	4.7E-02	AC020676.1	NT	ze94602.3f Soanes, senescent, fibroblasts, NHISF Homo sapiens cDNA clone IMAGE329511.3 similar to
9798	22892	36073	3.03	4.7E-02	AC020676.1	NT	ze94602.3f Soanes, senescent, fibroblasts, NHISF Homo sapiens cDNA clone IMAGE329511.3 similar to
10233	23034	35401	0.53	4.7E-02	BF035231.1	EST_HUMAN	ze94602.3f Soanes, senescent, fibroblasts, NHISF Homo sapiens cDNA clone IMAGE329511.3 similar to
10233	23034	35401	0.53	4.7E-02	BF035231.1	EST_HUMAN	ze94602.3f Soanes, senescent, fibroblasts, NHISF Homo sapiens cDNA clone IMAGE329511.3 similar to
11989	24632	38328	1.31	4.7E-02	U72621.1	NT	ze94602.3f Soanes, senescent, fibroblasts, NHISF Homo sapiens cDNA clone IMAGE329511.3 similar to

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Probes SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Mod Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11899	24832	38829	1.6	4.7E-02	U79621.1	NT	Box binding protein 1 (bax1) gene, partial cds
12300	28851	38829	1.86	4.7E-02	U79621.1	EST_HUMAN	Box binding protein 1 (bax1) gene, partial cds
280	13384	26300	1.01	4.8E-02	BE15383.1	EST_HUMAN	PMH-H10339-251199-003-q05 HT0339 Homo sapiens cDNA
763	13320	26749	2.62	4.8E-02	AE020485.1	NT	Escherichia coli O157:H7 serotype 135 of 400 of the complete genome
1318	14351		0.89	4.8E-02	AF04295.1	EST_HUMAN	PMH-H10339-251199-003-q05 HT0339 Homo sapiens cDNA
1338	14417	27722	3.79	4.8E-02	AV72759.1	EST_HUMAN	PMH-H10339-251199-003-q05 HT0339 Homo sapiens cDNA
2511	15512	29415	2.84	4.8E-02	AW29028.1	EST_HUMAN	PMH-H10339-251199-003-q05 HT0339 Homo sapiens cDNA
2855	13394	26300	2.34	4.8E-02	BE15383.1	EST_HUMAN	PMH-H10339-251199-003-q05 HT0339 Homo sapiens cDNA
3376	16104	29003	0.67	4.8E-02	BE15383.1	EST_HUMAN	PMH-H10339-251199-003-q05 HT0339 Homo sapiens cDNA
3255	16104	29008	1.07	4.8E-02	BE15383.1	EST_HUMAN	PMH-H10339-251199-003-q05 HT0339 Homo sapiens cDNA
4119	17235		1.21	4.8E-02	AF223463.1	NT	Mus musculus nucleolar RNA helicase [l20] (G2221) gene, complete cds
5036	19003	32122	1.49	4.8E-02	AF076962.1	NT	Hepelomiris burtoni gonadotroph-releasing hormone and GnRH-associated peptide precursor (GnRH2) gene, complete cds
6476	10521	32607	3.36	4.8E-02	X61024.1	NT	C. reinhardtii ap2 (ap2) mRNA
6476	10421	32608	3.36	4.8E-02	X61024.1	NT	C. reinhardtii ap2 (ap2) mRNA
7106	20313	33376	1.25	4.8E-02	AI146574.1	EST_HUMAN	Similar to contains L1 L1 L1 repetitive element
8357	21262	34485	0.52	4.8E-02	6978720	NT	Rattus norvegicus Cathelin H (Cath), mRNA
9214	22142	35497	3.8	4.8E-02	BE154004.1	EST_HUMAN	PMH-H10339-00400-009-G12 HT0339 Homo sapiens cDNA
11840	24691	38180	4.09	4.8E-02	AA013328.1	EST_HUMAN	Q27H03.1 Scores_NFL_C_GBC_ST Homo sapiens cDNA clone IMAGE1524737 3'
13016	25063		3.4	4.8E-02	X57006.1	NT	Human genome immunoglobulin lambda chain gene
409	13540	26463	2.77	4.8E-02	P22446	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1246	14282	27224	0.8	4.8E-02	AF005780.1	NT	Marburg virus strain MG.1Africa/Johannesburg/1975Ozlin VP30 gene, complete cds
1246	14282	27225	0.8	4.8E-02	AF005780.1	NT	Marburg virus strain MG.1Africa/Johannesburg/1975Ozlin VP30 gene, complete cds
1826	14849	27528	4.38	4.8E-02	P33162	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2122	11735	26141	1.85	4.8E-02	AE030064.1	NT	Xylinia fastidiosa, section 110 of 279 of the complete genome
3787	16818	29705	5.68	4.8E-02	AL16376.2	NT	Homo sapiens chromosome 21 segment HS210278
6476	19523	32701	1.5	4.8E-02	AJ400877.1	NT	Homo sapiens AQL3 gene, C6orf1 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6785	10818	33030	0.98	4.8E-02	AL103260.2	NT	Methanocaldococcus jannaschii carbon monoxide dehydrogenase large subunit (cdhA) gene, carbon monoxide dehydrogenase small subunit (cdhB) gene, complete cds
7205	20205	33450	0.64	4.8E-02	LM2487.1	NT	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7036	20052	33208	0.92	4.3E-02	AF469298.1	EST_HUMAN	nc85-1241 NCL CGAP_P2 Homo sapiens cDNA clone IMAGE:118886
6398	21272		0.44	4.3E-02	L12698.1	NT	Testis germ amnioblastoma syndrome gene, complete cds
9079	22008	35944	0.9	4.3E-02	AF260365.1	NT	Homo sapiens identical to 3 (US2) genes, complete cds, alternatively spliced
9356	22287	36960	1.16	4.3E-02	X53327.1	NT	H. sapiens cDNA for nuclear coat protein molecule
6399	22287	36961	1.16	4.3E-02	X53327.1	NT	NCL-1 cDNA for nuclear coat protein molecule
8477	13902	28942	2.57	4.2E-02	AU728327.1	EST_HUMAN	AU728327.NT29622 Homo sapiens cDNA clone NT29N200020.5
891	13444		2.51	4.2E-02	AU728327.1	EST_HUMAN	AU728327.NT29622 Homo sapiens cDNA clone NT29N200020.5
921	13873	29920	0.67	4.3E-02	AF009465.1	EST_HUMAN	nc94901.1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:2644584.3 similar to TR-Q63261 Q35261
1260	14376		1.34	4.3E-02	AF459565.1	NT	L1 RETROPOSON. ORF2 mRNA, contains L1.81.1 L1 repetitive element;
3732	16764	23851	1.63	4.3E-02	P22901	SWISSPROT	Thrombospondin adhesion molecule, segment 4/5
4214	17231	30100	0.79	4.2E-02	BE202606.1	EST_HUMAN	TRANSFORMING PROTEIN MAP
5812	18934	31603	0.73	4.2E-02	AF260107.1	NT	801196039F.NIH.MGC.19 Homo sapiens cDNA clone IMAGE:3903503.5
5812	18934	31604	0.73	4.2E-02	AF260107.1	NT	801196039F.NIH.MGC.19 Homo sapiens cDNA clone IMAGE:3903503.5
7323	18491	31284	0.79	4.2E-02	BE260265.1	EST_HUMAN	4 (CYP3A4) and cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7650	20372	34183	4.83	4.2E-02	AF279752.1	NT	601124558F.NIH.MGC.8 Homo sapiens cDNA clone IMAGE:2589519.9
7076	20907	34210	0.72	4.2E-02	AF739347.1	NT	Legionella pneumophila catalase-peroxidase (KatA)
9369	22297	35960	4.41	4.2E-02	P05095	SWISSPROT	A77804.7.HITF Homo sapiens cDNA clone HITF.A1104.8
10660	23546	36960	1.74	4.2E-02	C16650	SWISSPROT	ACTIN-TROPOMYOSIN-BOX-BRAIN PROTEIN 11(TBR-1) (TFS-59)
11752	24453	38134	2.3	4.2E-02	BE819822.1	EST_HUMAN	PWS-BN0174.269600.006 d10 BN0174 Homo sapiens cDNA
11752	24453	38135	2.3	4.2E-02	BE819822.1	EST_HUMAN	PWS-BN0174.269600.006 d10 BN0174 Homo sapiens cDNA
11638	24782	38270	1.95	4.2E-02	AF174043.1	NT	PRRS isolate PRRS/93 envelope glycoprotein gene, complete cds
12701	26989		3.73	4.2E-02	AI083494.1	EST_HUMAN	wf4010.41 NCL CGAP_Pant Homo sapiens cDNA clone IMAGE:2510859.3
533	13932	29513	0.67	4.1E-02	AF200630.1	NT	Homo sapiens HPST1 gene, intron 6
2725	15718	29716	1.05	4.1E-02	AE002350.2	NT	Chenry44 maturation, section 6 of 65 of the complete genome
3059	16507	29882	0.69	4.1E-02	BE297230.1	EST_HUMAN	601177607F.NIH.MGC.171 Homo sapiens cDNA clone IMAGE:333363.5
3069	16507	29883	0.69	4.1E-02	BE297230.1	EST_HUMAN	601177607F.NIH.MGC.171 Homo sapiens cDNA clone IMAGE:333363.5
4585	17503		5.96	4.1E-02	AF1863494.1	EST_HUMAN	CYP11A.M0172.100400.004 d10 M0172 Homo sapiens cDNA
5819	18910	32025	0.04	4.1E-02	BE251804.1	EST_HUMAN	601175350F.NIH.MGC.131 Homo sapiens cDNA clone IMAGE:334384.6
5819	18910	32025	0.04	4.1E-02	BE251804.1	EST_HUMAN	601175350F.NIH.MGC.131 Homo sapiens cDNA clone IMAGE:334384.6

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Probe Seq ID Seq ID NC:	Exon Seq ID Seq ID NC:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7203	20309		1.02	4.1E-02	Z5884.1	NT	A. bilineata mRNA for plasma membrane intrinsic protein 1a
7458	20308	34571	1.81	4.1E-02	AE002132.1	NT	Unpublished genomic section 33 of 59 of the complete genome
7506	20308	34166	1.56	4.1E-02	76824.7	NT	Homo sapiens KIA00867 protein (KIA00867), mRNA
8045	20305	34273	0.69	4.1E-02	L02110.1	NT	Mac molecule protein involved in the cAMP phosphodiesterase (rd beta PDE) gene, intron 1, with the protein insert encompassing the 5' end pseudogene (3' end) and 3' LTR
8234	21139	34471	2.95	4.1E-02	AF026196.1	NT	Fetus subgen neural cell adhesion molecule(L1 homodol (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitotic-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
8785	21715	35062	0.72	4.1E-02	P07857	SWISSPROT	ADAMTS 1(PRECURSOR (ADISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
9203	22131	35487	0.78	4.1E-02	P04687	SWISSPROT	ADAMTS 1(PRECURSOR (ADISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
9897	22622	36000	0.95	4.1E-02	AA372366.1	EST_HUMAN	ESTB4297 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
13040	25880	31779	12.28	4.1E-02	AJ271906.1	NT	Enkestatin repeat unit gene for placental glutamate synthetase, exon 1-12
1669	14659	27656	1.32	4.0E-02	AF075392.1	EST_HUMAN	nt088001 nt NCL CGAP P-28 Homo sapiens cDNA clone IMAGE233745 3'
3280	16337	29240	4.8	4.0E-02	AE040904.1	NT	Homo sapiens mRNA for PMA1471 protein, partial cds
3804	16893	29777	1.39	4.0E-02	L11910.1	NT	Human retinoblastoma susceptibility gene conts 1-27, complete cds
5273	18259	31111	0.7	4.0E-02	AE042287.1	NT	Homo sapiens PFS gene for 6-phosphogluconate synthase, complete cds
5378	18391	31201	1.05	4.0E-02	BF242745.1	EST_HUMAN	801877607F1NH_MGC_35 Homo sapiens cDNA clone IMAGE:1102620 5'
5554	18842	31520	5.92	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) gene, complete cds; and cytochrome P450
6488	19503	32378	1.61	4.0E-02	BF110434.1	EST_HUMAN	70290741 NCL CGAP_Luc2 Homo sapiens cDNA clone IMAGE3503890 3' amier to TR-075298 015298
8143	21052	34384	0.69	4.0E-02	L2368.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (sdmp) mRNA, complete cds
8217	21122		0.42	4.0E-02	AI_161533.2	NT	Adipocytes: Italian DNA databases 4, conts: fragment No. 35
8235	21140	34472	0.88	4.0E-02	AE030391.1	NT	Homo sapiens DNA for Fc gammaR molecule, complete cds
8235	21140	34473	0.88	4.0E-02	AE030391.1	NT	Homo sapiens DNA for Fc gammaR molecule, complete cds
8292	21195	34333	0.48	4.0E-02	AF28155.1	NT	Homo sapiens DNA for Fc gammaR molecule, complete cds
8278	22204	33561	2.41	4.0E-02	P08640	SWISSPROT	GLUCAMINASE 5162 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE, (1-4)-ALPHA-D-GLUCAN
10170	23031		0.72	4.0E-02	BF079375.1	EST_HUMAN	60218984F1NH_MGC_35 Homo sapiens cDNA clone IMAGE:2284724 5'
10182	23034	36486	2.46	4.0E-02	AF030941.1	NT	Mechanoblastin: human osteoblast, strain Marburg, Thioflavin red-stained subunit A
10480	23378		0.9	4.0E-02	D0949.1	NT	Human mRNA for KIA00092 gene, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1163	14194	27133	8.71	3.2E-02	AF062753.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68c allele, complete cds
2131	15144		1.04	3.2E-02	P29605	SWISSPROT	LARGE TEGUMENT PROTEIN
2885	13238	26157	1.01	3.2E-02	AJ02005.1	NT	Oryzias latipes c-myc gene encoding leucopostin-dependent ribo acid transporter
3179	16229	26123	17.23	3.2E-02	BE607553.1	EST_HUMAN	h0142431F1: NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3945727.5
3177	19808	20956	1.42	3.2E-02	AL03203.2	NT	Homo sapiens chromosome 21 segment HS21C033
4315	17329		17.61	3.2E-02	X847683.1	NT	H sapiens RP3 gene (XLRP gene 3)
4880	17870	30744	3.77	3.2E-02	AF11482.1	NT	Sedrinpa radica mullae (mull) gene, chloroplast gene encoding chloroplast protein, partial cds
4941	17940	30707	0.69	3.2E-02	AF067083.1	NT	Vitreoscilla sp. outer membrane protein, isomerase gene, complete cds, Trp repressor binding protein gene, partial cds, and unknown genes
5001	18108		0.92	3.2E-02	AF105905.1	NT	Mus musculus WHO class III region R10 gene, partial cds; BF C2, GSA, N322, G8, HSP70, HSP70, HSC70H, and anRNP genes, complete cds; G1A gene, partial cds; and unknown genes
6725	18798	31900	1.60	3.2E-02	X89708.1	NT	S. griseocannum WHG-Siv gene
6725	18798	31891	1.60	3.2E-02	X89709.1	NT	S. griseocannum WHG-Siv gene
6802	19335	33046	2.31	3.2E-02	M32437.1	NT	Rattus norvegicus left junction in cell line W18.14
6805	19838		27.96	3.2E-02	T86307.1	EST_HUMAN	y13H12.1: Scans fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:110087.3 similar to contains
6805	19838	33140	3.81	3.2E-02	AF179845.1	NT	Alu repetitive element contains LTR1 repetitive element;
8231	21139	34460	0.9	3.2E-02	11424048	NT	Segutis oculatus cytochrome P-450, subfamily IIB (phenobarbital-inducible) (CYP2B), mRNA
8401	21304	34639	0.46	3.2E-02	AA555015.1	EST_HUMAN	Homo sapiens cytochrome P-450, subfamily IIB (phenobarbital-inducible) (CYP2B), mRNA
8875	21805	35158	4.19	3.2E-02	6980503	NT	LIKE PROTEIN FUBI (HUMAN);
9466	22424		0.96	3.2E-02	AF107181.1	NT	Mus musculus fresh family member 32 (F32), mRNA
9766	22690	39075	1.32	3.2E-02	A1278971.1	EST_HUMAN	Homo sapiens chromosome 3 subtelomeric region
9766	22690	39076	1.32	3.2E-02	A1278971.1	EST_HUMAN	gnt1704.1: NC1 CGAP_Lus Homo sapiens cDNA clone IMAGE:182069.3
10599	23445		4.62	3.2E-02	AA179795.1	EST_HUMAN	gnt1704.1: NC1 CGAP_Lus Homo sapiens cDNA clone IMAGE:182069.3
10844	25730	37153	1.15	3.2E-02	U6702.1	NT	g54b42.1: Scans, junc, gntd, NHP3 Homo sapiens cDNA clone IMAGE:397161.9 similar to
12211	25945		1.49	3.2E-02	A133302.2	NT	g54b42.1: Scans, junc, gntd, NHP3 Homo sapiens cDNA clone IMAGE:397161.9 similar to
1287	14330		2.17	3.1E-02	6503416	NT	Nesaka mullae chemokine receptor CCR5 mRNA, complete cds
1331	14335	27514	1.12	3.1E-02	F18045	SWISSPROT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1400	14381	27508	1.12	3.1E-02	F18045	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN ALPHA3 CHAIN PRECURSOR (GF-ALPHA-3)
1529	15030		1.01	3.1E-02	Z59397.1	NT	Mus musculus adipocyte-related protein complex APC3, delta subunit (AP3delta)
1529	15030		1.01	3.1E-02	Z59397.1	NT	Oryzias latipes mRNAs for fatless protein
5446	18528	31252	1.22	3.1E-02	U75104.1	NT	Human tubulin inhibitory factor receptor (LIRF) gene, promoter and partial exon 1

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5645	18829		2.38	3.1E-02	AF17478.1	EST_HUMAN	z61436.1 NC1 GQAP GCR1 Homo sapiens cDNA clone IMAGE 703958 5'
5844	18916	37031	0.86	3.1E-02	BF60742.1	EST_HUMAN	g0306763.F1 NIH MGCG 57 Homo sapiens cDNA clone IMAGE 405768 5'
5915	20635	37104	0.42	3.1E-02	AJ391284.1	NT	Nucleolar matrix-binding DNA for region 2 (rib-2- and rib-3 homologs, uniconom genes) and (anking genes), strain FAMB3
10334	20420	36935	2.6	3.1E-02	AF094776.1	NT	Enterozoosuccinyl succinate surface protein precursor, gene, complete cds
1649	14977		1.74	3.0E-02	AF187128.1	NT	Phospholipid nitric oxide synthase oxidase [gene, partial cds; mitochondrial gene for mitochondrial product z65903.1] Soames, testis, NIH Homo sapiens cDNA clone IMAGE 727293 5'
2823	16921	28614	1.41	3.0E-02	AA024242.1	EST_HUMAN	Saccharomyces cerevisiae stem-loop mutation suppressor SSL2, gene, complete cds
3625	16991	29691	1.32	3.0E-02	M64176.1	NT	Pseudomonas fluorescens family 1 aminotransferase gene, complete cds
3721	16793	20841	3.77	3.0E-02	AF247944.1	NT	QV2-S10296-180200-040-050 S10296 Homo sapiens cDNA
3805	16839		0.78	3.0E-02	AA920223.1	EST_HUMAN	EST174530 Pterid gland III Homo sapiens cDNA 5' end
4027	17054		0.95	3.0E-02	AA920223.1	EST_HUMAN	Homo sapiens neurogranin 2 (NR2P2) gene, complete cds, alternatively spliced
6186	18177	31022	8.94	3.0E-02	AF281074.1	NT	Homo sapiens neurogranin 2 (NR2P2) gene, complete cds, alternatively spliced
6186	18177	31023	8.94	3.0E-02	AF281074.1	NT	Homo sapiens neurogranin 2 (NR2P2) gene, complete cds, alternatively spliced
5976	18954		3.18	3.0E-02	AB045793.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds
6803	19847	32724	0.7	3.0E-02	N68015.1	EST_HUMAN	z65810.1 Soames fetal liver, spleen INFLS Homo sapiens cDNA clone IMAGE 234600 5' similar to contains element TART repetitive element:
6803	19847	32725	0.7	3.0E-02	N68015.1	EST_HUMAN	z65810.1 Soames fetal liver, spleen INFLS Homo sapiens cDNA clone IMAGE 234600 5' similar to contains element TART repetitive element:
7008	20304	33563	2.45	3.0E-02	AJ242005.1	NT	Oryzopsis eipho mRNA for inducible nitric oxide synthase (NOS gene)
7235	20144	33583	2.68	3.0E-02	BE869445.1	EST_HUMAN	g01512208.F1 NIH MGCG 71 Homo sapiens cDNA clone IMAGE 3913948 5'
7235	20144	33584	2.68	3.0E-02	BE869445.1	EST_HUMAN	g01512208.F1 NIH MGCG 71 Homo sapiens cDNA clone IMAGE 3913948 5'
7426	20125	33583	2.14	3.0E-02	AF213984.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFkB1) gene, complete cds
7426	20125	33584	2.14	3.0E-02	AF213984.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFkB1) gene, complete cds
7601	20590	33625	1.19	3.0E-02	AJ65624.1	NT	Human dyx19p1 gene
8019	20935		0.88	3.0E-02	BF240361.1	EST_HUMAN	g0158460.F1 NIH MGCG 57 Homo sapiens cDNA clone IMAGE 407458 5'
8163	22108	35460	0.03	3.0E-02	BE512670.1	EST_HUMAN	g01710268.F1 NIH MGCG 18 Homo sapiens cDNA clone IMAGE 354947 5'
8230	22278	35464	0.83	3.0E-02	BF240361.1	EST_HUMAN	g01710268.F1 NIH MGCG 18 Homo sapiens cDNA clone IMAGE 354947 5'
8381	22719		1.85	3.0E-02	BF240361.1	EST_HUMAN	g01710268.F1 NIH MGCG 18 Homo sapiens cDNA clone IMAGE 354947 5'
8381	22719	37361	1.85	3.0E-02	BF240361.1	EST_HUMAN	g01710268.F1 NIH MGCG 18 Homo sapiens cDNA clone IMAGE 354947 5'
10297	20202	37160	0.63	3.0E-02	AF20178.1	NT	Thymidylate synthase, 100 kDa of 100 kDa isoform, complete cds
11651	24682	36923	2.47	3.0E-02	AF01183.1	EST_HUMAN	HSA0401HS TEST1 Human adult testis, Homo sapiens cDNA clone IMAGE 234600 5' similar to contains element TART repetitive element:

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1214	24655	38456	8.71	3.0E-02	AF049218.1	EST_HUMAN	pcp7004.1 NC1 CGAP, 1341 Homo sapiens cDNA clone IMAGE:611283
1258	26958	31373	2.68	3.0E-02	BC020161.1	EST_HUMAN	hsp62.04.1 Scarsa fetal liver splen N18L5 Homo sapiens cDNA clone IMAGE:134403
1273	26469		7.82	3.0E-02	AF095585.1	EST_HUMAN	OV4-1N0038-270400-187-405 N0038 Homo sapiens cDNA
1292	26031		4.22	3.0E-02	AF049687.1	NT	Rat1a transposon UDP-Galactose 4-epimerase beta-1,4-galactose 4-epimerase mRNA, complete cds
3033	16095	26686	1.12	2.9E-02	BF056441.1	EST_HUMAN	hsp62.04.1 Scarsa fetal liver splen N18L5 Homo sapiens cDNA clone IMAGE:389068
3033	16095	26687	1.12	2.9E-02	BC056441.1	EST_HUMAN	hsp62.04.1 Scarsa fetal liver splen N18L5 Homo sapiens cDNA clone IMAGE:389068
4034	17031	26621	0.81	2.9E-02	H72653.1	EST_HUMAN	hsp62.04.1 Scarsa fetal liver splen N18L5 Homo sapiens cDNA clone IMAGE:233130
4070	17098	26979	0.66	2.9E-02	O15440	SWISSPROT	MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 5 (ABC TRANSPORTER MOAT-2) (PAB011) (SMRP)
5144	16139	30981	0.81	2.9E-02	X68107.1	NT	S. vulgaris pepC gene for PEP carboxylase
5144	16139	30982	0.81	2.9E-02	X68107.1	NT	S. vulgaris pepC gene for PEP carboxylase
6200	18414		3.86	2.9E-02	R09112.1	EST_HUMAN	Y25020.1 Scarsa fetal liver splen N18L5 Homo sapiens cDNA clone IMAGE:127888
6208	16349	32517	1.31	2.9E-02	AF060223.1	NT	Site specific deoxyribonuclease II mRNA, complete cds
6545	16588	32775	6.16	2.9E-02	BF032231.1	EST_HUMAN	hsp62.04.1 Scarsa fetal liver splen N18L5 Homo sapiens cDNA clone IMAGE:385558
7266	20239	33489	0.87	2.9E-02	AJ391284.1	NT	Nisseria meningitidis DNA for region 2 (thrB- and thrC-homologs, unknown genes) and flanking genes, strain FAM18
7679	20554	33947	10.47	2.9E-02	BE271437.1	EST_HUMAN	hsp62.04.1 Scarsa fetal liver splen N18L5 Homo sapiens cDNA clone IMAGE:314680
7827	20798	34000	0.54	2.9E-02	D52414.1	EST_HUMAN	Buchnera aphidicola natural host Schlechtendillia chinensis glucuronate-6-phosphate dehydrogenase (gcd) gene, partial cds
8577	21008	34653	1.01	2.9E-02	AF126279.1	NT	Buchnera aphidicola natural host Schlechtendillia chinensis glucuronate-6-phosphate dehydrogenase (gcd) gene, partial cds
8577	21608	34654	1.01	2.9E-02	AF126279.1	NT	Buchnera aphidicola natural host Schlechtendillia chinensis glucuronate-6-phosphate dehydrogenase (gcd) gene, partial cds
10183	25074	36474	2.06	2.9E-02	AW875079.1	EST_HUMAN	CHG-PT0014-071259-051-c24 PT0014 Homo sapiens cDNA
10183	25074	36475	2.06	2.9E-02	AW875079.1	EST_HUMAN	CHG-PT0014-071259-051-c24 PT0014 Homo sapiens cDNA
10386	25275		0.85	2.9E-02	AF079597.1	EST_HUMAN	EST1389005 MAGC neurexin-like MAGC Homo sapiens cDNA
10386	25275	37143	1.17	2.9E-02	AF000064.1	NT	Acropora patula genomic DNA, section 777
11465	19420	31350	2.04	2.9E-02	X62094.1	NT	Sheep gene for ultra high-sulfur keratin protein
12583	25653		1.73	2.9E-02	X62094.1	EST_HUMAN	hsp62.04.1 Scarsa fetal liver splen N18L5 Homo sapiens cDNA clone IMAGE:102562
887	13666		0.78	2.9E-02	AF091053.1	EST_HUMAN	hsp62.04.1 Scarsa fetal liver splen N18L5 Homo sapiens cDNA
3425	19400	28573	1.77	2.9E-02	AF060353.1	NT	Homo sapiens retinal ficolin (FICOLIN) gene, exon 2
3425	19400	28574	1.77	2.9E-02	AF060353.1	NT	Homo sapiens retinal ficolin (FICOLIN) gene, exon 2
3976	16130	31672	10.95	2.9E-02	BE740681.1	EST_HUMAN	hsp62.04.1 Scarsa fetal liver splen N18L5 Homo sapiens cDNA clone IMAGE:324887
7120	26324	33585	1.35	2.9E-02	178601.1	EST_HUMAN	hsp62.04.1 Scarsa fetal liver splen N18L5 Homo sapiens cDNA clone IMAGE:108455

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID	Exon SEQ ID	ORF SEQ ID NO.	Exposition Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
66033	216533	351388	-1.67	2.8E-02	AJ056200.1	NT	<i>Cratichneumon plantigenus</i> mRNA for homeocytin leucine zipper protein (hb-1)
66034	216534	351389	-1.67	2.8E-02	AJ056200.1	NT	2550606.01 NCBI_GDB - GDB1 Homo sapiens cDNA clone IMAGE:171466.5
66035	224650	348358	-0.92	2.8E-02	AF307862.1	EST - HUMAN	Cavia porcellus mRN4777 ratifying potassium channel K2.1 (KCND2), gene, complete cds
66036	9749	327473	-30.937	1.23	2.8E-02	AF187872.1	Archaeoglobus fulgidus section 15 of 172 of the complete genome
66037	227668	361163	-0.65	2.8E-02	AJ001692.1	NT	<i>Chlamydomonas reinhardtii</i> strain 15th-homologous protein (FL2.0) mRNA, complete cds
66038	12204	250309	-38.642	2.8E-02	J236907.1	NT	Human germline T-cell receptor beta chain Dogma-like hydroxylase-like, TRV1, TRV2, TRV3, TRV4, TRV5, TRV6, TRV7, TRV8, TRV9, TRV10, TRV11, TRV12, TRV13, TRV14, TRV15, TRV16, TRV17, TRV18, TRV19, TRV20, TRV21, TRV22, TRV23, TRV24, TRV25, TRV26, TRV27, TRV28, TRV29, TRV30, TRV31, TRV32, TRV33, TRV34, TRV35, TRV36, TRV37, TRV38, TRV39, TRV40, TRV41, TRV42, TRV43, TRV44, TRV45, TRV46, TRV47, TRV48, TRV49, TRV50, TRV51, TRV52, TRV53, TRV54, TRV55, TRV56, TRV57, TRV58, TRV59, TRV60, TRV61, TRV62, TRV63, TRV64, TRV65, TRV66, TRV67, TRV68, TRV69, TRV70, TRV71, TRV72, TRV73, TRV74, TRV75, TRV76, TRV77, TRV78, TRV79, TRV80, TRV81, TRV82, TRV83, TRV84, TRV85, TRV86, TRV87, TRV88, TRV89, TRV90, TRV91, TRV92, TRV93, TRV94, TRV95, TRV96, TRV97, TRV98, TRV99, TRV100, TRV101, TRV102, TRV103, TRV104, TRV105, TRV106, TRV107, TRV108, TRV109, TRV110, TRV111, TRV112, TRV113, TRV114, TRV115, TRV116, TRV117, TRV118, TRV119, TRV120, TRV121, TRV122, TRV123, TRV124, TRV125, TRV126, TRV127, TRV128, TRV129, TRV130, TRV131, TRV132, TRV133, TRV134, TRV135, TRV136, TRV137, TRV138, TRV139, TRV140, TRV141, TRV142, TRV143, TRV144, TRV145, TRV146, TRV147, TRV148, TRV149, TRV150, TRV151, TRV152, TRV153, TRV154, TRV155, TRV156, TRV157, TRV158, TRV159, TRV160, TRV161, TRV162, TRV163, TRV164, TRV165, TRV166, TRV167, TRV168, TRV169, TRV170, TRV171, TRV172, TRV173, TRV174, TRV175, TRV176, TRV177, TRV178, TRV179, TRV180, TRV181, TRV182, TRV183, TRV184, TRV185, TRV186, TRV187, TRV188, TRV189, TRV190, TRV191, TRV192, TRV193, TRV194, TRV195, TRV196, TRV197, TRV198, TRV199, TRV200, TRV201, TRV202, TRV203, TRV204, TRV205, TRV206, TRV207, TRV208, TRV209, TRV210, TRV211, TRV212, TRV213, TRV214, TRV215, TRV216, TRV217, TRV218, TRV219, TRV220, TRV221, TRV222, TRV223, TRV224, TRV225, TRV226, TRV227, TRV228, TRV229, TRV230, TRV231, TRV232, TRV233, TRV234, TRV235, TRV236, TRV237, TRV238, TRV239, TRV240, TRV241, TRV242, TRV243, TRV244, TRV245, TRV246, TRV247, TRV248, TRV249, TRV250, TRV251, TRV252, TRV253, TRV254, TRV255, TRV256, TRV257, TRV258, TRV259, TRV260, TRV261, TRV262, TRV263, TRV264, TRV265, TRV266, TRV267, TRV268, TRV269, TRV270, TRV271, TRV272, TRV273, TRV274, TRV275, TRV276, TRV277, TRV278, TRV279, TRV280, TRV281, TRV282, TRV283, TRV284, TRV285, TRV286, TRV287, TRV288, TRV289, TRV290, TRV291, TRV292, TRV293, TRV294, TRV295, TRV296, TRV297, TRV298, TRV299, TRV300, TRV301, TRV302, TRV303, TRV304, TRV305, TRV306, TRV307, TRV308, TRV309, TRV310, TRV311, TRV312, TRV313, TRV314, TRV315, TRV316, TRV317, TRV318, TRV319, TRV320, TRV321, TRV322, TRV323, TRV324, TRV325, TRV326, TRV327, TRV328, TRV329, TRV330, TRV331, TRV332, TRV333, TRV334, TRV335, TRV336, TRV337, TRV338, TRV339, TRV340, TRV341, TRV342, TRV343, TRV344, TRV345, TRV346, TRV347, TRV348, TRV349, TRV350, TRV351, TRV352, TRV353, TRV354, TRV355, TRV356, TRV357, TRV358, TRV359, TRV360, TRV361, TRV362, TRV363, TRV364, TRV365, TRV366, TRV367, TRV368, TRV369, TRV370, TRV371, TRV372, TRV373, TRV374, TRV375, TRV376, TRV377, TRV378, TRV379, TRV380, TRV381, TRV382, TRV383, TRV384, TRV385, TRV386, TRV387, TRV388, TRV389, TRV390, TRV391, TRV392, TRV393, TRV394, TRV395, TRV396, TRV397, TRV398, TRV399, TRV400, TRV401, TRV402, TRV403, TRV404, TRV405, TRV406, TRV407, TRV408, TRV409, TRV410, TRV411, TRV412, TRV413, TRV414, TRV415, TRV416, TRV417, TRV418, TRV419, TRV420, TRV421, TRV422, TRV423, TRV424, TRV425, TRV426, TRV427, TRV428, TRV429, TRV430, TRV431, TRV432, TRV433, TRV434, TRV435, TRV436, TRV437, TRV438, TRV439, TRV440, TRV441, TRV442, TRV443, TRV444, TRV445, TRV446, TRV447, TRV448, TRV449, TRV450, TRV451, TRV452, TRV453, TRV454, TRV455, TRV456, TRV457, TRV458, TRV459, TRV460, TRV461, TRV462, TRV463, TRV464, TRV465, TRV466, TRV467, TRV468, TRV469, TRV470, TRV471, TRV472, TRV473, TRV474, TRV475, TRV476, TRV477, TRV478, TRV479, TRV480, TRV481, TRV482, TRV483, TRV484, TRV485, TRV486, TRV487, TRV488, TRV489, TRV490, TRV491, TRV492, TRV493, TRV494, TRV495, TRV496, TRV497, TRV498, TRV499, TRV500, TRV501, TRV502, TRV503, TRV504, TRV505, TRV506, TRV507, TRV508, TRV509, TRV510, TRV511, TRV512, TRV513, TRV514, TRV515, TRV516, TRV517, TRV518, TRV519, TRV520, TRV521, TRV522, TRV523, TRV524, TRV525, TRV526, TRV527, TRV528, TRV529, TRV530, TRV531, TRV532, TRV533, TRV534, TRV535, TRV536, TRV537, TRV538, TRV539, TRV540, TRV541, TRV542, TRV543, TRV544, TRV545, TRV546, TRV547, TRV548, TRV549, TRV550, TRV551, TRV552, TRV553, TRV554, TRV555, TRV556, TRV557, TRV558, TRV559, TRV560, TRV561, TRV562, TRV563, TRV564, TRV565, TRV566, TRV567, TRV568, TRV569, TRV570, TR

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORT SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
5169	14191	31033	1.26	2.9E-02	AE02074.1	NT	Unfractionated rat liver RNA section 151 of 226 of the complete chromosome 1
5227	18216	31062	2.49	2.9E-02	AW241164.1	EST_HUMAN	h2304141 NCI CON_389 Homo sapiens cDNA clone IMAGE370383 3' similar to SW1069_HUMAN
5059	19120	31063	0.87	2.9E-02	AF101552.2	EST_HUMAN	U-130411 HTH THE PROTEIN NUC-0009
5058	19120	31063	0.87	2.9E-02	AF101552.2	EST_HUMAN	U-130411 HTH THE PROTEIN NUC-0009
5454	19599	31064	1.51	2.9E-02	AI299303.1	EST_HUMAN	h2304141 NCI CON_389 Homo sapiens cDNA clone IMAGE370383 3' similar to SW1069_HUMAN
6693	19729	33029	2.29	2.9E-02	BE52746.1	EST_HUMAN	h2304141 NCI CON_389 Homo sapiens cDNA clone IMAGE370383 3' similar to SW1069_HUMAN
7140	20248	33498	0.78	2.9E-02	Z69044.1	EST_HUMAN	h2304141 NCI CON_389 Homo sapiens cDNA clone IMAGE370383 3' similar to SW1069_HUMAN
7236	20147	33597	0.78	2.9E-02	Z69044.1	EST_HUMAN	h2304141 NCI CON_389 Homo sapiens cDNA clone IMAGE370383 3' similar to SW1069_HUMAN
7078	20147	33911	0.71	2.9E-02	PT1884	EST_HUMAN	h2304141 NCI CON_389 Homo sapiens cDNA clone IMAGE370383 3' similar to SW1069_HUMAN
6072	22001	35955	0.87	2.9E-02	AA60946.1	EST_HUMAN	h2304141 NCI CON_389 Homo sapiens cDNA clone IMAGE370383 3' similar to SW1069_HUMAN
6608	22669	36270	1.45	2.9E-02	11452020	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
10239	23127	36529	0.77	2.9E-02	AF114952.1	NT	Secitacryonase dieneinase NRRL Y-12354(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene
10239	23127	36530	0.77	2.9E-02	AF114952.1	NT	Secitacryonase dieneinase NRRL Y-12354(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene
10698	23773	37199	4.93	2.9E-02	AL163305.2	EST_HUMAN	h2304141 NCI CON_389 Homo sapiens cDNA clone IMAGE370383 3' similar to SW1069_HUMAN
11825	24745	37199	2.19	2.9E-02	AA278351.1	EST_HUMAN	h2304141 NCI CON_389 Homo sapiens cDNA clone IMAGE370383 3' similar to SW1069_HUMAN
11695	24837	36330	1.87	2.9E-02	AW150047.1	EST_HUMAN	h2304141 NCI CON_389 Homo sapiens cDNA clone IMAGE370383 3' similar to SW1069_HUMAN
555	13024	29932	1.51	2.9E-02	AF193130.1	EST_HUMAN	h2304141 NCI CON_389 Homo sapiens cDNA clone IMAGE370383 3' similar to SW1069_HUMAN
555	13024	29933	1.51	2.9E-02	AF193130.1	EST_HUMAN	h2304141 NCI CON_389 Homo sapiens cDNA clone IMAGE370383 3' similar to SW1069_HUMAN
835	13800	29827	13.09	2.9E-02	BE974314.1	EST_HUMAN	h2304141 NCI CON_389 Homo sapiens cDNA clone IMAGE370383 3' similar to SW1069_HUMAN
694	13947	29894	4.47	2.9E-02	BE974314.1	EST_HUMAN	h2304141 NCI CON_389 Homo sapiens cDNA clone IMAGE370383 3' similar to SW1069_HUMAN
2613	19902	29894	2.54	2.9E-02	U12571.1	NT	Rattus norvegicus nebulin-3A mRNA, complete cds
2607	19049	26551	1.86	2.9E-02	X68697.1	NT	H. sapiens mRNA for luciferin chlorophyll a/c binding protein, 10p1
2607	19049	26552	1.86	2.9E-02	X68697.1	NT	H. sapiens mRNA for luciferin chlorophyll a/c binding protein, 10p1
4120	18403	30027	1.28	2.9E-02	BE179166.1	EST_HUMAN	h2304141 NCI CON_389 Homo sapiens cDNA clone IMAGE370383 3' similar to SW1069_HUMAN
4120	18403	30028	1.28	2.9E-02	BE179166.1	EST_HUMAN	h2304141 NCI CON_389 Homo sapiens cDNA clone IMAGE370383 3' similar to SW1069_HUMAN
4301	17515	30161	0.19	2.9E-02	AW192114.1	EST_HUMAN	h2304141 NCI CON_389 Homo sapiens cDNA clone IMAGE370383 3' similar to SW1069_HUMAN
5387	18993	30161	0.19	2.9E-02	AW192114.1	EST_HUMAN	h2304141 NCI CON_389 Homo sapiens cDNA clone IMAGE370383 3' similar to SW1069_HUMAN
5912	15881	33069	0.38	2.9E-02	AF16276.1	EST_HUMAN	h2304141 NCI CON_389 Homo sapiens cDNA clone IMAGE370383 3' similar to SW1069_HUMAN
9434	19161		4.75	2.9E-02	BE370126.1	EST_HUMAN	h2304141 NCI CON_389 Homo sapiens cDNA clone IMAGE370383 3' similar to SW1069_HUMAN

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6463	10498	32016	4.02	2.5E-02	BE14688.1	EST_HUMAN	60157303.F1 NIH MCC-3 Homo sapiens cDNA, clone IMAGE:3028054.5'
6593	18934	32016	0.83	2.5E-02	L2002.1	NT	Chlamydomonas reinhardtii YSP-3 mRNA, complete cds
8113	21027	34353	1.72	2.5E-02	BF53722.1	EST_HUMAN	AB010565.F1 NIH COAP B66.3 Homo sapiens cDNA, clone IMAGE:4213409.5'
8113	21027	34354	1.72	2.5E-02	BF53722.1	EST_HUMAN	AB010565.F1 NIH COAP B66.3 Homo sapiens cDNA, clone IMAGE:4213409.5'
8208	21285	34800	0.48	2.5E-02	BE29409.1	EST_HUMAN	Chromodomain protein class I DNA, p202 (p202) (PHF2) gene, complete cds
8208	21285	34801	0.48	2.5E-02	BE29409.1	EST_HUMAN	Chromodomain protein class I DNA, p202 (p202) (PHF2) gene, complete cds
8208	21463	35263	0.78	2.5E-02	021713.1	EST_HUMAN	60105020.F1 NIH MCC-36 Homo sapiens cDNA, clone IMAGE:3344278.5'
10358	22142	35674	0.78	2.5E-02	021713.1	SWISSPROT	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
10358	22142	35675	0.78	2.5E-02	021713.1	NT	D melanogaster 26S ribosomal RNA, D2 domain
11959	22495	37377	0.98	2.5E-02	A147615.1	EST_HUMAN	ab22462.x1 Soares, pregnant, uterus, NHPU Homo sapiens cDNA, clone IMAGE:186932.3'
11249	24173	37020	2.37	2.5E-02	010335	SWISSPROT	HYPOHETICAL_467_KD PROTEIN C18G10.05 IN CHROMOSOME1
11249	24173	37921	2.37	2.5E-02	010335	SWISSPROT	HYPOHETICAL_467_KD PROTEIN C18G10.05 IN CHROMOSOME1
11269	24218	37968	4.36	2.5E-02	A123763.1	NT	Bos taurus partial actin9 gene, exon 17-19
11318	24237						Mac musculus major histocompatibility locus class II region, major histocompatibility protein class II alpha chain (IiAlpha) and major histocompatibility protein class II beta chain (IiBeta) gene, complete cds; butyrophilin-like (NCG), butyrophilin-1b
12181	25017		3.87	2.5E-02	AF050157.1	NT	Homo sapiens gene for LECT2, complete cds
12215	25049		1.74	2.5E-02	AB007546.1	NT	Pseudomonas sp. transposon TnsC47 DNA
12477	25885		2.05	2.5E-02	X59509.1	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC53603), mRNA
12653	25749		1.7	2.5E-02	11433220	NT	Homo sapiens mitogen-activated protein kinase kinase 15 (K15) (K15), complete cds
12740	25380		2.18	2.5E-02	U00109.1	NT	Dicycatalium discoidium putative protein kinase kinase 15 (K15) (K15), complete cds
184	13283	26200	1.01	2.4E-02	AB179892.1	EST_HUMAN	h77d71.x1 Soares, fetal liver spleen, TNF.S1 Homo sapiens cDNA, clone IMAGE:2070109.3'
1621	14651	27614	1.4	2.4E-02	H63844.1	EST_HUMAN	h77d71.x1 Soares, fetal liver spleen, TNF.S1 Homo sapiens cDNA, clone IMAGE:2070109.3'
2048	15915	28075	1.71	2.4E-02	P01601	SWISSPROT	H2 CLASS1 HISTOCOMPATIBILITY ANTIGEN, K.B ALPHA CHAIN PRECURSOR (H-2K(B))
2048	15915	28075	1.71	2.4E-02	P01601	SWISSPROT	H2 CLASS1 HISTOCOMPATIBILITY ANTIGEN, K.B ALPHA CHAIN PRECURSOR (H-2K(B))
4475	174847	30346	2.83	2.4E-02	J05110.1	NT	T thermophilus calcium-binding 26 kDa (CBP 26) protein mRNA, complete cds
4641	17847	30511	1.5	2.4E-02	P01601	SWISSPROT	H2 CLASS1 HISTOCOMPATIBILITY ANTIGEN, K.B ALPHA CHAIN PRECURSOR (H-2K(B))
5204	18279	31120	1.1	2.4E-02	B02702	NT	Homo sapiens hypothetical protein FL1084 (FL1084), mRNA
6420	19054	32879	1.05	2.4E-02	U00680.1	EST_HUMAN	h65904.x1 Soares, fetal liver, spleen, TNF.S1 Homo sapiens cDNA, clone IMAGE:418791.3'
6520	19550	32914	0.81	2.4E-02	NS11090.1	NT	Chicken myoglobin-related dihydro-1C kinase substrate (MARCKS) mRNA, complete cds
9520	19550	32914	0.81	2.4E-02	NS11090.1	NT	Chicken myoglobin-related dihydro-1C kinase substrate (MARCKS) mRNA, complete cds
7600	20528	33515	0.79	2.4E-02	J20573.1	EST_HUMAN	HS040CA.Y1.T Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7607	20528	33515	0.83	2.4E-02	J20573.1	NT	Put gene for uncoupling protein (UCP)
7607	20542	33553	0.83	2.4E-02	X12625.1	NT	Put gene for uncoupling protein (UCP)

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Probe Seq ID NC:	Exon Seq ID NC:	ORF Seq ID NC:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5387	21330	34590	0.86	2.4E-02	P58602	SWISSPROT	HENIOCTIN PRECURSOR (HUMORAL ECTIN)
5388	21330	34590	0.86	2.4E-02	P58602	SWISSPROT	HENIOCTIN PRECURSOR (HUMORAL ECTIN)
5389	21330	34591	0.74	2.4E-02	AF181907.1	EST_HUMAN	RC3-310185-293504/19-0285101-66 Homo sapiens cDNA
5390	21493		0.61	2.4E-02	U10780.1	NT	Human related nucleoside 5' long terminal repeat
5392	21493		0.61	2.4E-02	U10780.1	NT	Human related nucleoside 5' long terminal repeat
9009	21938		0.87	2.4E-02	H76378.1	EST_HUMAN	nt2024 at Scarses fetal liver spleen INT.S. Homo sapiens cDNA clone IMAGE233570 3' similar to contains Alu repetitive element; contains ASR repetitive element;
9005	22024	33580	2.18	2.4E-02	N93442.1	EST_HUMAN	z58571.1 at Scarses fetal liver spleen INT.S. Homo sapiens cDNA clone IMAGE234668 3' similar to contains Alu repetitive element; contains ASR repetitive element;
9538	22465	35623	0.6	2.4E-02	AE001126.1	NT	Borealis burgoniensis (section 11 of 70) of the complete genome
9591	22488	35540	0.59	2.4E-02	AA62960.1	EST_HUMAN	z581608.1 at Scarses fetal liver spleen INT.S. Homo sapiens cDNA clone IMAGE743934 3' similar to glc.04422 SLET
10322	23211	36523	2.67	2.4E-02	AF502954.1	EST_HUMAN	AMALOID POLYPEPTIDE PRECURSOR (HUMAN)/contains Alu repetitive element; contains element XTR
10487	23375	35760	3.35	2.4E-02	AA46894.1	EST_HUMAN	nt07512.41 NCL CGAP_Thyl Homo sapiens cDNA clone IMAGE243583 similar to contains Alu repetitive element; contains element PIR5 repetitive element;
12005	24847	38344	2.3	2.4E-02	AF108905.1	NT	Mus musculus major histocompatibility locus class III region Hic70i gene, partial cds, enRNP, G7A, N G23, Mus homolog, CLCP, NG24, NG25, and NG26 genes, complete cds, and unknown genes
12005	24847	38345	2.3	2.4E-02	AF108905.1	NT	Mus musculus major histocompatibility locus class III region Hic70i gene, partial cds, enRNP, G7A, N G23, Mus homolog, CLCP, NG24, NG25, and NG26 genes, complete cds, and unknown genes
12296	25105		4.99	2.4E-02	6927009	NT	Bacteriophage BL07, complete genome
12428	25105	31875	2.48	2.4E-02	6759633	NT	Mus musculus DnaE homolog 1 (E co3) (DnaE1), mRNA
12590	25235	31626	1.85	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
12590	25235	31697	1.86	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
12633	25330		3.1	2.4E-02	A206826.1	NT	Osmorhiza elegans mRNA for non-soluble subunit of mitochondrial succinate dehydrogenase, complete
1895	14316		8.98	2.4E-02	U03040.1	EST_HUMAN	patgiga1 at Scarses fetal liver, 100% Homo sapiens cDNA clone IMAGE268204 5'
1897	14326		8.73	2.3E-02	U31455.1	NT	Homo sapiens mammary tumor-associated protein INTS (1/3) gene, exon 4
2123	15176	28390	2.77	2.3E-02	Z71289.1	NT	S cerevisiae chromosome IV reading frame ORF YOL245c
3149	15730	28370	5.03	2.3E-02	Z20372.1	EST_HUMAN	HSAACAD1P, Human Fetal Brain Whole Tissue Homo sapiens cDNA
3778	16889		0.65	2.3E-02	U12435.1	NT	CebA beta-galactosidase-binding protein (L GAL53) mRNA, 3' end

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expressed Signal	Most Similar (Top) Ht BLAST E Value	Top Ht Accession No.	Top Ht Database Source
4248	17264	30130	0.91	2.3E-02 L24796.1	NT	Gallus gallus contigenn 45.6 (Cx265.0) gene, complete cds
4248	17264	30131	0.91	2.3E-02 L24762.1	EST_HUMAN	Gallus gallus contigenn 45.6 (Cx265.0) gene, complete cds
4527	175635	30398	1.12	2.3E-02 AF069107.1	NT	CMA-HM085-290.002-169-04 NM0089 Homo sapiens cDNA
4559	175638	30428	1.12	2.3E-02 BE035225.1	EST_HUMAN	CMA-MT0115-071690-315-007 MT0118 Homo sapiens cDNA
4559	175638	30428	1.12	2.3E-02 BE035225.1	EST_HUMAN	CMA-MT0115-071690-315-007 MT0118 Homo sapiens cDNA
4590	18405	30429	1.15	2.3E-02 AV165498.1	EST_HUMAN	w25598.1 NC1 CGAP_ U2 Homo sapiens cDNA clone IMAGE:270671.1
4590	18405	30429	1.15	2.3E-02 AV165498.1	EST_HUMAN	w25598.1 NC1 CGAP_ U2 Homo sapiens cDNA clone IMAGE:270671.1
4705	17170	30573	3.03	2.3E-02 BF029487.1	EST_HUMAN	80167227Rf NIH_MGC_ J2 Homo sapiens cDNA clone IMAGE:382893.5
4705	17170	30573	3.03	2.3E-02 BF029487.1	EST_HUMAN	80167227Rf NIH_MGC_ J2 Homo sapiens cDNA clone IMAGE:382893.5
5141	18139	30978	0.92	2.3E-02 AT93177.1	EST_HUMAN	q25603.35 NC1 CGAP_ NRH1 Homo sapiens cDNA clone IMAGE:384386.5
5141	18139	30978	0.92	2.3E-02 AT93177.1	EST_HUMAN	q25603.35 NC1 CGAP_ NRH1 Homo sapiens cDNA clone IMAGE:384386.5
5104	18156	31003	1.02	2.3E-02 AV1844307.1	EST_HUMAN	R2C-RN051-280100-011-407 ON0057 Homo sapiens cDNA
5590	18838	31517	3.68	2.3E-02 UB6303.1	EST_HUMAN	Cauliculer acetabularis lipoxygenase IV PaeL subunit (perE) gene, complete cds, and prolamyl-CoA carboxylase beta chain (pcarB) homolog genes, partial cds
6183	19328	32706	0.5	2.3E-02 BF04644.1	EST_HUMAN	8018292Rf NIH_MGC_ J77 Homo sapiens cDNA clone IMAGE:4042829.3
6908	19693	35157	4.37	2.3E-02 AF16157.1	NT	Ardopsops pallens DNA chromosome 1, coding fragment No. 17
7320	18488	31290	1.11	2.3E-02 BE14175.1	EST_HUMAN	NF04-H1030-071099-002-299-10080 Homo sapiens cDNA
7987	20794	34098	0.43	2.3E-02 AF163103.2	NT	Homo sapiens chromosome 21 segment :IS27C103
8456	21388	34727	6.96	2.3E-02 UB9391.0	NT	Human plectin (PLECT) gene, exon 3-52, and complete cds
9041	21910	35529	0.97	2.3E-02 AJ248105.1	NT	Homo sapiens RXR α gene for thyroid-containing component X, exons 1-11
9041	21910	35529	0.97	2.3E-02 AJ248105.1	NT	Homo sapiens RXR α gene for thyroid-containing component X, exons 1-11
9254	22162	35536	0.8	2.3E-02 AF033306.1	EST_HUMAN	w41014.5 Homo sapiens cDNA clone IMAGE:290291.47
9254	22162	35537	0.8	2.3E-02 AF033306.1	EST_HUMAN	w41014.5 Homo sapiens cDNA clone IMAGE:290291.47
9351	22607	35660	0.81	2.3E-02 AF11556	SWISSPROT	HYPOPHOSPHATE DEHYDROGENASE IN CHROMOSOME 11 PRECURSOR
10373	23352	36604	0.79	2.3E-02 F05532	SWISSPROT	CHROMATIN ASSEMBLY PROTEIN KAPC3
10383	24118	36825	1.23	2.3E-02 F05532	SWISSPROT	Fibrin chain C12 NG units section 85 of 400 of the complete precursor
10383	24118	36825	1.23	2.3E-02 F05532	SWISSPROT	Fibrin chain C12 NG units section 85 of 400 of the complete precursor
12221	26147	37558	2.04	2.3E-02 AF02108.1	SWISSPROT	GLUCONAMYLASE SIBP2 REQUISITOR (GLUCAN 1+ALPHA-D GLUCOSIDASE) (1+-ALPHA-D GLUCAN HYDROLASE)
12214	26048	37558	1.41	2.3E-02 AF159132.1	EST_HUMAN	Meliponine eras fushi keratin-factor 1 mRNA, complete cds
12408	26736	37558	5.09	2.3E-02 BE176833.1	EST_HUMAN	60117095Rf NIH_MGC_ J21 Homo sapiens cDNA clone IMAGE:3549587.5
12691	26481	317505	3.4	2.3E-02 UB60431.1	NT	Shropyniensis sp. alpha-1,3/4-fucosidase precursor gene, complete cds
20259	25908		3.37	2.3E-02 UJ1071.1	NT	Drosophila discoidium extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF D NC	Expressi Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7611	13818	26747	2.86	2.3E-02	AF016207.1	NT	Columbia 16α nucleoside epiphosphatase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
7791	1773	14759	1.22	2.3E-02	4657440	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
2028	10245	28040	1.24	2.3E-02	Z83001.1	NT	<i>S. pneumoniae</i> rpsA gene and open reading frames
2774	15633	23759	1.24	2.3E-02	AF006933.1	NT	Mus musculus rpsA gene and open reading frames
3456	16636		1.69	2.3E-02	AA07786.1	EST	Mus musculus rpsA gene and open reading frames
3715	16747		1.46	2.3E-02	AF068094.1	EST	Human rpsA gene and open reading frames
3520	16948	29630	1.15	2.3E-02	AF001317.1	EST	Human rpsA gene and open reading frames
3395	17022	28912	0.65	2.3E-02	Z74233.1	EST	Human rpsA gene and open reading frames
4726	17731		0.9	2.3E-02	Z61979	SWISSPROT	Human rpsA gene and open reading frames
6509	19053	33743	0.51	2.3E-02	AF002222.1	EST	Human rpsA gene and open reading frames
7617	20585	32848	3.24	2.3E-02	AF006933.1	EST	Human rpsA gene and open reading frames
8443	21873	35233	1.89	2.3E-02	AF016162.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 27
8843	21873	35234	1.89	2.3E-02	AF016162.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 27
9398	22266	35659	0.58	2.3E-02	Z79485.1	NT	Human rpsA gene and open reading frames
10210	23101	36591	2.26	2.3E-02	AB026898.1	NT	Human rpsA gene and open reading frames
10210	23101	36592	2.26	2.3E-02	AB026898.1	NT	Human rpsA gene and open reading frames
10701	23687		1.17	2.3E-02	6875140	EST	Human rpsA gene and open reading frames
11854	24560	34631	1.60	2.3E-02	BE791007.1	EST	Human rpsA gene and open reading frames
12636	26329		2.8	2.3E-02	AF003563.1	EST	Human rpsA gene and open reading frames
442	13313		6.53	2.1E-02	ZV016022.1	EST	Human rpsA gene and open reading frames
471	13542		6.53	2.1E-02	AF023726.1	EST	Human rpsA gene and open reading frames
1290	14320	27266	5.86	2.1E-02	U72075.1	NT	Human rpsA gene and open reading frames
1414	14444		1.06	2.1E-02	AF001936.1	NT	Human rpsA gene and open reading frames
1414	14444		1.06	2.1E-02	AF001936.1	NT	Human rpsA gene and open reading frames
1806	14832	27398	0.88	2.1E-02	P02438	SWISSPROT	Human rpsA gene and open reading frames
1806	14832	27601	0.88	2.1E-02	P02438	SWISSPROT	Human rpsA gene and open reading frames
1806	14832	27601	0.88	2.1E-02	P02438	SWISSPROT	Human rpsA gene and open reading frames
1977	14905	27979	1.02	2.1E-02	AF009090.1	NT	Human rpsA gene and open reading frames

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Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3048	10326	28066	0.95	2.1E-02	BC077546.1	EST_HUMAN	PtACE10546:120100-091.41; B10546 Homo sapiens cDNA
3058	10328	28070	0.95	2.1E-02	BC077546.1	EST_HUMAN	PtACE10546:120100-091.41; B10546 Homo sapiens cDNA
3064	10332	28073	0.95	2.1E-02	AA70262.1	EST_HUMAN	PtACE10546:120100-091.41; B10546 Homo sapiens cDNA
3102	10355	28075	0.95	2.1E-02	NZ02683.1	EST_HUMAN	PtACE10546:120100-091.41; B10546 Homo sapiens cDNA
3102	10355	28066	0.95	2.1E-02	BC077546.1	EST_HUMAN	PtACE10546:120100-091.41; B10546 Homo sapiens cDNA
3102	10356	28067	0.95	2.1E-02	BC077546.1	EST_HUMAN	PtACE10546:120100-091.41; B10546 Homo sapiens cDNA
3645	10681	28078	1.38	2.1E-02	AA461271.1	EST_HUMAN	PtACE10546:120100-091.41; B10546 Homo sapiens cDNA
4227	17243	30111	0.72	2.1E-02	J70283.1	NT	S cerevisiae chromosome IV coding frame ORF YOL245c
4414	17425	30977	0.97	2.1E-02	BF34655.1	EST_HUMAN	60231300071 NCI CGAP Bmi1 Homo sapiens cDNA clone IMAGE4157151
4554	17593	30422	2.02	2.1E-02	U44944.1	NT	Borrelia burgdorferi element c33-2, <i>src2</i> and <i>src3</i> genes, complete cds, and unknown genes
4665	17573	30439	1.59	2.1E-02	U08127.1	EST_HUMAN	w391.d11.x1 Scores: NSF: P8: SW: OT: PA: P: 31 Homo sapiens cDNA clone IMAGE231508.3
4823	17824	30363	5.16	2.1E-02	U06501.1	NT	A. Italiane mitochondrial genome, part A
4033	17032	30791	0.86	2.1E-02	AB23432.1	EST_HUMAN	W54105.x1 NCI CGAP Kdr1 Homo sapiens cDNA clone IMAGE284428.3
5839	18907	33022	0.81	2.1E-02	AA737026.1	EST_HUMAN	CU44HT0244:11109-040-008 HT0244 Homo sapiens cDNA
7420	20110	33360	0.78	2.1E-02	BF086100.1	EST_HUMAN	Q79-QN0058-120000-326-w12 GNC058 Homo sapiens cDNA
9084	22013	35370	0.92	2.1E-02	6792328	NT	Mus musculus sorting motif 1 (Src1), mRNA
10034	22834	35522	0.81	2.1E-02	AA484288.1	EST_HUMAN	am35407.41 Striatogene schizobrain S11 Homo sapiens cDNA clone IMAGE1620732.3 similar to contains
10157	23048	35447	2.31	2.1E-02	AJ243215.1	NT	Alu repetitive element/contains element MER11 repetitive element;
10157	23048	35446	2.31	2.1E-02	AJ243215.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10489	23377	36792	1.41	2.1E-02	U29324.1	NT	Streptococcus pneumoniae lipoteichoic acid, excludase, repressor protein, release, UrmC/MucB homolog, and
10663	23449	36871	0.71	2.1E-02	AA484288.1	EST_HUMAN	am35407.41 Striatogene schizobrain S11 Homo sapiens cDNA clone IMAGE1620732.3 similar to contains
12638	18429		13.78	2.1E-02	U02718.1	NT	Homo sapiens putative p38HRA pseudogene for hair keratin, exons 2 to 7
18026	26667	31737	12.1	2.1E-02	AF463915.1	NT	Ascaris lumbricoides major outer membrane protein Omap precursor (omax) gene, complete cds
18	13134	26020	0.77	2.0E-02	BF02382.1	EST_HUMAN	765108.x1 NCI CGAP J7-28 Homo sapiens cDNA clone IMAGE330658.3 similar to contains MER13
10	13135	26021	7.06	2.0E-02	AY006565.1	EST_HUMAN	MER1 repetitive element;
278	13373	26287	3.11	2.0E-02	U02718.1	NT	U02718.1 Homo sapiens cDNA clone IMAGE330658.3 similar to contains MER13
316	13407	26255	2.79	2.0E-02	AA455535.1	EST_HUMAN	am35407.41 Striatogene schizobrain S11 Homo sapiens cDNA clone IMAGE330658.3 similar to contains
823	13850	26817	1.86	2.0E-02	6753635	NT	Mus musculus DMS homolog 1 (E. coli) (DMS1), mRNA

Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1114	14198	27095	135.42	2.0E-02	AF096935.1	NT	Homo sapiens genomic region containing hypermutable mini-satellites chromosome 1 [1,638,33] of Homo sapiens
1227	14254	27207	1.04	2.0E-02	86222491	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1227	14254	27208	1.04	2.0E-02	86222491	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1690	14617	27895	1.45	2.0E-02	8622433	NT	Homo sapiens hypothetical protein FLJ10468 (FLJ10468), mRNA
1690	14617	27896	1.45	2.0E-02	8622433	NT	Homo sapiens hypothetical protein FLJ10468 (FLJ10468), mRNA
2848	18555		2.16	2.0E-02	AL161632.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3128	19134	28020	1.75	2.0E-02	BF026232.1	EST_HUMAN	T951608.x1 NIG CGAP_F238 Homo sapiens cDNA clone IMAGE3308998.3 similar to contains MER1.13 MER1 repetitive element;
3187	19239		1.42	2.0E-02	7365474	NT	Mus musculus scema domain, transmembrane domain (TM), and cytoplasmic domain, (annexin) 8B (Sema8B), mRNA
3274	19322		1.54	2.0E-02	AF05568.1	NT	Arabidopsis thaliana CP2-2 zinc finger protein FZF mRNA, complete cds
4022	17117	20092	1.44	2.0E-02	M18095.1	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRCGP) mRNA, 3' end
5295	18271	31119	0.86	2.0E-02	AA468538.1	EST_HUMAN	aa16510.11 Soares, NIH/NIH, ST Homo sapiens cDNA clone IMAGE819307.5'
5349	18332	31180	0.86	2.0E-02	Z21058.1	EST_HUMAN	HSAJADMI1 TEST1, Human adult testis tissue Homo sapiens cDNA clone CA
8370	19332		0.97	2.0E-02	BF045913.1	EST_HUMAN	CNG-2N0038-10080-542-06 QN0388 Homo sapiens cDNA
8631	18002	32017	0.41	2.0E-02	U04776.1	NT	Centothalpis megans sea-2 mRNA, complete cds
8115	19174	32304	0.8	2.0E-02	33521.2	NT	Dicotyledon discoidalis VII unconventional myosin (myo) gene, complete cds
7682	20003	34216	0.86	2.0E-02	AF000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-650400 nt, position (47)
7682	20003	34219	0.86	2.0E-02	AF000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-650400 nt, position (47)
10389	20278		2.21	2.0E-02	U70408.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
10947	20753	37159	2.12	2.0E-02	AA049432.1	EST_HUMAN	hw17002.x1 NIG CGAP_F4611 Homo sapiens cDNA clone IMAGE229810.3'
11047	24719	37460	5.81	2.0E-02	Z73056.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 93192
11610	24791	38222	2.1	2.0E-02	D8181.1	NT	Enase catalase DNA for Trichostema/aeaw1720-lyase, c-amp etc cds
12107	24648	38350	1.58	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANKG), transcript variant 1, mRNA
12107	24648	38491	1.58	2.0E-02	AA049538.1	EST_HUMAN	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANKG), transcript variant 1, mRNA
12241	18271	31119	1.06	2.0E-02	AF151032.2	NT	aa16510.11 Soares, NIH/NIH, ST Homo sapiens cDNA clone IMAGE819307.5'
12673	19589		1.94	2.0E-02	AF151032.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
13085	25008		6.43	2.0E-02	18009.1	EST_HUMAN	hw17002.x1 NIG CGAP_F311 Homo sapiens cDNA clone IMAGE914166 similar to contains L1.1 L1
717	13775	20886	1.72	1.0E-02	AA57204.1	EST_HUMAN	EMPI-SPRACLES (EMPI-SPRACLES) PROTEIN
1639	14670	27653	1.13	1.0E-02	P15408	SWISSPROT	EMPI-SPRACLES (EMPI-SPRACLES) PROTEIN
2033	15070	26070	3.41	1.0E-02	AL103303.2	NT	Homo sapiens chromosome 21, segment H521C103
2033	15070	26071	3.41	1.0E-02	AL103303.2	NT	Homo sapiens chromosome 21, segment H521C103

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4174	17195		1.26	1.8E-02 AA681446.1	EST_HUMAN	EST_HUMAN	42404 at Source. testis. N1T Homo sapiens cDNA clone IMAGE:140935.3'
4837	17618	39407	1.47	1.8E-02 AA681446.1	EST_HUMAN	SWISSPROT	0V4207021.30.1250071.541 DT0021 Homo sapiens cDNA
5070	18397	33917	1.71	1.8E-02 OA0010	SWISSPROT	SWISSPROT	HYPOPHYSICAL PROTEIN DUB4624.2
6048	19047	32679	0.03	1.8E-02 AE002181.1	NT	NT	Nucleolar phosphoprotein group B strain NC88 section 160 of 208 of the complete genome
6548	19887	32878	0.03	1.8E-02 AE002181.1	NT	NT	Nucleolar phosphoprotein group B strain NC88 section 160 of 208 of the complete genome
7121	20320	33569	9.91	1.8E-02 P14310	EST_HUMAN	SWISSPROT	601765208FT NH MGCC 20 Homo sapiens cDNA clone IMAGE:4025260.5'
7873	20820	34103	0.46	1.8E-02 BF125800.1	EST_HUMAN	EST_HUMAN	601765208FT NH MGCC 20 Homo sapiens cDNA clone IMAGE:4025260.5'
7901	20820	34103	0.54	1.8E-02 BF125800.1	EST_HUMAN	EST_HUMAN	601765208FT NH MGCC 20 Homo sapiens cDNA clone IMAGE:4025260.5'
8700	21037	34094	0.86	1.8E-02 U37001.1	NT	NT	Mac muscular carboxylic anhydrase IV gene, complete cds
9037	21986	35256	0.87	1.8E-02 AA681446.1	EST_HUMAN	EST_HUMAN	0V22.NT075.220.460.155.049 NN1073 Homo sapiens cDNA
9078	22007	35363	1.33	1.8E-02 AA681446.1	EST_HUMAN	EST_HUMAN	Mac muscular microtubule-associated protein 2 (Mac2), mRNA
10025	22325	38313	0.57	1.8E-02 BF241924.1	EST_HUMAN	EST_HUMAN	601877028FT NH MGCC 35 Homo sapiens cDNA clone IMAGE:41059303.5'
10026	22926	38314	0.57	1.8E-02 BF241924.1	EST_HUMAN	EST_HUMAN	601877028FT NH MGCC 35 Homo sapiens cDNA clone IMAGE:41059303.5'
10168	23059		2.33	1.8E-02 AA681446.1	EST_HUMAN	EST_HUMAN	463609 at Source. testis. N1T Homo sapiens cDNA clone IMAGE:184921.8' similar to gbL11872.2 ZINC
10565	23451	36972	1.73	1.8E-02 BE71827.1	EST_HUMAN	EST_HUMAN	FNFR PROTEIN 91 (HUMAN);
10721	23607	37036	1.4	1.8E-02 X69533.1	EST_HUMAN	EST_HUMAN	001465546FT NH MGCC 87 Homo sapiens cDNA clone IMAGE:3865963.5'
11037	23821	37365	0.59	1.8E-02 DT6330	SWISSPROT	SWISSPROT	L-sialin mRNA for myomodulin neuropeptide precursor
11037	23821	37364	0.59	1.8E-02 DT6330	SWISSPROT	SWISSPROT	HYALURONAN-MEDIATED MOTILITY RECEPTOR (INTRACELLULAR HYALURONIC ACID BINDING PROTEIN) (RECEPTOR FOR HYALURONAN-MEDIATED MOTILITY)
11889	23989	37404	1.55	1.8E-02 AB002337.2	NT	SWISSPROT	HYALURONAN-MEDIATED MOTILITY RECEPTOR (INTRACELLULAR HYALURONIC ACID BINDING PROTEIN) (RECEPTOR FOR HYALURONAN-MEDIATED MOTILITY)
11889	23989	37404	1.55	1.8E-02 AB002337.2	NT	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
12040	24832	38386	2.8	1.8E-02 AF000006.1	NT	NT	Pyrodictus koiichii OT3 genome DNA, 118501-1486000 nt, position (67)
12052	24898	38396	3.11	1.8E-02 U62740.1	NT	NT	Zea mays scd6 ribosomal protein P2a-3 (rps26-3) mRNA, partial cds
13030	25720		1.63	1.8E-02 AF20180.1	NT	NT	Plasmodium falciparum erythrocyte membrane-associated glut protein antigen 332 (Ag332) gene, partial cds
931	13983	26028	1.35	1.7E-02 BE94966.1	EST_HUMAN	EST_HUMAN	00151000FT NH MGCC 44 Homo sapiens cDNA clone IMAGE:3883210.5'
1813	14338	27910	2.31	1.7E-02 AW67168.1	EST_HUMAN	EST_HUMAN	HS4403 at Source. NF_1_C0C.S1 Homo sapiens cDNA clone IMAGE:2683740.3' similar to contains L1.11.1 repetitive element
1813	14338	27911	2.31	1.7E-02 AW67168.1	EST_HUMAN	EST_HUMAN	HS4403 at Source. NF_1_C0C.S1 Homo sapiens cDNA clone IMAGE:2683740.3' similar to contains L1.11.1 repetitive element
1834	14315		2.73	1.7E-02 AL036182.2	NT	NT	Homo sapiens chromosome 21 segment HS27C004
2125	15138		10.95	1.7E-02 AB004616.1	NT	NT	Oncobagrus cylindricus mRNA for mltgammag28, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) HT BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2312	15320	2821	1.05	1.7E-02	S1168.1	NT	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
2308	15302		44.07	1.7E-02	1981498	NT	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
3041	19393	2856	0.74	1.7E-02	A147915.1	EST_HUMAN	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
3071	19398		5.93	1.7E-02	A147915.1	EST_HUMAN	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
3071	19398		5.93	1.7E-02	A147915.1	EST_HUMAN	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
3071	19398		0.72	1.7E-02	P04229	SWISSPROT	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
4293	17281		1.14	1.7E-02	A040618.1	EST_HUMAN	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
4296	17310		2.21	1.7E-02	R02608.1	EST_HUMAN	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
4594	17572	30435	1.04	1.7E-02	A055276.1	EST_HUMAN	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
4845	17651	30516	1.58	1.7E-02	A057183.1	EST_HUMAN	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
4827	17629	30596	1.57	1.7E-02	V09841.1	NT	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
4927	17929		8.93	1.7E-02	A015074.1	EST_HUMAN	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
5200	18192	31034	0.65	1.7E-02	0981289	NT	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
6385	19414	32579	1.74	1.7E-02	A109247.1	EST_HUMAN	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
6747	19791		0.49	1.7E-02	Z8368.1	NT	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
6861	19893	33106	1.8	1.7E-02	A038930.1	EST_HUMAN	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
7403	20102	33337	1.13	1.7E-02	A100933.1	NT	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
7570	20906	33764	1.86	1.7E-02	9400716	NT	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
7748	20970	33777	0.88	1.7E-02	L07896.1	NT	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
7748	20970	33779	0.88	1.7E-02	L07896.1	NT	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
8207	21113		2.17	1.7E-02	A101070.1	NT	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
8207	21113		2.17	1.7E-02	A101070.1	NT	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
8970	21328	34861	1.1	1.7E-02	U24841.1	NT	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
10221	23112	38914	1.31	1.7E-02	A040554.1	EST_HUMAN	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
12199	23934	38934	1.98	1.7E-02	5962007	NT	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
12593	25891	31480	2.08	1.7E-02	A1403462.1	EST_HUMAN	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
13073	25397	31728	1.63	1.7E-02	A046028.1	EST_HUMAN	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
334	13005		2.07	1.8E-02	A021629.1	NT	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2
1683	14719	27075	3.49	1.8E-02	Y18886.1	NT	Intercallicin (NR441) [Osteoblasts], Granocyte, 356 nt, segment 1 of 2

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar (Tao) HT BLAST E Value	Top HT Accession No.	Top HT Database Source	Top HT Descriptor
2264	15274	26279	1.1	1.0E-02	G64179	SWISSPROT	LIVER CARBOXYL ESTERASE Z2 PRECURSOR (EGASYN) (ESTERASE-22)
2264	15274	26280	1.1	1.0E-02	G64179	SWISSPROT	LIVER CARBOXYL ESTERASE Z2 PRECURSOR (EGASYN) (ESTERASE-22)
2600	10398	23653	1.31	1.0E-02	AJ003463.1	NT	Homo sapiens NCI COAP gene, Homo sapiens cDNA clone IMAGE:570697
2601	10398	23654	1.32	1.0E-02	AJ003463.2	EST_HUMAN	Homo sapiens NCI COAP gene, Homo sapiens cDNA clone IMAGE:570697
2744	10737	28584	1.42	1.0E-02	AB011633.1	NT	Homo sapiens NCI COAP gene, Homo sapiens cDNA clone IMAGE:570697
3587	10624	28627	0.6	1.0E-02	AF195052.1	EST_HUMAN	3-5'UTR-109200-082-207 C10219 Homo sapiens cDNA
4271	17267		2.09	1.0E-02	AF109203.1	NT	Max musculus major histocompatibility complex region NG27, NG28, RP228, NACH, endonuclease, NG28, KIFC1, Fnc-binding protein, BING1, leucine, RAG3S-like, K22, BING1, beta-1, 3-galactosyl transferase, and
4402	17414	30281	1.14	1.0E-02	AF195407.1	EST_HUMAN	RS915 gene, complete cds; Sacm21 gene, partial
5135	18131	30672	0.94	1.0E-02	AA655347.1	EST_HUMAN	h17f12.21 NCI COAP, P22 Homo sapiens cDNA clone IMAGE:1189103 similar to gb:M24002
5135	18131	30673	0.94	1.0E-02	AA655347.1	EST_HUMAN	PROSTATIC ACID PHOSPHATASE PRECURSOR (HUMAN);
5203	18194	31039	1.06	1.0E-02	AF09132.1	EST_HUMAN	h17f12.21 NCI COAP, P22 Homo sapiens cDNA clone IMAGE:1189103 similar to gb:M24002
5434	18501	31241	0.32	1.0E-02	AI281385.1	EST_HUMAN	PROSTATIC ACID PHOSPHATASE PRECURSOR (HUMAN);
5818	18300	32003	1.29	1.0E-02	g64179	NT	h17f12.21 NCI COAP, P22 Homo sapiens cDNA clone IMAGE:1189103 similar to gb:M24002
5924	10953	33164	2.06	1.0E-02	AB015261.1	NT	Max musculus major histocompatibility complex region NG27, NG28, RP228, NACH, endonuclease, NG28, KIFC1, Fnc-binding protein, BING1, leucine, RAG3S-like, K22, BING1, beta-1, 3-galactosyl transferase, and
7261	20170	33410	0.95	1.0E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7261	20170	33411	0.95	1.0E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
8170	21077	34407	0.85	1.0E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8608	21029	34674	0.70	1.0E-02	AJ277005.1	NT	Homo sapiens perlecan gene for tubby (mouse) homolog and LM01 gene for LIM domain only 1 protein
8767	21067		2.09	1.0E-02	N05151.1	NT	Human spc111 gene for pericentriolar material 1
10545	23426		2.79	1.0E-02	AF019764.1	NT	Drosophila melanogaster enhancer of polycomb (E[PC]) mRNA, complete cds
10602	23767	37214	1.7	1.0E-02	AA672916.1	EST_HUMAN	h17f12.21 NCI COAP, P22 Homo sapiens cDNA clone IMAGE:574290 similar to SW:TELO_RABIT
10602	23767	37215	1.7	1.0E-02	AA672916.1	EST_HUMAN	h17f12.21 NCI COAP, P22 Homo sapiens cDNA clone IMAGE:574290 similar to SW:TELO_RABIT
11347	25946	37700	2.4	1.0E-02	Z94028.1	NT	G. gallus microsatellite DNA (E1008) (c110E11)
11601	24557	38040	2.39	1.0E-02	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11601	24557	38041	2.4	1.0E-02	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11943	24767	38283	2.23	1.0E-02	AB173585.1	EST_HUMAN	h17f12.21 NCI COAP, P22 Homo sapiens cDNA clone IMAGE:574290 similar to SW:TELO_RABIT
12417	15374	25279	2.97	1.0E-02	G64179	SWISSPROT	LIVER CARBOXYL ESTERASE Z2 PRECURSOR (EGASYN) (ESTERASE-22)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source
12417	5274	26260	2.37	1.5E-02	Q04175	SWISSPROT
7716	13832		3.52	1.5E-02	862732	EST_HUMAN
2157	15169	26171	3.65	1.5E-02	N53251	EST_HUMAN
2188	15169	26204	4.31	1.5E-02	AF16184.2	EST_HUMAN
3198	15169	26204	4.31	1.5E-02	AF16184.2	EST_HUMAN
3198	15169	26204	4.31	1.5E-02	AF16184.2	EST_HUMAN
3198	15169	26204	4.31	1.5E-02	AF16184.2	EST_HUMAN
3783	16819	25077	0.88	1.5E-02	BF02942.1	EST_HUMAN
4239	17255	30121	0.93	1.5E-02	AA160697.1	EST_HUMAN
5846	18320	31178	1.05	1.5E-02	AA160697.1	EST_HUMAN
6847	19590	32777	1.02	1.5E-02	Q06711	SWISSPROT
7703	20435		1.73	1.5E-02	11467262	NT
7800	20729	34031	1.39	1.5E-02	11418713	NT
8315	21220	34250	0.77	1.5E-02	AE00347.1	NT
8514	21396	34726	1.7	1.5E-02	AF163303.2	NT
8461	21392	34724	4.2	1.5E-02	11417739	NT
9389	22817	35076	0.88	1.5E-02	BF34554.1	EST_HUMAN
10001	22818		0.55	1.5E-02	AF05074.1	NT
10089	22948	35337	1.39	1.5E-02	D44608.1	NT
10327	23216	35526	1.48	1.5E-02	R32657.1	EST_HUMAN
10327	23216	35526	1.48	1.5E-02	R32657.1	EST_HUMAN
11044	23926	37336	0.53	1.5E-02	BE265719.2	EST_HUMAN
11610	24519	37688	2.52	1.5E-02	L40065.1	NT
11650	24666	38025	1.73	1.5E-02	AF111283.1	NT
12618	25778		2.73	1.5E-02	AF175834.1	EST_HUMAN
440	13611		1.51	1.4E-02	AE002302.2	NT
1145	14787	27126	3.18	1.4E-02	770695	NT
1284	14317		1.27	1.4E-02	U33900.1	NT
1324	14388		2.43	1.4E-02	AF07779.1	NT
1332	14488		1.2	1.4E-02	AF123785.1	EST_HUMAN
3359	16307	23211	2.05	1.4E-02	AF163098.2	NT
3458	16465	23402	0.78	1.4E-02	AF174212.1	EST_HUMAN

Experiments

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Probe ID SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top HIT Accession No.	Top HRD Diabetes Source	Top HIT Descriptor
3543	16391	29484	0.95	1.4E-02 AL161983.2	NT		Auricopias Italiana DNA chromosome 4, contig fragment No. 82
3543	19481	29485	0.69	1.4E-02 AL161388.2	NT		Auricopias Italiana DNA chromosome 4, contig fragment No. 82
3590	16917	29520	0.95	4.90E-02	9503628	NT	Homo sapiens coagulation factor XII (Hageman factor) [F12], mRNA
3724	17076	29644	0.32	1.4E-02 G99919.1B	EST_HUMAN		Mus musculus histocompatibility 2, complement component factor B (I2-B), mRNA
4002	17910	30438	0.32	1.4E-02 AW062888.1	EST_HUMAN		E5374761 IMAGE resequences; IAGG Homo sapiens cDNA
4002	17910	30446	0.61	1.4E-02 AW062888.1	EST_HUMAN		E5374761 IMAGE resequences; IAGG Homo sapiens cDNA
4773	17778	30947	0.77	1.4E-02 G992391	EST_HUMAN		Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
4773	17778	30947	0.81	1.4E-02 G992391	EST_HUMAN		Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
4983	17992	30989	0.97	1.4E-02 BE733142.1	EST_HUMAN		B0107430FT NIH_MGC_21 Homo sapiens cDNA clone IMAGE384280 5'
4983	17992	30940	0.83	1.4E-02 BE733142.1	EST_HUMAN		B0107430FT NIH_MGC_21 Homo sapiens cDNA clone IMAGE384280 5'
6001	28974		0.93	1.4E-02 J91338.1	NT		Hesperia LASS-B pseudogene 3
6682	19718	32018	4.64	1.4E-02 MA69000.1	EST_HUMAN		nT10dA_1 NC1_CGAP_B2 Homo sapiens cDNA clone IMAGE:1026600 similar to contains AUI repetitive element
6682	19718	32919	4.54	1.4E-02 AA59030.1	EST_HUMAN		nT10dA_1 NC1_CGAP_B2 Homo sapiens cDNA clone IMAGE:1026600 similar to contains AUI repetitive element
9495	22168		1.50	1.4E-02 AG20273.1	NT		Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
9495	22383	35745	1.01	1.4E-02 U61702.1	NT		Candida bodinii methanol oxidase (ACO1) gene, complete cds
9688	22621	38001	1.28	1.4E-02 AT72995.1	NT		Homo sapiens SPPL2 gene for secreted phosphoprotein 24 precursor, exon 1-8
9698	23843	35520	1.22	1.4E-02 BC44396.1	EST_HUMAN		B01076230FT NIH_MGC_12 Homo sapiens cDNA clone IMAGE:344241 5'
11034	23990		0.77	1.4E-02 AL163181.2	NT		Homo sapiens chromosome 21 segment HS21C918
11034	23990	37390	0.64	1.4E-02 ZN5936.1	NT		Zmays KlotterS1 (Kot-S1) gene
12537	25132	36100	2.93	1.4E-02 D08498.1	NT		Human FHLN1 gene for filamentous alpha-beta receptor
12537	25132	36100	2.38	1.4E-02 AS24985.1	NT		Auricopias Italiana DNA chromosome 4, contig fragment 1 (SPAC01), mRNA
12538	25500		2.38	1.4E-02 AS24985.1	NT		Auricopias Italiana DNA chromosome 4, contig fragment 1 (SPAC01), mRNA
1588	26840	27669	2.17	1.3E-02 AL163301.2	NT		Homo sapiens chromosome 21 segment HS21C001
1588	26840	27677	2.17	1.3E-02 BS027414.1	EST_HUMAN		Homo sapiens chromosome 21 segment HS21C001
3203	19308	29712	2.24	1.3E-02 AF169198.1	EST_HUMAN		R07129475Ft NIH_MGC_36 Homo sapiens cDNA clone IMAGE:238323 3'
3203	19308	29712	2.24	1.3E-02 BF097081.1	EST_HUMAN		R07129475Ft NIH_MGC_36 Homo sapiens cDNA clone IMAGE:238323 3'
4032	17079		1.23	1.3E-02 AF169198.1	NT		Mus musculus beta-sarcoglycan gene, complete cds
5019	18208		0.98	1.3E-02 U02654.1	NT		Homo genitipes T-cell receptor beta chain TORBVY15141T, TORV/1951P, TORV/285/P, TORBV15141T, TORBV15141T, HMB, bclL, TORBV/285IP, TORBV/AS1, TORBV/AS1,
5314	18398	30932	0.71	1.3E-02 DG6671.1	NT		TORBV/AS1, TORBV/AS1, TRY4, TRY6, TRY7, TRY8, TORBD1, TORBV/HS1, TORBV/HS2>

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) HT BLAST E Value	Top HT Accession No.	Top Hit Database Source	Top HT Descriptor
5426	18398	31284	1.31	1.3E-02	AL049396.2	NT	Mus musculus chromosome X contig2; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 82, zinc finger protein 280
5428	18399	31285	1.31	1.3E-02	AL049396.2	NT	Mus musculus chromosome X contig2; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 82, zinc finger protein 280
5405	18453	32625	1.35	1.3E-02	U09017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, lipid cdc, neuronal apoptosis inhibitory protein (napi) and survival motor neuron protein (smn) genes, complete cds
6439	18486	32662	0.93	1.3E-02	M65952.1	NT	Geminin (Geminin 1.5-hydroxylase esterase)/copanase activator mRNA, complete cds
7298	18487	31287	1.64	1.3E-02	AL161546.2	NT	Archidopsis thaliana DNA chromosome 4, contig fragment No. 48
7298	18487	31288	1.64	1.3E-02	AL161546.2	NT	Archidopsis thaliana DNA chromosome 4, contig fragment No. 48
8012	20929	34297	4.84	1.3E-02	A031863.1	EST_HUMAN	sw60505.v1 Soares, parathyroid, tumor, N/AHPA Homo sapiens cDNA clone IMAGE164807.2 3' similar to contains Alu repetitive element;
8418	21321	34264	0.48	1.3E-02	AF153963.1	NT	Homo sapiens ecotaxone-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
9051	21890	35337	1.91	1.3E-02	AF160061.1	NT	Homo sapiens human endogenous retrovirus W gag/c3.37 (g) gag (gag) gene, complete cds
10703	23359	37016	2.22	1.3E-02	M63700.1	NT	Mouse kidney androgen-regulated protein (KARP) gene, complete cds
10771	23359	37016	0.84	1.3E-02	A001304.1	NT	Cherrydell trichostellin section 31 of 87 of the complete genome
11430	24346	37760	3.78	1.3E-02	AW268583.1	EST_HUMAN	vc34ed3.v1 Soares, NHL_T_GBC_S1 Homo sapiens cDNA clone IMAGE2815030 3'
11430	24346	37761	3.78	1.3E-02	AW268583.1	EST_HUMAN	vc34ed3.v1 Soares, NHL_T_GBC_S1 Homo sapiens cDNA clone IMAGE2815030 3'
12708	25814		2.51	1.3E-02	X57760.1	NT	Yeast ABP1 gene for actin binding protein
12708	25397		1.86	1.3E-02	6630068	NT	Human herpesvirus 8B, complete genome
12931	25712		74.42	1.3E-02	AF152268.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
227	13325		10.45	1.2E-02	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, PPA2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
375	13491	20576	2.86	1.2E-02	A0050096.1	EST_HUMAN	zfp501.1.1 Soares ratia NZS-HR Homo sapiens cDNA clone IMAGE331640 5' similar to contains element L1 repetitive element;
475	13496	20466	1.51	1.2E-02	F93898	SWISSPROT	HYPOTHETICAL 1711 ND PROTEIN IN PUR3 REGION
762	13816	26746	10.78	1.2E-02	AF18622.1	EST_HUMAN	gribelin2.1.1 Soares, testis, NT Homo sapiens cDNA clone IMAGE1754970 3' similar to contains L1.1; L1 repetitive element;
2193	15321	20395	1.98	1.2E-02	AL153132.2	NT	Homo sapiens chromosome 21 segment HS21C019
2407	15470	25870	1.03	1.2E-02	AF172330.1	EST_HUMAN	381 600X1.1 Soares, NHL_T_GBC_S1 Homo sapiens cDNA clone IMAGE2865402 3'
2505	15507	25900	1.15	1.2E-02	AF163162.2	NT	381 600X1.1 Soares, NHL_T_GBC_S1 Homo sapiens cDNA clone IMAGE2865402 3'
2520	15521	25824	1.28	1.2E-02	BC383916.1	EST_HUMAN	60108009F1 NHL MGC 10 kb human cDNA clone IMAGE2454001 5'
2520	15521	25825	1.28	1.2E-02	BC383916.1	EST_HUMAN	60108009F1 NHL MGC 10 kb human cDNA clone IMAGE2454001 5'
2522	15522	25870	1.85	1.2E-02	AF172330.1	EST_HUMAN	381 600X1.1 Soares, NHL_T_GBC_S1 Homo sapiens cDNA clone IMAGE2865402 3'
3148	16189		8.71	1.2E-02	A0073416.1	EST_HUMAN	pm38608.11 Stragano ovarian cancer (8602210) Homo sapiens cDNA clone IMAGE55520 5'

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3331	16377	20277	2.38	1.3E-02	R63053.1	EST_HUMAN	H11268 at Soares placenta N22-HP Homo sapiens cDNA clone IMAGE:138003 3'
4990	17956	30646	1.05	1.2E-02	0754367	NT	Mus musculus interferon regulatory factor 5 (IRF5) mRNA
5025	18022	30990	2.33	1.2E-02	U94383.1	NT	Human headlump hemopoietic colony initiation 24-like protein gene, headlump/hemopoietic (HLA-H) gene, R694d gene, and sodium phosphate transporter (NPT3) gene, complete cds
5172	18184		1.82	1.2E-02	AB011769.1	NT	Oncoapoptosis-related Col1A1 mRNA, partial cds
5219	18209	31055	2.09	1.2E-02	AF173764.1	EST_HUMAN	AV373764.HTF Homo sapiens cDNA clone HTF5HG11 3'
5683	18662		0.47	1.2E-02	AA176918.1	EST_HUMAN	ab2910 at Soares testis, NIH Homo sapiens cDNA clone 1844235 3'
5669	19026	32149	2.02	1.2E-02	D75693.1	NT	Rana sacposa mRNA for calreticulin, complete cds
6355	19404	32571	0.95	1.2E-02	AF045955.1	NT	Homo sapiens wbcort1 (WBCORT1) and wbcort6 (WBCORT6) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7351	20347	33516	5.05	1.2E-02	AF176412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7672	20406	33505	1.02	1.2E-02	H02167.1	EST_HUMAN	y5412 at Soares placenta N22-HP Homo sapiens cDNA clone IMAGE:138055 3'
7656	20629	33527	11.85	1.2E-02	AV173205.1	EST_HUMAN	AV173205.HTF Homo sapiens cDNA clone HTF-BJ019 5'
7088	20807	34223	0.57	1.2E-02	BF219950.1	EST_HUMAN	801882949F1.NH_KGC_87 Homo sapiens cDNA clone IMAGE:496253 5'
8578	21597	34562	2.50	1.2E-02	Q11205	SWISSPROT	CYP-NA-CYD5E1.NEURALINATE-BETA-GALACTOSIDASE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-S) (GAL-NA-COS) (GAL-BETA-1,3-GALNA-CALPHA-2,3-SIALYLTRANSFERASE) (ST3GAL.2) (SIAT-4B)
8705	21636	34583	0.58	1.2E-02	R69831.1	EST_HUMAN	y49106 at Soares placenta N22-HP Homo sapiens cDNA clone IMAGE:142019 3'
8770	21700	35045	1.30	1.2E-02	AF103912.1	NT	Homo sapiens fringe protein mRNA, partial cds
8770	21700	35046	1.38	1.2E-02	AF103912.1	NT	Homo sapiens fringe protein mRNA, partial cds
9447	22376		0.5	1.2E-02	T76987.1	EST_HUMAN	y772018 at Soares fetal liver spleen INL5 Homo sapiens cDNA clone IMAGE:113774 3'
10165	23056	36455	2.19	1.2E-02	AB031015.1	NT	Novaki-like virus group 2 gene for capsid protein, complete cds
10165	23057	36458	5.07	1.2E-02	C18119.1	EST_HUMAN	Novaki-like virus group 2 gene for capsid protein, complete cds
12938	25005		1.4	1.2E-02	AJ246003.1	EST_HUMAN	Novaki-like virus group 2 gene for capsid protein, complete cds
12938	25006		1.49	1.1E-02	AJ247035.1	EST_HUMAN	C18119 Human placenta cDNA (Tfujura) Homo sapiens cDNA clone GEN:457708 5'
1353	14762	27732	1.22	1.1E-02	X75491.1	NT	zmbf011.31 Stratiopsis neopneumoniae (p337231) Homo sapiens cDNA clone IMAGE:330524 3'
1735	14762	27733	1.22	1.1E-02	X75491.1	NT	H sapiens LIPA gene, exon 4
2062	15059	26959	4.39	1.1E-02	BF146363.1	EST_HUMAN	H sapiens LIPA gene, exon 4
2520	15973		4.58	1.1E-02	BF146363.1	EST_HUMAN	zmbf011.31 Stratiopsis neopneumoniae (p337231) Homo sapiens cDNA clone IMAGE:330524 3'
3654	16821	26625	2.68	1.1E-02	AG6386.1	EST_HUMAN	apb010 at NCI-GARP_Ov02 Homo sapiens cDNA clone IMAGE:221959 3' similar to SV-XCP_HUMAN
4250	17219		0.71	1.1E-02	AF181390.1	EST_HUMAN	zmbf011.31 Stratiopsis neopneumoniae (p337231) Homo sapiens cDNA clone IMAGE:330524 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	QRT SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7037	20273	33529	1.02	1.0E-02/22964.0.1	NT	NT	Zmap, UterusRNA pseudogene
9428	22834	36223	8.21	1.0E-02/36353.1.1	EST_HUMAN	EST_HUMAN	601495075F1 NIH_MGC_601 Homo sapiens cDNA clone IMAGE3883177.5'
9528	22834	36223	8.21	1.0E-02/36353.1.1	EST_HUMAN	EST_HUMAN	601495075F1 NIH_MGC_601 Homo sapiens cDNA clone IMAGE3883177.5'
11710	24612		2.1	1.0E-02/AF157559.1	NT	NT	CH146n locus, putative 7 kb gene RNA-binding protein mRNA, complete cds; nucleotide order; full length of gene for
11739	24641		1.41	1.0E-02/AF175961.1	EST_HUMAN	EST_HUMAN	HEAT SHOCK PROTEIN HSP 90-ALPHA (HUMAN) contains 10 repetitive element (contains element 1) MER6
11836	24641	38519	1.98	1.0E-02/AF175961.1	EST_HUMAN	EST_HUMAN	HEAT SHOCK PROTEIN HSP 90-ALPHA (HUMAN) contains 10 repetitive element (contains element 1) MER6
12366	25671		1.97	1.0E-02/362303	SWISSPROT	SWISSPROT	SPICEOSOME ASSOCIATED PROTEIN (SAP 82) (SPLING FACTOR 3A SUBUNIT 2) (SFA308)
12409	25766	31972	3.12	1.0E-02/AF163562.1	EST_HUMAN	EST_HUMAN	RC2-D10077-120300-016-H22 D10077 Homo sapiens cDNA
12422	25805		4.28	1.0E-02/570330.1	NT	NT	Homo sapiens renal disintegrin (RDP) gene, complete cds
12017	26335		2.04	1.0E-02/362844.1	NT	NT	H sapiens gene for I/e910063 antigen
918	13970	25917	1.44	9.0E-03/AF169126.1	EST_HUMAN	EST_HUMAN	WH4290.1 NCI_C63AP_KidT1 Homo sapiens cDNA clone IMAGE2883433.3' similar to contains element
1201	14324		1.31	9.0E-03/BE781869.1	EST_HUMAN	EST_HUMAN	MER22/MER22 repetitive element;
2418	15422	29423	2.28	9.0E-03/AL161569.2	NT	NT	Antibodyp1616 NIH_MGC_87 Homo sapiens cDNA clone IMAGE3873346.5'
2427	15431	29423	1.26	9.0E-03/AF09834.1	NT	NT	Mus musculus MHC class III protein RP7 (Rp1) mRNA, partial cds
2540	15002	28903	1.05	9.0E-03/AF121744.1	EST_HUMAN	EST_HUMAN	qf6008.X1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE1854281.3'
2540	15002	28904	1.05	9.0E-03/AF121744.1	EST_HUMAN	EST_HUMAN	qf6008.X1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE1854281.3'
3063	10002	28903	0.74	9.0E-03/AF121744.1	EST_HUMAN	EST_HUMAN	qf6008.X1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE1854281.3'
3063	10002	28904	0.74	9.0E-03/AF121744.1	EST_HUMAN	EST_HUMAN	qf6008.X1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE1854281.3'
3738	19768	28904	0.83	9.0E-03/AF121744.1	EST_HUMAN	EST_HUMAN	S. carolinensis thermoplasma gene, complete cds
6390	18352	31202	0.81	9.0E-03/AF1676126.1	NT	NT	Homo sapiens mRNA for putative ankyrin repeat containing protein (ORF1)
6021	18353		1.01	9.0E-03/AF1676126.1	EST_HUMAN	EST_HUMAN	w7706a.X1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE2991031.3'
9820	19560		4.43	9.0E-03/BE74988.1	EST_HUMAN	EST_HUMAN	601579438F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE3351752.5'
7872	20798	34102	0.99	9.0E-03/AF142196.1	EST_HUMAN	EST_HUMAN	qf57612.X1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE185974.3'
7891	20817	34123	0.9	9.0E-03/AF142196.1	EST_HUMAN	EST_HUMAN	Homo sapiens hypothetical protein FLH10560 (FLH10560) mRNA
9485	21387		0.84	9.0E-03/AF169891.1	EST_HUMAN	EST_HUMAN	DNF2P454L0412.7.434 (gynymy. hsd) Homo sapiens cDNA clone DKFZ54541.0422.9'
8824	21754		0.99	9.0E-03/AF223391.1	NT	NT	Homo sapiens cation channel apolipoprotein (CACNA1E) gene, exon 7, 48, and partial cds, alternatively spliced
13376	25295	34987	1.71	9.0E-03/P25808	SWISSPROT	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
11424	24340		2.38	9.0E-03/AF160001.1	EST_HUMAN	EST_HUMAN	60151088F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE2892181.5'
11451	24357		1.13	9.0E-03/BE36356.1	EST_HUMAN	EST_HUMAN	60151088F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE2892181.5'

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	OFF SEQ ID NO:	Expression Signal	Most Similar (Top) HT BLAST E Value	Top HT Accession No.	Top HT Database Source	Top HT Descriptor
12137	24077	38478	4.04	8.0E-03	AF565860.1	NT	Homo sapiens mitogen-activated serine/threonine kinase (IMAGE51) gene, complete cds
12291	25102		2.46	8.0E-03	ME2036.1	NT	Oryzopsis cinnamomea aff. 2a Homo mRNA, complete cds
12334	25130		5.42	8.0E-03	AB393101.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
718	26526	26526	0.96	7.0E-03	AF527183.1	NT	Conyocarpoidium parvum HC-10 gene, complete cds
719	13172	26527	0.9	7.0E-03	AF527183.1	NT	Conyocarpoidium parvum HC-10 gene, complete cds
1003	14032	26528	3.85	7.0E-03	AF543376.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1143	14185	27123	2.85	7.0E-03	AV137112.1	EST_HUMAN	AV137112 HTF Homo sapiens cDNA clone HTFAZ10.8
1301	14422		1.34	7.0E-03	Q01000	SWISSPROT	FORHEAD BOX PROTEIN D3 HNFXPH TRANSSCRIPTION FACTOR GENESIS (HEPATOCYTE
1422	14453	27407	3.81	7.0E-03	AA069284.1	EST_HUMAN	NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2 (NFK-2)
1522	14953	27514	3.39	7.0E-03	AF563566.1	EST_HUMAN	ab758403.11 Stragalone fetal retina 197202 Homo sapiens cDNA clone IMAGE:883148.3
2274	16220	28292	1.69	7.0E-03	P04620	SWISSPROT	MG1602.21 Soanes_NEL_7_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739.3
3831	16861	20744	0.97	7.0E-03	AF144468.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3830	16809	20790	0.99	7.0E-03	AF109344.1	EST_HUMAN	U1H-B13.4b-c-10-JUJ.1 NCI_Q6AP_S05 Homo sapiens cDNA clone IMAGE:2733901.3
4105	16891	20744	0.7	7.0E-03	AF144468.1	EST_HUMAN	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (A1beta10) mRNA, complete cds
4709	17174		1.02	7.0E-03	AF165088.1	EST_HUMAN	U1H-B13.4b-c-10-JUJ.1 NCI_Q6AP_S05 Homo sapiens cDNA clone IMAGE:2733901.3
5110	18107		1.98	7.0E-03	AL163278.2	NT	HNBA05.Y1 NCI_Q6AP_GU1 Homo sapiens cDNA clone IMAGE:2689926.9
5334	18318	31166	0.96	7.0E-03	AB107415.1	EST_HUMAN	Homo sapiens chromosome 21 segment H821C078
6031	19003		0.0	7.0E-03	H71108.1	EST_HUMAN	wt10602.1 NCI_Q6AP_Lu119 Homo sapiens cDNA clone IMAGE:2481028.3 similar to contains Alu repetitive element/contains element LTR6 repetitive element
6350	23946		5.23	7.0E-03	AF161059.1	EST_HUMAN	yf52g01.17 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:211024.5 similar to
6609	19010	32764	1.96	7.0E-03	V169251.1	EST_HUMAN	phiX10729 CLUSTERIN PRECURSOR (HUMAN)
6816	19846	33056	2.87	7.0E-03	AA327125.1	EST_HUMAN	RC1-CT02665-096400-018-008 CT02685 Homo sapiens cDNA
6846	19876	33062	0.63	7.0E-03	BE657365.1	EST_HUMAN	z53301.01 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:342716.5
7438	20180	33423	1.98	7.0E-03	BE229133.1	EST_HUMAN	EST336971 Cohn1 Homo sapiens cDNA 5' end
7945	20885	34170	5.7	7.0E-03	Z23938.1	NT	TG4640.43 NCI_Q6AP_Bm202 Homo sapiens cDNA clone IMAGE:330647.3 similar to TR-013387
7948	20895	34171	6.7	7.0E-03	Z23938.1	NT	Q13587 HYPOPHYSICAL PROTEIN 36/39A_2, contains TARI.12 TARI TARI repetitive element
8430	21362	34701	0.57	7.0E-03	AJ224043.1	NT	Scorbutic chromosome II reading frame ORF 13L0717w
8430	21362	34702	0.57	7.0E-03	AJ224043.1	NT	Homo sapiens 899 kb contig between ALL1 and CCR1 on chromosome 21q22, segment 3/3
8589	21620	34902	3.04	7.0E-03	BE176607.1	EST_HUMAN	Homo sapiens 899 kb contig between ALL1 and CCR1 on chromosome 21q22, segment 3/3

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
56033	22638		0.76	7.0E-03	AF111093.2	NT	Homo sapiens <i>serpine1</i> (serpin) transcripts, subunit 1 gene, complete cds, and unknown genes
							W4010.11 Sources fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:248946 3' similar to contains
10122	23013	36410	0.67	7.0E-03	N62878.1	EST_HUMAN	At repetitive element
10242	23133	36556	2.9	7.0E-03	P43832	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10242	23133	36537	2.9	7.0E-03	P43832	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10760	23881		1.12	7.0E-03	A037378.1	EST_HUMAN	AV18/3730 GAG Homo sapiens cDNA clone G1647.09 5'
10950	23981		0.97	7.0E-03	A070074.1	EST_HUMAN	AV18/3730 GAG Homo sapiens cDNA clone G1647.09 5'
11266	24180	37638	2.48	7.0E-03	A030852.1	EST_HUMAN	Bot. tauris mRNA for ND502, complete cds
11340	24239	37668	1.65	7.0E-03	AJ040482.1	NT	Homo sapiens partial MUC3B gene, exon 1-25
11340	24239	37669	1.65	7.0E-03	AJ040482.1	NT	Homo sapiens partial MUC3B gene, exon 1-25
11740	24250	37660	1.65	7.0E-03	B230325.1	EST_HUMAN	Homo sapiens partial MUC3B gene, exon 1-25
12305	25422		1.63	7.0E-03	B230325.1	EST_HUMAN	Homo sapiens partial MUC3B gene, exon 1-25
12881	26478		1.60	7.0E-03	Y17455.1	EST_HUMAN	Homo sapiens LSRF2 gene, penultimate exon
13003	26478		1.60	7.0E-03	AL103300.2	NT	Homo sapiens chromosome 21 segment H821C100
							h222405.1 Sources, N17, 3BG, S1 Homo sapiens cDNA clone IMAGE:2510224 3' similar to
1298	14303	27250	8.83	6.0E-03	AW511148.1	EST_HUMAN	h222405.1 Sources, N17, 3BG, S1 Homo sapiens cDNA clone IMAGE:2510224 3' similar to
1298	14303	27261	8.83	6.0E-03	AW511148.1	EST_HUMAN	h222405.1 Sources, N17, 3BG, S1 Homo sapiens cDNA clone IMAGE:2510224 3' similar to
2633	16866	28884	4.43	6.0E-03	A3739135.1	EST_HUMAN	h222405.1 Sources, N17, 3BG, S1 Homo sapiens cDNA clone IMAGE:2510224 3' similar to
2633	16863	28885	4.43	6.0E-03	A3739135.1	EST_HUMAN	h222405.1 Sources, N17, 3BG, S1 Homo sapiens cDNA clone IMAGE:2510224 3' similar to
3291	16338		2.68	6.0E-03	H76950.1	EST_HUMAN	h222405.1 Sources, N17, 3BG, S1 Homo sapiens cDNA clone IMAGE:2510224 3' similar to
							h222405.1 Sources, N17, 3BG, S1 Homo sapiens cDNA clone IMAGE:2510224 3' similar to
3350	16390		1.02	6.0E-03	AF400338.1	NT	h222405.1 Sources, N17, 3BG, S1 Homo sapiens cDNA clone IMAGE:2510224 3' similar to
							h222405.1 Sources, N17, 3BG, S1 Homo sapiens cDNA clone IMAGE:2510224 3' similar to
3440	16481	20398	0.87	6.0E-03	U08890.1	NT	h222405.1 Sources, N17, 3BG, S1 Homo sapiens cDNA clone IMAGE:2510224 3' similar to
3440	16481	20398	0.87	6.0E-03	U08890.1	NT	h222405.1 Sources, N17, 3BG, S1 Homo sapiens cDNA clone IMAGE:2510224 3' similar to
3440	16481	20398	0.87	6.0E-03	U08890.1	NT	h222405.1 Sources, N17, 3BG, S1 Homo sapiens cDNA clone IMAGE:2510224 3' similar to
3768	17610	29847	2.75	6.0E-03	P107686.1	EST_HUMAN	h222405.1 Sources, N17, 3BG, S1 Homo sapiens cDNA clone IMAGE:2510224 3' similar to
3768	17610	29847	2.75	6.0E-03	P107686.1	EST_HUMAN	h222405.1 Sources, N17, 3BG, S1 Homo sapiens cDNA clone IMAGE:2510224 3' similar to
3844	16873	20756	1.05	6.0E-03	S764029.1	EST_HUMAN	h222405.1 Sources, N17, 3BG, S1 Homo sapiens cDNA clone IMAGE:2510224 3' similar to
3907	17024	29514	0.68	6.0E-03	AW194728.1	EST_HUMAN	h222405.1 Sources, N17, 3BG, S1 Homo sapiens cDNA clone IMAGE:2510224 3' similar to
4040	17047		1.54	6.0E-03	B2350103.1	EST_HUMAN	h222405.1 Sources, N17, 3BG, S1 Homo sapiens cDNA clone IMAGE:2510224 3' similar to
							h222405.1 Sources, N17, 3BG, S1 Homo sapiens cDNA clone IMAGE:2510224 3' similar to
4322	17346		1.30	6.0E-03	U082022.1	NT	h222405.1 Sources, N17, 3BG, S1 Homo sapiens cDNA clone IMAGE:2510224 3' similar to
4453	17441		0.92	6.0E-03	N58465.1	EST_HUMAN	h222405.1 Sources, N17, 3BG, S1 Homo sapiens cDNA clone IMAGE:2510224 3' similar to

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Top Hit

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession	Top Hit Database Source	Top Hit Descriptor
4471	17452		2.1	6.0E-23	A076833.1	EST_HUMAN	683311.11 Scores, bestis, NHT Homo sapiens cDNA clone IMAGE:1635124.3
49308	17500	30675	8.41	6.0E-03	AA324942.1	EST_HUMAN	EST127116 Corbellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5295	18261		1.08	6.0E-03	AA32492.1	NT	Human gamma UBE L Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5274	18280	31112	1.05	6.0E-03	AA62527.1	EST_HUMAN	W6120.121 COGAP COG6 Homo sapiens cDNA clone IMAGE:2310143.3
5340	18293	31172	0.85	6.0E-03	AA62527.1	EST_HUMAN	W6120.121 COGAP COG6 Homo sapiens cDNA clone IMAGE:2310143.3
6392	25647	32609	0.64	6.0E-03	9827621	EST_HUMAN	W6120.121 COGAP COG6 Homo sapiens cDNA clone IMAGE:2310143.3
7126	20332	32058	0.79	6.0E-03	011094	SWISSPROT	Varicella virus, complete genome
7176	18447	31316	0.69	6.0E-03	BE233748.1	EST_HUMAN	SYNAPSIN II
7620	20355	33848	0.43	6.0E-03	BE233748.1	EST_HUMAN	001112339T NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3333172.5
7620	20357	33849	0.43	6.0E-03	AA24442.1	EST_HUMAN	EST119496 Uterus tumor 1 Homo sapiens cDNA 5' end
8090	21057	34332	0.77	6.0E-03	AA24442.1	EST_HUMAN	EST119496 Uterus tumor 1 Homo sapiens cDNA 5' end
8308	21124	34549	0.43	6.0E-03	AF12889.1	NT	Human telomerase reverse transcriptase (TERT) gene, exons 7-10 and complete cds
8359	21294	37500	0.51	6.0E-03	AA24311.1	SWISSPROT	PAS-RELATED PROTEIN RAP-28
8440	21372	34713	14.27	6.0E-03	AC03596.1	EST_HUMAN	Human DMBT1 candidate tumor suppressor gene, exons 1 to 55
8552	21433	34824	2.83	6.0E-03	AN760337.1	EST_HUMAN	onf34a1 M10.1b1 MERT10 repetitive element;
8624	21553		1.74	6.0E-03	EP331018.1	EST_HUMAN	RO-UM0051-210303-032-902 UM0051 Homo sapiens cDNA
10393	22876	36264	0.14	6.0E-03	DT0484.1	NT	RO-UM0051-210303-032-902 UM0051 Homo sapiens cDNA IMAGE:3815628.6
10546	23442		2.49	6.0E-03	AC02981.1	EST_HUMAN	Subcutaneous panniculitis (SPE) virus mRNA for fusion protein
10558	25492	36978	1.14	6.0E-03	AC02981.1	EST_HUMAN	Subcutaneous panniculitis (SPE) virus mRNA for fusion protein
10795	23675	37200	0.88	6.0E-03	AA621955.1	NT	Human sapiens Ovarian acid-hydrolase and cAMP-regulated phosphoprotein 19 (AORP-19) mRNA, complete cds
10890	23774	37200	0.82	6.0E-03	BA63045.1	NT	M10Homo sapiens complete plasmid plasmid pV1 DNA
11195	24171	37559	2.31	6.0E-03	AN062184.1	EST_HUMAN	EST314257 MAGE resequences, MAGE Homo sapiens cDNA
11250	24174		2.31	6.0E-03	AN062184.1	EST_HUMAN	EST314257 MAGE resequences, MAGE Homo sapiens cDNA
11420	24337	37795	5.63	6.0E-03	U14558.1	NT	Mouse nuclear zinc-finger protein mRNA, complete cds
11421	24337	37795	4.02	6.0E-03	U14558.1	NT	Mouse nuclear zinc-finger protein mRNA, complete cds
12364	25168		2.77	6.0E-03	AF101495.1	NT	0015727.06T NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747.5
12504	25742		7.19	6.0E-03	AE000833.1	NT	Rhizobacter capsulatus strain S81303, partial genome
12577	25796		2.38	6.0E-03	U00790.1	NT	Methanobacterium thermoautotrophicum from base 429102 to 492295 (section 39 of 113) of the complete genome
12627	25310		1.73	6.0E-03	Q30229	SWISSPROT	Phenylalanyl-tRNA synthetase (PheRS) from Homo sapiens
12627	25310		1.73	6.0E-03	Q30229	SWISSPROT	Phenylalanyl-tRNA synthetase (PheRS) from Homo sapiens

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12986	25487		2.9	5.0E-03	B672610.1	EST_HUMAN	6014232.1 FI NHG.C. 68 Homo sapiens cDNA clone IMAGE:388338.5
12914	25497		1.49	5.0E-03	AJ259453.1	NT	Bos taurus cDNA clone for SLC6A10, cell surface, cell surface
228	13326	26243	4.80	5.0E-03	X67344.1	NT	H sapiens DNA, DNB, HLA-21, P22, LMP7, TAP1, LMP7, TAP2, DOB, DOB2 and RINGA, 9, 18 and 14 genes
682	13753	26596	1.93	5.0E-03	L29105.1	NT	Chlamydia trachomatis partial ORF8; aminocyclase synthase, complete cds; complete ORF-A, and gpe- like protein, complete cds
682	13753	26670	1.93	5.0E-03	L29105.1	NT	Chlamydia trachomatis partial ORF8; aminocyclase synthase, complete cds; complete ORF-A, and gpe- like protein, complete cds
683	13753	26669	2.31	5.0E-03	L29105.1	NT	Chlamydia trachomatis partial ORF8; aminocyclase synthase, complete cds; complete ORF-A, and gpe- like protein, complete cds
693	13753	26670	2.31	5.0E-03	L29105.1	NT	Chlamydia trachomatis partial ORF8; aminocyclase synthase, complete cds; complete ORF-A, and gpe- like protein, complete cds
1139	14181	27110	1.03	5.0E-03	AJ13457.1	EST_HUMAN	At6g04060.1 Arabidopsis thaliana mRNA for DEAD box RNA helicase RH3
1590	14621		1.11	5.0E-03	A134607.1	EST_HUMAN	g016065.1 Homo sapiens cDNA clone IMAGE:1735980.3
2730	16773	28716	2.35	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2978	16930	28932	0.79	5.0E-03	B673005.1	EST_HUMAN	601194756.F1 NHG.C. 7 Homo sapiens cDNA clone IMAGE:338790.5
3181	16231	29120	5.03	5.0E-03	T67623.1	EST_HUMAN	Y65106.31 Soera infant brain TNIB Homo sapiens cDNA clone IMAGE:22983.3
3198	16246		2.2	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3208	16356	29154	1.43	5.0E-03	R71794.1	EST_HUMAN	Y65902.21 Soera breast DNA Bst Homo sapiens cDNA clone IMAGE:16696.3
3322	16368		0.67	5.0E-03	AJ297357.1	NT	Homo sapiens partial LMOT gene for LIM domain containing protein 1 and KIAA0851 gene
3764	16796	29085	6.51	5.0E-03	AF147449.2	NT	Citrus sinensis seed storage protein cDNA, complete cds
3822	16842	29736	0.71	5.0E-03	U38514.1	NT	M thermophilus complete plasmid pT7-DNA
4026	17053	29943	1.09	5.0E-03	X68508.1	NT	EST172121 Soera liver Homo sapiens cDNA 5' and
4045	17092		1.85	5.0E-03	AA320675.1	EST_HUMAN	Y67610.71 Soera liver Homo sapiens cDNA clone IMAGE:340066.5
4408	17420	30284	0.81	5.0E-03	H78395.1	EST_HUMAN	Citrus sinensis seed storage protein cDNA, complete cds
4410	18852	29736	0.99	5.0E-03	U38941.1	NT	Citrus sinensis seed storage protein cDNA, complete cds
4718	17725	30195	0.52	5.0E-03	AJ131015.1	NT	Homo sapiens SCL gene locus
4832	17853	30703	1.35	5.0E-03	A1762367.1	EST_HUMAN	601502.11 Normal Human Tubular Bone Cells Homo sapiens cDNA clone NHTBC-011502 random
5045	18042	30698	1.11	5.0E-03	P16255	SWISSPROT	SPERMATOCYTOGENIC CELL CAPSULE SELLANDROPROTEIN (MCS)
6006	19070	32196	5.98	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PAVA (PARALYTIC-PROTEIN)

Table 4

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database	Top Hit Descriptor
3701	18739	29924	0.8	4.0E-03	AF46283.1	EST_HUMAN	AV46283.GC Homo sapiens cDNA clone GLC4D02.3
3335	18732	29915	0.7	4.0E-03	U01696	SWISSPROT	GLYCYLATE RECEPTOR 8T (GLYCYLATE RECEPTOR-LIKE PROTEIN OLF1)
4095	17032	29222	0.8	4.0E-03	AF59886.1	NT	Mus musculus tumor susceptibility protein 101 (tsp101) gene, complete cds
4091	17106		2.28	4.0E-03	AJ011712.1	NT	Homo sapiens PINK11 gene, exon 1-11 (end joined CDS)
4723	17728	30192	0.98	4.0E-03	AF172754.1	EST_HUMAN	chr16:68.45 Striocyte lung (p63722) Homo sapiens cDNA clone IMAGE:491142.3 similar to complete ALU repetitive element
4325	18509	31159	1.58	4.0E-03	A466686.1	EST_HUMAN	2586201.1 Soares, fetal liver, adeno_3_NHLS_31 Homo sapiens cDNA clone IMAGE:436009.3
5395	18508		1.02	4.0E-03	AF18104.1	EST_HUMAN	UFR3-ST1028-110700-028-456 ST1028 Homo sapiens cDNA
5438	18538	31381	1.67	4.0E-03	AF170389.1	NT	Drosophila melanogaster mps2077 (mps2077) mRNA, complete cds
5554	18601	31638	20.71	4.0E-03	AF168326.1	NT	Rattus norvegicus beta-casom binding protein mRNA, complete cds
6004	18068	32195	2.46	4.0E-03	P04198	SWISSPROT	(HPR3)
6008	18072	32197	1.61	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE-LABELLED TROPHOZYTE ANTIGEN PRECURSOR
6321	18371	32262	3.62	4.0E-03	U2180.1	EST_HUMAN	DKF227611014.117.761 (synonym: haryz) Homo sapiens cDNA clone DKF227611014.5
6481	19528	32704	0.81	4.0E-03	AF1756072.1	EST_HUMAN	Rattus norvegicus spin gene, complete cds
6554	19035	32760	1.35	4.0E-03	BE24943.1	EST_HUMAN	hp4607.x1 NCI CGAP CG8 Homo sapiens cDNA clone IMAGE:2348682.3
6595	19034	33222	1.34	4.0E-03	AJ813222.1	EST_HUMAN	01070070157 NIH IMAGE_12 Homo sapiens cDNA clone IMAGE:3491854.5
7082	20288	33547	1.49	4.0E-03	U78408.1	NT	#3271.1et Soares, testis, NIH Homo sapiens cDNA clone 1362043.5
7425	20124	33961	1.01	4.0E-03	AL163278.2	NT	Lycopodium obscurum knotted 3 protein (TK3) mRNA, complete cds
7425	20124	33962	1.01	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21078
7602	20469	33787	4.55	4.0E-03	Q02617	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7635	20763	34065	1.34	4.0E-03	AB01483.1	EST_HUMAN	0579712.x1 NCI CGAP_L024 Homo sapiens cDNA clone IMAGE:2271814.3
7837	20765	34068	0.59	4.0E-03	BE570170.1	EST_HUMAN	7651802.x1 NCI CGAP_L024 Homo sapiens cDNA clone IMAGE:3281043.3
7948	20870		0.75	4.0E-03	X02106.1	NT	H. sapiens hgbk1 gene
8521	21462	34795	0.38	4.0E-03	G07102	SWISSPROT	ADAMTS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 6)
8528	21557	34909	0.99	4.0E-03	AF111944.1	NT	(ADAMTS-5) (ADAMTS) (AGGRECANASE-2) (ADMP-2) (ADAMTS 11)
9273	22201	35556	7.83	4.0E-03	AF533983.1	EST_HUMAN	Protein tyrosine phosphatase 122 (PTP122) (PTP122) gene, partial cds
9416	22374		3.38	4.0E-03	AL163208.2	NT	hschr11.1 Soares, NIH_T_OCR_31 Homo sapiens cDNA clone IMAGE:2080013.3 similar to contains ALU repetitive element
9436	22374	35746	3.38	4.0E-03	AL163219.2	NT	Homo sapiens chromosome 21 segment HS21009
10037	23328	36743	0.52	4.0E-03	AF56941.2	EST_HUMAN	HPK3.12.1 Boer, testis, NIH Homo sapiens cDNA clone IMAGE:109180.5
10394	23750	37173	0.54	4.0E-03	AL161393.2	NT	Human chromosome 21 segment HS21009
11041	23623		0.38	4.0E-03	AL163291.2	NT	Homo sapiens chromosome 21 segment HS21001

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Table 4

Single Exon Probes Expressed in Adult Liver

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4693	17961	30819	3.2	3.0E-03	BE791945.1	EST_HUMAN	601462741.HIT_MGC (Homo sapiens cDNA clone IMAGE334543.6)
5201	18276	31124	1.08	3.0E-03	46381448	NT	Homo sapiens RAP1, GTPase activating protein 1 (GAP1/G31) mRNA
5201	18276	31125	1.08	3.0E-03	46381448	NT	Homo sapiens RAP1, GTPase activating protein 1 (GAP1/G31) mRNA
8447	18268	31254	3.68	3.0E-03	56022485	NT	Homo sapiens lymphoblast protein FLJ10339 (FLJ10339) mRNA
5747	18828	31971	1.85	3.0E-03	ALJ24981.1	NT	Mac musculus mRNA for lymphoblast protein (ORF2) (F10339)
5821	18983	32006	1.02	3.0E-03	U93323.1	NT	Mac musculus H2A1 alpha chain (H2A1) gene, H2A1 beta 2 chain (H2A1B2) gene, H2A1 beta 1 chain (H2A1B1) gene, low molecular weight protein 2 (Lmo2) (Lmo2) gene, complete cds
6834	19040	33060	10.99	3.0E-03	AA46701.1	EST_HUMAN	act13101.1 Soares. NHRNP_1, S1: Homo sapiens cDNA clone IMAGE313183.6
7374	20038	33657	0.95	3.0E-03	D37877.1	NT	Fugu tubulin mRNA for sodium channel alpha subunit, partial cds
7571	20307	33765	1.27	3.0E-03	AA11418.1	NT	Myxomycetes marasmius pop38 gene for putative chitinase
7846	20398	34160	3.97	3.0E-03	P26669	SWISSPROT	Oriza sativa gene for t23P protein, complete cds
8376	21260	34611	0.47	3.0E-03	AB221736.1	EST_HUMAN	Oriza sativa gene for t23P protein, complete cds
8517	21148	34761	0.97	3.0E-03	BF333058.1	EST_HUMAN	Oriza sativa gene for t23P protein, complete cds
8517	21148	34761	0.97	3.0E-03	BF333058.1	EST_HUMAN	Oriza sativa gene for t23P protein, complete cds
8734	21054	35009	1.74	3.0E-03	N62590.1	EST_HUMAN	Oriza sativa gene for t23P protein, complete cds
8960	21820	35498	0.95	3.0E-03	M03498.1	NT	Oriza sativa gene for t23P protein, complete cds
9029	21908	35519	1.18	3.0E-03	P01989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2/A1)
9052	21981	35538	1.91	3.0E-03	AL163265.2	NT	Homo sapiens chromosome 21 segment HS210088
9148	22076		1.4	3.0E-03	Q6Q681	SWISSPROT	NONSTRUCTURAL PROTEIN N V
9543	22470		11.85	3.0E-03	AW16374.1	EST_HUMAN	HHH10.41 NC1, COAP_GU1 Homo sapiens cDNA clone IMAGE2949151.3 similar to contains L1, L1
9598	22824	35888	4.20	3.0E-03	AL101893.2	NT	residue domain 1
9620	22846	35817	7.85	3.0E-03	AA10793.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
9949	22846		0.85	3.0E-03	DC0001.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
10162	23053		0.77	3.0E-03	P03355	SWISSPROT	HISTONE H2B.2 (HUMAN);
10279	23120		7.22	3.0E-03	P06872	SWISSPROT	Synedrales sp. P06803 complete genome, 3/27/2760-40289
10407	23236	36716	1.06	3.0E-03	P11369	SWISSPROT	POLYPROTEIN CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H
10501	23338	36960	1.44	3.0E-03	P01989	SWISSPROT	ORIGAMIS-RELATED POLYPROTEIN CONTAINS: REVERSE TRANSCRIPTASE; RIBONUCLEASE H
10636	23326	36960	4.3	3.0E-03	AL163003.2	NT	RETROVIRUS-RELATED POLYPROTEIN CONTAINS: REVERSE TRANSCRIPTASE; RIBONUCLEASE H
11283	24704		1.97	3.0E-03	5303028	NT	RETROVIRUS-RELATED POLYPROTEIN CONTAINS: REVERSE TRANSCRIPTASE; RIBONUCLEASE H
11627	20398	34160	1.03	3.0E-03	AB221736.1	NT	Heterogeneous nuclear ribonucleoprotein A2 homolog 1 (HNRNP A2/A1)
11819	24740	36231	1.98	3.0E-03	AF00222.1	NT	Homo sapiens cDNA clone IMAGE2949151.3 similar to contains L1, L1
11819	24740	36231	1.98	3.0E-03	AF00222.1	NT	Phenylalanyl tRNA synthetase mRNA, partial cds

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Probe SEQ ID NO.	Eno SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (19) Hit BLAST E Value	Top Hit Accession	Top Hit Database Source	Top Hit Description
4519	17528		1.9	2.0E-03	U50741.1	NT	Puclarin retinoid major outer capsid protein (VP7) mRNA, complete cds
4534	17543		1.19	2.0E-03	U02470.386.1	EST_HUMAN	UH-HWJC rat g-33 Q1 rat N1 CGAP. S168 Homo sapiens cDNA clone IMAGE:276413.3'
4539	17548	30409	1.9	2.0E-03	U00547.046.1	EST_HUMAN	HA0507 Homo sapiens fetal liver cDNA library Homo sapiens cDNA
4562	17567	30535	1.95	2.0E-03	U42512.1	EST_HUMAN	Drosophila melanogaster shortlegless class 2 (sls) mRNA, complete cds
4562	17567	30536	1.96	2.0E-03	U42512.1	NT	Drosophila melanogaster shortlegless class 2 (sls) mRNA, complete cds
4819	17820	30659	1.25	2.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, wntn 740, and partial cds, alternatively spliced
4834	17825		1.47	2.0E-03	U87775.1	EST_HUMAN	yef6022-1. X-linked antibiotic resistance protein gene (EDA), wntn 2 and flanking repeat regions
5147	18142	30657	0.93	2.0E-03	AF06828.1	SWISSPROT	HYPOPHYSICAL 37.4 KD PROTEIN TM0485 IN CHROMOSOME III
5176	18161	31013	0.79	2.0E-03	U49899	EST_HUMAN	Homo sapiens concentrative nucleoside transporter (CNT1) gene, wntn 12
5271	18257	31108	0.84	2.0E-03	AF187974.1	NT	Cereals domesticus cwh19 gene for immunoglobulin heavy chain variable region
5370	18295		0.71	2.0E-03	U216167.1	NT	8010793897 NIH JMG5. 5 Homo sapiens cDNA clone IMAGE:2662426.3'
5393	18345		1.00	2.0E-03	BE019822.1	EST_HUMAN	bb010793897 NIH JMG5. 66 Homo sapiens cDNA clone IMAGE:4104862.3'
5676	18748	31660	1.74	2.0E-03	AF0114693.1	NT	Homo sapiens mRNA for KIAA0693 protein, partial cds
5922	18583	32057	2.21	2.0E-03	AF0114693.1	EST_HUMAN	MP22.U0025-300300-102-02 U0025 Homo sapiens cDNA
5950	18978	32065	0.49	2.0E-03	AF179911.1	EST_HUMAN	MP22.U0025-300300-102-02 U0025 Homo sapiens cDNA
6069	19078	32068	0.98	2.0E-03	AF179911.1	EST_HUMAN	Xenopus laevis xanillin mRNA, complete cds
5910	19078	32067	1.98	2.0E-03	U83711.1	NT	Xenopus laevis xanillin mRNA, complete cds
6348	18398	32664	3.82	2.0E-03	U73247.7	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT 8
6348	18398	32665	4.92	2.0E-03	U73247.7	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT 8
6603	18944	32828	2.28	2.0E-03	U06263	SWISSPROT	CARBOXYL AMINOACID-RELATED PROTEIN 2 PRECURSOR (CARP-2) (CA-RP-II) (CA-X)
6603	18944	32827	2.28	2.0E-03	U06263	SWISSPROT	CARBOXYL AMINOACID-RELATED PROTEIN 2 PRECURSOR (CARP-2) (CA-RP-II) (CA-X)
6605	19346	32829	7.05	2.0E-03	AF030187.1	EST_HUMAN	8010874947 NIH JMG5. 37 Homo sapiens cDNA clone IMAGE:4121408.3'
6645	18934	32876	2.61	2.0E-03	GM4704	SWISSPROT	ADAMTS-7 PRECURSOR (ADAMTS-7) (ADAMTS-7) (ADAMTS-7)
6645	18935	32876	2.61	2.0E-03	GM4704	SWISSPROT	ADAMTS-7 PRECURSOR (ADAMTS-7) (ADAMTS-7) (ADAMTS-7)
6651	19711	32871	1.22	2.0E-03	U46161.1	NT	adenosine mRNA for pppRNA synthetase (pys5)
6688	19048		1.25	2.0E-03	AF091089.1	EST_HUMAN	hcd890v.1. Sources: Drosophila, cdon. MH20 Homo sapiens cDNA clone IMAGE:25241.77 similar to SW-FL26 HUMAN.P47614.055 RIROSOALM Protein.128. 22 cdc14n element USR1. 7 cdc14n element.1
6929	19259	33179	0.68	2.0E-03	AF477333.1	EST_HUMAN	21341.11. Sources: fetal liver, spleen. 1NF15. S11 Homo sapiens cDNA clone IMAGE:450652.3'
7295	18424	31334	1.421	2.0E-03	AF030187.1	NT	8010874947 NIH JMG5. 37 Homo sapiens cDNA clone IMAGE:4121408.3'
7431	20193	33427	3.29	2.0E-03	AF067996.1	EST_HUMAN	GM4704.H3556.01299.054-001 B170565 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7604	20443	33726	0.7	2.0E-03	AJ26882.1	EST_HUMAN	un65411.1 NC_004616 Homo sapiens cDNA clone IMAGE:168585 3'
7673	20507	33966	0.74	2.0E-03	U6039.1	EST_HUMAN	pat 791011 Soares fetal liver spleen INFL3 Homo sapiens cDNA clone IMAGE:14906 5'
8053	20976	34281	1.35	2.0E-03	P07354	SWISSPROT	PROTEOLYTIC LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
8629	21560	34596	2.84	2.0E-03	AW56204.1	EST_HUMAN	H07606.1f Soares INFL3_C8C.51 Homo sapiens cDNA clone IMAGE:289408 3' similar to TR038976
8796	21726	35074	6.05	2.0E-03	N0287.1	EST_HUMAN	cytochrome P-450, polypeptide 21HJM Homo sapiens cDNA clone IMAGE:264423 3' similar to contains 1-132 L1 nucleotide element
8793	21726	35076	6.05	2.0E-03	N0287.1	EST_HUMAN	cytochrome P-450, polypeptide 21HJM Homo sapiens cDNA clone IMAGE:264423 3' similar to contains 1-132 L1 nucleotide element
8840	21770	35116	0.34	2.0E-03	Q62350	SWISSPROT	HYPOPHYSICAL 32.8 KD PROTEIN C5G6.06 IN CHROMOSOME 1
8843	21783	35148	1.26	2.0E-03	P10137	SWISSPROT	LAMININ ALPHA1 CHAIN PRECURSOR (LAMININ A CHAIN)
8815	21845	35199	0.83	2.0E-03	G03655.5	NT	Homo sapiens Retina derived POU domain factor-1 (RPF-1), mRNA
8815	21845	35200	0.83	2.0E-03	G03655.5	NT	Homo sapiens Retina derived POU domain factor-1 (RPF-1), mRNA
8830	21869	35229	1.03	2.0E-03	AU136976.1	EST_HUMAN	AU136979 PLACE1 Homo sapiens cDNA clone IMAGE:100439 6'
8900	21919		0.66	2.0E-03	AJ40087.1	NT	Homo sapiens ASGL3 gene, C1orf15 gene, C11orf16 gene and C11orf17 gene
8737	18076	32095	0.79	2.0E-03	AW76911.1	EST_HUMAN	MF2-UM0025-300500-102-R02 UM0025 Homo sapiens cDNA
8737	18076	32096	0.79	2.0E-03	AW76911.1	EST_HUMAN	MF2-UM0025-300500-102-R02 UM0025 Homo sapiens cDNA
8737	18076	32096	0.79	2.0E-03	AW76911.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
9782	22706	35000	0.9	2.0E-03	AF224059.1	NT	UBE2D3 genes, complete cds
10056	22972	35361	0.65	2.0E-03	H02632.1	EST_HUMAN	cytochrome P-450, fetal liver spleen INFL3 Homo sapiens cDNA clone IMAGE:194293 3'
10056	22972	35362	0.68	2.0E-03	H00632.1	EST_HUMAN	cytochrome P-450, fetal liver spleen INFL3 Homo sapiens cDNA clone IMAGE:194293 3'
10687	22880	35280	3.48	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEPARANCHON) (CYTOTACTIN) (GMEIN) (JI)
10182	23003	35464	1.19	2.0E-03	P49862	SWISSPROT	(MIOTENDOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP-160-226) (TENASCIN-C) (TN-C)
10182	23003	35464	1.19	2.0E-03	P49862	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10214	23135	35639	0.65	2.0E-03	AF067732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL-10) gene, complete cds
10214	23135	35640	0.65	2.0E-03	AF067732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL-10) gene, complete cds
10426	23315	35732	1.09	2.0E-03	AW56426.1	EST_HUMAN	Q15-Q10665-060400-144-0H1 OT0004 Homo sapiens cDNA
10545	23431	35735	6.4	2.0E-03	AA031376.1	EST_HUMAN	cytochrome P-450, fetal liver spleen INFL3 Homo sapiens cDNA clone IMAGE:694794 3'
11464	24370		2.49	2.0E-03	M06534.1	NT	Human osteonin gene
11920	20976	34281	2.33	2.0E-03	P07354	SWISSPROT	PROTEOLYTIC LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11975	24818		2.4	2.0E-03	BF30069.1	EST_HUMAN	RC3-B10333-110600-115-g01 B10333 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4776	17760	30560	0.73	1.0E-03 U25446.1	NT	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
4837	17936	30793	2.83	1.0E-03 AN73486.1	EST_HUMAN	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
4838	17937	30794	2.83	1.0E-03 AN73486.1	EST_HUMAN	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
4839	17937	31045	4.81	1.0E-03 BF15067.1	EST_HUMAN	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
5420	18371	31045	2.18	1.0E-03 BF15067.1	EST_HUMAN	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
5421	18371	31477	3.16	1.0E-03 M200961.1	EST_HUMAN	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
5897	18624	31477	3.26	1.0E-03 M200961.1	EST_HUMAN	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
5841	18716	31677	3.26	1.0E-03 A06542.1	NT	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
5841	18716	31677	2.69	1.0E-03 K03332.1	NT	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
5841	18716	31677	2.69	1.0E-03 K03332.1	NT	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
5764	18837	31940	0.9	1.0E-03 BF70469.1	EST_HUMAN	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
5770	18843	31940	1.63	1.0E-03 O02338.1	SWISSPROT	SWISSPROT	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
5829	18900	32014	0.66	1.0E-03 N41974.1	EST_HUMAN	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
5829	18900	32015	0.66	1.0E-03 N41974.1	EST_HUMAN	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
6110	19170	32902	0.51	1.0E-03 M77352.1	EST_HUMAN	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
6113	19182		0.48	1.0E-03 BF64163.1	EST_HUMAN	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
6283	19309		3.24	1.0E-03 X07659.1	NT	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
6284	19346	32513	1.06	1.0E-03 BE069362.2	EST_HUMAN	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
6433	19460		8.03	1.0E-03 11520170	NT	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
6591	19932	37814	1.11	1.0E-03 TR7761.1	EST_HUMAN	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
6674	19711		1.56	1.0E-03 AW002585.1	EST_HUMAN	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
7060	20086	33319	1.56	1.0E-03 L77570.1	NT	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
7513	20452	33237	2.47	1.0E-03 D16820.1	NT	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
7607	20832		2.62	1.0E-03 AJ220042.1	NT	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
8088	21000	34322	1.52	1.0E-03 U02111.2	NT	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
8197	21074	34304	3.28	1.0E-03 M63376.1	NT	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
8224	21129	34400	0.86	1.0E-03 BE580044.1	EST_HUMAN	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
8469	21400	34740	0.77	1.0E-03 AF270581.1	NT	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
8528	21459	34922	5.96	1.0E-03 AJ251974.1	NT	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes
8722	21652	34949	0.87	1.0E-03 AJ422720.1	EST_HUMAN	EST_HUMAN	Chorionadhesin domain, apical leader RNA (SL3 alpha) (SL3) and (SL5) genes

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10199	23030		1.57	8.0E-04	AB337203.1	NT	Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) mRNA for beta-amyloid synthase, complete cds
1506	14637		1.27	8.0E-04	J094663.1	NT	Human GAPDH mRNA for beta-amyloid synthase, complete cds
3993	17020	22910	0.68	8.0E-04	R07008.1	EST_HUMAN	Human GAPDH mRNA for beta-amyloid synthase, complete cds
4276	17250		8.2	8.0E-04	P03047	SWISSPROT	Human GAPDH mRNA for beta-amyloid synthase, complete cds
4678	17177	30743	0.32	8.0E-04	P03047	SWISSPROT	Human GAPDH mRNA for beta-amyloid synthase, complete cds
11595	21436		2.32	8.0E-04	AA377094.1	EST_HUMAN	Human GAPDH mRNA for beta-amyloid synthase, complete cds
1162	24647		2.32	8.0E-04	AA377094.1	EST_HUMAN	Human GAPDH mRNA for beta-amyloid synthase, complete cds
1451	14571	27855	1.54	7.0E-04	U19384.1	EST_HUMAN	Human GAPDH mRNA for beta-amyloid synthase, complete cds
2421	14226	26426	0.50	7.0E-04	U19384.1	EST_HUMAN	Human GAPDH mRNA for beta-amyloid synthase, complete cds
2753	15796	26769	1.18	7.0E-04	AL183210.2	NT	Human GAPDH mRNA for beta-amyloid synthase, complete cds
3334	18370	29271	1.05	7.0E-04	4856170.1	NT	Human GAPDH mRNA for beta-amyloid synthase, complete cds
6333	19393	32051	0.73	7.0E-04	AA518212.1	EST_HUMAN	Human GAPDH mRNA for beta-amyloid synthase, complete cds
9619	19501	32778	0.47	7.0E-04	AB333875.1	EST_HUMAN	Human GAPDH mRNA for beta-amyloid synthase, complete cds
9747	19524		2.27	7.0E-04	AI070931.1	EST_HUMAN	Human GAPDH mRNA for beta-amyloid synthase, complete cds
7697	20853		0.81	7.0E-04	AK024446.1	NT	Human GAPDH mRNA for beta-amyloid synthase, complete cds
10320	23209	36920	0.65	7.0E-04	P13467	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10320	23209	36921	0.35	7.0E-04	P13467	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11698	24840		2.33	7.0E-04	U78027.1	NT	Human GAPDH mRNA for beta-amyloid synthase, complete cds
12023	24936	36906	2.84	7.0E-04	Z00591.1	EST_HUMAN	Human GAPDH mRNA for beta-amyloid synthase, complete cds
12746	26366		14.51	7.0E-04	BE07841.1	EST_HUMAN	Human GAPDH mRNA for beta-amyloid synthase, complete cds
12663	26121		4.19	7.0E-04	R17338.1	EST_HUMAN	Human GAPDH mRNA for beta-amyloid synthase, complete cds
12690	26546		4.86	7.0E-04		6005950	Human GAPDH mRNA for beta-amyloid synthase, complete cds
2748	15748		0.86	6.0E-04	BF341380.1	EST_HUMAN	Human GAPDH mRNA for beta-amyloid synthase, complete cds
4044	17071	25957	1.77	6.0E-04	U68263.1	EST_HUMAN	Human GAPDH mRNA for beta-amyloid synthase, complete cds
4281	17285	30161	4.06	6.0E-04	U6593.1	NT	Human GAPDH mRNA for beta-amyloid synthase, complete cds
4652	17661	30420	1.54	6.0E-04	BE17435.1	EST_HUMAN	Human GAPDH mRNA for beta-amyloid synthase, complete cds
4652	17661	30421	1.54	6.0E-04	BE17435.1	EST_HUMAN	Human GAPDH mRNA for beta-amyloid synthase, complete cds
5391	18373	31213	1.08	6.0E-04	P12259	SWISSPROT	COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR)
5391	18373	31214	1.08	6.0E-04	P12259	SWISSPROT	COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR)
8447	21379		3.72	6.0E-04	P4608	SWISSPROT	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (GLUT5)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8894	21026		0.67	6.0E-04	H02947.1	EST_HUMAN	Y04611.1 Score: 9196 gend_N3HPG Homo sapiens cDNA clone IMAGE:281866 5' similar to contains LORI repetitive element;
10488	28374		4.07	6.0E-04	AL048597.2	EST_HUMAN	DFZ285900224.1 581 (genom): Tumor) Homo sapiens cDNA clone DAF2568812224
10582	28498	38864	2.41	6.0E-04	H010850.1	EST_HUMAN	PC2840122504004121HT ENO120 Homo sapiens cDNA
10827	22713		0.95	6.0E-04	AF287479.1	NT	Lymphoblastoid cell line B-cellular matrix protein precursor (ECV8) mRNA, complete cDNA
11016	24763	38280	2.88	6.0E-04	AF229421.1	EST_HUMAN	Human sapiens 989 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/8
11889	24811	38337	4.82	6.0E-04	AF013847.1	EST_HUMAN	U14600.200401.1 NCL CGAP S101 Homo sapiens cDNA clone IMAGE:270825 3'
12041	24768		2.18	6.0E-04	AF013847.1	EST_HUMAN	U14600.200401.1 NCL CGAP S101 Homo sapiens cDNA clone IMAGE:270825 3'
12029	28100		2.18	6.0E-04	AF013847.1	EST_HUMAN	U14600.200401.1 NCL CGAP S101 Homo sapiens cDNA clone IMAGE:270825 3'
12724	13739	28848	8.11	6.0E-04	AF013847.1	EST_HUMAN	PC2840122504004121HT ENO120 Homo sapiens cDNA
1871	13739	28848	8.11	6.0E-04	AF013847.1	EST_HUMAN	PC2840122504004121HT ENO120 Homo sapiens cDNA
1821	14452		1.8	6.0E-04	AF013847.1	EST_HUMAN	PC2840122504004121HT ENO120 Homo sapiens cDNA
3474	18514	29413	1.07	6.0E-04	AA548631.1	EST_HUMAN	U14600.200401.1 NCL CGAP S101 Homo sapiens cDNA clone IMAGE:104794 3' similar to contains Au recessive element.
3778	18810	29897	0.92	6.0E-04	Q9UKP4	SWISSPROT	ADAMTS 7 (ADAMTS-7) (ADAMTS-7)
5660	18734	31841	2.82	6.0E-04	AF246054.1	NT	Bov taurin micromolar calmodulin activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6010	19040	33170	6.5	6.0E-04	AA145050.1	EST_HUMAN	z533828.1 Stratiogene colon (R507204) Homo sapiens cDNA clone IMAGE:586953 5'
7769	20599	33990	13.89	6.0E-04	M23004.1	NT	Gonella gonella involution gene medium allele, complete cds
8834	21465	34806	5.87	6.0E-04	AF08982.1	EST_HUMAN	g41306.1 Score: 9196 gend_N3HPG Homo sapiens cDNA clone IMAGE:172919 3' similar to pc251602_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN) contains Au repetitive element;
8878	21808	35161	0.83	6.0E-04	AA814519.1	EST_HUMAN	MER22222.1 NCL CGAP S101 Homo sapiens cDNA clone IMAGE:1393223 3' similar to contains element repetitive element;
9817	22723	38100	2.14	6.0E-04	AA84045.1	EST_HUMAN	q98903.1 Score: 9196 gend_N3HPG Homo sapiens cDNA clone IMAGE:1393223 3' similar to K2746F Homo sapiens cDNA clone IMAGE:1393223 3' similar to REPELITIVE ELEMENT
9910	22898	38986	0.89	6.0E-04	AB07965.1	EST_HUMAN	z533828.1 NCL CGAP S101 Homo sapiens cDNA clone IMAGE:270825 3'
10148	23027	39524	4.14	6.0E-04	AA1270098.1	EST_HUMAN	Human familial Alzheimer's disease (FAMAD) gene, complete cds
11773	23655		0.83	6.0E-04	U63871.1	NT	Human familial Alzheimer's disease (FAMAD) gene, complete cds
14413	24329		2.26	6.0E-04	AL048597.2	EST_HUMAN	DFZ285900224.1 581 (genom): Tumor) Homo sapiens cDNA clone DAF2568812224
12135	18734	31841	14.44	6.0E-04	AF246054.1	NT	Bov taurin micromolar calmodulin activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
12375	25751		2.07	6.0E-04	AA145050.1	EST_HUMAN	PC2840122504004121HT ENO120 Homo sapiens cDNA clone IMAGE:586953 5'

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
413	13496		1.71	4.0E-04	AF214462.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:410487 5'
686	10756	26973	1.2	4.0E-04	U52746.1	NT	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
972	13925	26972	1.22	4.0E-04	AF20263.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
972	13925	26973	1.23	4.0E-04	AF20263.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
1484	14515	27476	3.44	4.0E-04	AF176396.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
2096	19110	28114	1.23	4.0E-04	AF182770.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
2147	19110	28114	1.23	4.0E-04	AF182770.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
2673	19939	28668	2.08	4.0E-04	AF168824.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
3414	14949	28932	0.92	4.0E-04	AF168824.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
3526	16564		1.13	4.0E-04	AF163267.2	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
4429	17440	30299	4.02	4.0E-04	AA576331.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
4429	17440	30300	4.02	4.0E-04	AA576331.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
4653	17655	30628	1.11	4.0E-04	AA608324.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
5222	19211	31057	3.87	4.0E-04	BE500660.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
5309	19283		0.86	4.0E-04	BE178660.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
7644	20579	33874	1.26	4.0E-04	P48442	SWISSPROT	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
7662	20584		4.7	4.0E-04	AF161660.2	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
8179	21086	34420	0.71	4.0E-04	AF122076.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
9100	22039	36384	1.02	4.0E-04	AF247172.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
9109	22039	36390	2.16	4.0E-04	U25607.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
12114	23105	36505	3.89	4.0E-04	AF026999.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
13358	23244		0.71	4.0E-04	AF132866.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
14716	26728		2.21	4.0E-04	AF175452.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
1581	12457	26164	3.52	3.0E-04	AF114942.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
208	13807	26224	6.76	3.0E-04	P14289	SWISSPROT	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
603	13857	27955	1.97	3.0E-04	U53911.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
1663	14355	27955	1.96	3.0E-04	AF03100.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
1793	14973		0.76	3.0E-04	AF03100.1	EST_HUMAN	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626
3354	16386	28280	0.83	3.0E-04	P26147	SWISSPROT	5'UTR/5S4PT NH ₂ MOC 55 Homo sapiens cDNA clone IMAGE:2304039 3' similar to 7RQ18626

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Exegration Signal	Most Similar (Top) HT BLAST E Value	Top HI Accession No.	Top HR Database Source	Top HI Descriptor
4047	17074	25640	3.18	3.0E-04/A26448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)	Homo sapiens Xq pseudoclonal region, segment 1/2
4141	17162		1.67	3.0E-04/AZ17735.1	NT	Homo sapiens Xq pseudoclonal region, segment 1/2	RQHQ10041-X10899-028 HT0014 Homo sapiens cDNA
4152	17302		1.41	3.0E-04/BE14090.1	EST - HUMAN	EST - HUMAN	PJ0101030-100200-007 *g12 HT10359 Homo sapiens cDNA
4630	17920		6.87	3.0E-04/BS15378.1	EST - HUMAN	EST - HUMAN	QV8-Q70045-229-446-008 DT0048 Homo sapiens cDNA
4902	17931	30848	0.77	3.0E-04/AW39373.1	EST - HUMAN	EST - HUMAN	Homo sapiens chromosome 21 segment HS21C081
6343	19431		5.48	3.0E-04/AL163382.1	EST - HUMAN	EST - HUMAN	Homo sapiens chromosome 21 segment HS21C078
7132	20240	33460	3.75	3.0E-04/AL163278.2	NT	NT	RCAN1-N0027-00040G-011-508 N10027 Homo sapiens cDNA
7331	18466	51275	0.62	3.0E-04/AA1869381.1	EST - HUMAN	SWISSPROT	FIBRINOBYST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FORR3)
8031	20497	34284	0.85	3.0E-04/F23446	EST - HUMAN	SWISSPROT	FIBROBLAST SOURCE TIE2 HT1 Homo sapiens cDNA clone IMAGE:195471.5 similar to go/M82782
8635	21705	35112	4.88	3.0E-04/F22407	EST - HUMAN	EST - HUMAN	VACUOLAR ATP-SYNTHASE IS 18 KD PROTEOLIPID SUBUNIT (HUVA)
10431	23320	39737	1.19	3.0E-04/A405095.1	EST - HUMAN	EST - HUMAN	HT1711.X1 Spines, thymus_NHR.H1 Homo sapiens cDNA clone IMAGE-2513276.3
10674	23909	39662	0.79	3.0E-04/A092121	EST - HUMAN	EST - HUMAN	92Ag65.1 Spores, testis_H1 Homo sapiens cDNA clone 1391288.3 similar to go/V96072.605
10988	23823	37290	3.8	3.0E-04/AY181201.1	EST - HUMAN	EST - HUMAN	ncf3684.1 NC1_GCAP_F32 Homo sapiens cDNA clone IMAGE:1014300 similar to contains 1.12 L1 repetitive element;
12342	26984	51372	4.37	3.0E-04/A238001.1	EST - HUMAN	EST - HUMAN	Homo sapiens mRNA for KIA08749 protein, partial cds
12874	25791	51678	2.28	3.0E-04/A3018522.1	NT	NT	CDC2B47L.B1c.Y1.F477 (eryonycin flutrin) Homo sapient cDNA clone D1F25647.188.5'
13041	25577		2.71	3.0E-04/AL134831	EST - HUMAN	EST - HUMAN	Homo sapiens SCG101 gene, complete cds
188	18298	28201	1.65	2.0E-04/D217768.1	NT	NT	protein 1 (ABPRP1) genes, complete cds
501	13571	29489	2.28	2.0E-04/AF140737.1	EST - HUMAN	EST - HUMAN	AJ474077 HEMBB1 Homo sapiens cDNA clone HEL485001233.3'
832	19894	28639	8.04	2.0E-04/U06524.1	EST - HUMAN	EST - HUMAN	Human tyrosinase gene
932	13984	25030	8.04	2.0E-04/U06524.1	NT	NT	Human tyrosinase gene
1207	14246		3.43	2.0E-04/A236021.1	EST - HUMAN	EST - HUMAN	glb6d411.Y1 Spores, NFL_1_OBG.5' Homo sapiens cDNA clone IMAGE:1855052.3 similar to contains MER3 like M233 repetitive element;
1214	14252		1.51	2.0E-04/AL163303.2	NT	NT	Homo sapiens chromosome 21 segment HS21C093
1606	14578		1.23	2.0E-04/D27426.1	NT	NT	SACS6508.4 S. flandria cspN17.P22 gene
2109	15210		0.88	2.0E-04/A417860.1	EST - HUMAN	EST - HUMAN	SACS6508.4 S. Scores-only from NCHO1 Homo sapiens cDNA clone IMAGE:740337.3 similar to contains ALO repetitive element;
2611	15609	28914	5.18	2.0E-04/H09511.1	NT	NT	Human gamma T-cell receptor beta chain TC9BV1754.1T, TC9BV251, TC9BV106/P, TC9BV269/P, TC9BV4551, TC9BV4514.1T, HWB wt, TC9BV285/P, TC9BV245A, TC9BV145A, TC9BV451A, TC9BV451AT, IRY4, IRY4, IRY7, IRYA, TC9BR1, TC9BV1US1, TC9BV182.2

Table 4

consideration of

Session

Accession	Gene	Source	No.	BLAST E Value	Signal	DNOC	NO.
am136209.1	Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1531760.3	EST_HUMAN	1	1.12E-523.1	0.98	100.61	28592
Homo sapiens subunit, beta, 4 (TUBB4) mRNA		EST_HUMAN	1	2.0E-04	2.0E-04	20326	3382
U02.610363.070500-194407.B10539 Homo sapiens cDNA		EST_HUMAN	1	2.0E-04	0.9832317.1	3477	16536
Human Yonine kinase TXK (XK) gene, exons 9 and 10		NT	1	2.0E-04	US73541.1	26400	3504
EST350550 MAGE sequences, MAGEP Homo sapiens cDNA		EST_HUMAN	1	2.0E-04	AW197049.1	17313	25902
Phosducin vulgata invertebrate reduciase (PVNR2) gene, complete cds		NT	1	2.0E-04	AW197049.1	778	3696
y01.e11.1. Sources: _anal_gland_NSHGP Homo sapiens cDNA clone IMAGE:232569.6		EST_HUMAN	1	2.0E-04	H09263.1	4241	17257
y01.e11.1. Sources: _anal_gland_NSHGP Homo sapiens cDNA clone IMAGE:232569.6		EST_HUMAN	1	2.0E-04	H09263.1	4780	17765
Gallus gallus prothoracic 28. kDa subunit homolog mRNA, complete cds		EST_HUMAN	1	2.0E-04	U03226.1	4811	17910
Danio rerio haemoglobin, exons 1 to 5, partial cds		NT	1	2.0E-04	AB037707.1	17610	31028
Homo sapiens ARPP3 (arrestin-related protein 3, yeast) homolog (ACTR3), mRNA		EST_HUMAN	1	2.0E-04	AF070170.1	5514	18100
Homo sapiens ARPP3 (arrestin-related protein 3, yeast) homolog (ACTR3), mRNA		EST_HUMAN	1	2.0E-04	7822389.1	5527	18264
Homo sapiens ARPP3 (arrestin-related protein 3, yeast) homolog (ACTR3), mRNA		EST_HUMAN	1	2.0E-04	7822389.1	5532	18268
U0454352 GLC Homo sapiens cDNA clone GLOC0010.1		EST_HUMAN	1	2.0E-04	AV654352.1	5735	18268
NC0361.1.NCI CGAP U93 Homo sapiens cDNA clone GLOC0010.1		EST_HUMAN	1	2.0E-04	AV654352.1	5748	18821
EST11191 U93 Homo sapiens cDNA 5' and similar to EST containing O family repeat		EST_HUMAN	1	2.0E-04	A326962.1	5855	19023
Homo sapiens cell cycle progression 3 protein (DN3) mRNA		EST_HUMAN	1	2.0E-04	AF47063.1	6172	19220
Mus musculus cell cycle coupled receptor gene, complete cds, and pinwheel gene		NT	1	2.0E-04	AF47063.1	6466	19461
U012712.1 MAMM1 Homo sapiens cDNA clone MAMM1/000798.5		EST_HUMAN	1	2.0E-04	AU121712.1	7593	20535
U010387.1.180300-167-470 U0387 Homo sapiens cDNA		EST_HUMAN	1	2.0E-04	AB000603.1	7709	20641
LINE1 REVERSE TRANSCRIPTASE HOMOLOGY		SWISSPROT	1	2.0E-04	P03548	8526	21061
MYOEMIN 2 (MFPROTIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)		SWISSPROT	1	2.0E-04	P54206	80778	20850
Sclerium Yopocytinon phytochrome F (PHYF) gene, partial cds		NT	1	2.0E-04	U33444.2	8533	21464
Sclerium Yopocytinon phytochrome F (PHYF) gene, partial cds		NT	1	2.0E-04	U33444.2	8533	21464
Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)		NT	1	2.0E-04	AB026983.1	8651	21791
Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)		NT	1	2.0E-04	AB026983.1	8651	21791
Homo sapiens FRAB3 common fragile region, diastemotic triphosphate hydrolase (FHT) gene, exon 5		NT	1	2.0E-04	AB026983.1	8891	21791
Human immunoglobulin Gmu) and G(delta) heavy chain genes (constant regions)		NT	1	2.0E-04	U57353.1	9128	22706
GASTRULA ZINC FINGER PROTEIN XLG30.1		SWISSPROT	1	2.0E-04	P19715	8302	22240
RC3-H10254-151066-011-045 H10254 Homo sapiens cDNA		EST_HUMAN	1	2.0E-04	U03226.1	9533	22968
		EST_HUMAN	1	2.0E-04	U03226.1	9533	23366

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Table 4
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Probe SEQ ID NC:	Exon SEQ ID NC:	ORF SEQ ID NC:	Expression Signal	Mean (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10520	25407	38519	2.56	2.0E-04	AF46377.1	EST_HUMAN	208541.1 Sarcosin, NNT Homo sapiens cDNA, clone IMAGE:742854.5
11286	24207	37857	3.82	2.0E-04	AF73933.1	EST_HUMAN	UV730373 HTF Homo sapiens cDNA, clone HTF43A03.5
11618	24525		2.47	2.0E-04	AJ25218.1	NT	Homo sapiens EST142322 gene, complete cds
11760	24651	38132	3.46	2.0E-04	AF460292.1	EST_HUMAN	401114.1 NCL CGAP G661 Homo sapiens cDNA, clone IMAGE:271193.5
11858	24748	38246	2.82	2.0E-04	AF199740.1	EST_HUMAN	UJH381.1 srm-c40-0.1a st NCL CGAP S343 Homo sapiens cDNA, clone IMAGE:271193.5
13068	25548		130.57	2.0E-04	D87575.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
793	13848	20782	2.47	1.0E-04	H89046.1	EST_HUMAN	Y07026.1 Sarcosin, NNT Homo sapiens cDNA, clone IMAGE:20854.5 similar to contains L1 L1 repetitive element
1102	14146	27083	2.17	1.0E-04	P11389	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE, ENDONUCLEASE]
1141	14183	27120	3.59	1.0E-04	AF013847.1	EST_HUMAN	UJH300-sab-e-09-0-UL1 NCL CGAP S343 Homo sapiens cDNA, clone IMAGE:270825.5
1141	14183	27121	3.60	1.0E-04	AF013847.1	EST_HUMAN	UJH300-sab-e-09-0-UL1 NCL CGAP S343 Homo sapiens cDNA, clone IMAGE:270825.5
1350	14591		2.59	1.0E-04	U02016.1	NT	Angiogenesis-related protein 1 (A11) gene, complete cds
1651	14682	27644	2.55	1.0E-04	AF14806.1	NT	Kap1's sarcoma-associated herpesvirus ORF 68 gene, partial cds, and ORF 69, hepatitis, v-FLP, v-cyclin, latent nuclear antigen, ORF K14, v-QPCR, putative phosphatase/fornylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1651	14682	27644	2.55	1.0E-04	AF14806.1	NT	Kap1's sarcoma-associated herpesvirus ORF 68 gene, partial cds, and ORF 69, hepatitis, v-FLP, v-cyclin, latent nuclear antigen, ORF K14, v-QPCR, putative phosphatase/fornylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1850	14907	27852	1.23	1.0E-04	AF043432.1	NT	Equine calicivirus, complete cds
2036	15980	25680	1.05	1.0E-04	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (OXPE2) gene, complete cds
2036	15980	25681	1.05	1.0E-04	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (OXPE2) gene, complete cds
2748	16751	28726	0.91	1.0E-04	BE218633.1	EST_HUMAN	UJH606.1 NCL CGAP L202 Homo sapiens cDNA, clone IMAGE:317656.5
2748	16751	28727	0.91	1.0E-04	BE218633.1	EST_HUMAN	UJH606.1 NCL CGAP L202 Homo sapiens cDNA, clone IMAGE:317656.5
3328	18374	20275	1.42	1.0E-04	Q16293	SWISSPROT	SPICE-ONE ASSOCIATED PROTEIN 62 (SAP 62) (SPICING FACTOR 3A SUBUNIT 2) (SF3A69)
3798	19829	29716	0.9	1.0E-04	AF460282.1	EST_HUMAN	SPICE-ONE ASSOCIATED PROTEIN 62 (SAP 62) (SPICING FACTOR 3A SUBUNIT 2) (SF3A69)
4145	17166	30049	1.81	1.0E-04	U04242.1	NT	Mouse alpha 1 type-IV collagen mRNA
4170	17181	30063	1.62	1.0E-04	AF017272.1	EST_HUMAN	UJH722 GLO Homo sapiens cDNA, clone GLO8004.5
4760	17504	30446	1.83	1.0E-04	P06547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5231	18219	31066	1.34	1.0E-04	7620216	NT	Homo sapiens U04297.1 gene product (U04297), mRNA
5231	18219	31067	1.34	1.0E-04	7620216	NT	Homo sapiens U04297.1 gene product (U04297), mRNA
5074	19193	32268	1.74	1.0E-04	P06547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6148	16207	32945	0.48	1.0E-04	T10915.1	EST_HUMAN	TSF Heart Homo sapiens cDNA clone F3
6148	16207	32945	0.38	1.0E-04	T10915.1	EST_HUMAN	TSF Heart Homo sapiens cDNA clone F3
6107	19746	32945	0.98	1.0E-04	AA177111.1	EST_HUMAN	p232.2.31 NCL CGAP_P3 Homo sapiens cDNA clone F3
7151	20239	33513	0.6	1.0E-04	AA59501.1	EST_HUMAN	Y2504.1 NCL CGAP_A1 Homo sapiens cDNA clone IMAGE:93849 3' similar to p1407262
7400	20488	33777	14.75	1.0E-04	AA251980.1	EST_HUMAN	KALLMAN SYNORME PROTEIN PRECURSOR (HUMAN) contains AU repetitive element
8004	20488	33777	15.42	1.0E-04	AA251980.1	EST_HUMAN	Y27010.1 NCL CGAP_Ox32 Homo sapiens cDNA clone IMAGE:165693 3'
8574	21506	34846	1.13	1.0E-04	AA60465.1	EST_HUMAN	AB9498.1 Sialoprotein lung (663720) Homo sapiens cDNA clone IMAGE:165693 3'
8878	22791	36181	2.74	1.0E-04	AA80220.1	EST_HUMAN	W64608.1 Scaevola NCL_GBC_S1 Homo sapiens cDNA clone IMAGE:184545 3'
8889	22801	36188	1.38	1.0E-04	OB8959	SWISSPROT	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (GV8) (ATH 8)
9559	23654	37183	0.82	1.0E-04	T77163.1	EST_HUMAN	MT208.11 Scars fetal liver colicin TNF- α Homo sapiens cDNA clone IMAGE:113774 5'
10172	22083	36460	1.81	1.0E-04	10683878	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
10575	22951	37024	5.84	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10711	22997	37024	1.04	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11781	24080	38418	2.01	1.0E-04	M28587.1	NT	Mouse alpha leukocyte interferon gene, complete cds
12077	24917	35460	1.95	1.0E-04	AB032095.1	EST_HUMAN	Homo sapiens mRNA for KIAA1142 protein, partial cds
12116	24917	35460	2	1.0E-04	AB032095.1	EST_HUMAN	Y4697.2.1 Scars, NHL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815618 3'
12146	24986	38486	1.98	1.0E-04	Q06695	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NIG-CA)
12146	24986	38487	1.98	1.0E-04	Q06695	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NIG-CA)
12215	29050	29702	1.48	1.0E-04	AA251885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
722	13780	29702	2.01	9.0E-05	AA718833.1	EST_HUMAN	ahf5c11.1 Scars, testis, NHL Homo sapiens cDNA clone 1282495 3'
6382	18314	31203	1.17	9.0E-05	AF150193.1	NT	Homo sapiens putative tumor suppressor mRNA
6190	19247	32393	1.15	9.0E-05	Q06715	SWISSPROT	PCLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
8011	20928	34245	0.79	9.0E-05	AW204938.1	EST_HUMAN	UI-HH-ar-4-06-01.1 NCL CGAP_Su83 Homo sapiens cDNA clone IMAGE:2720263 3'
8011	20928	34246	0.79	9.0E-05	AW204938.1	EST_HUMAN	UI-HH-ar-4-06-01.1 NCL CGAP_Su83 Homo sapiens cDNA clone IMAGE:2720263 3'
10009	22926	36715	2.67	9.0E-05	D36006.1	NT	Homo sapiens gene for cholecystikinin type-A receptor, complete cds
10011	22928	36715	3.12	9.0E-05	AF120962.1	NT	Homo sapiens methyl-GDP binding protein 1 (MBD1) gene, exon 10b
11576	24486	37953	3.04	9.0E-05	AW073078.1	EST_HUMAN	rs34905.1 NCL CGAP_P18 Homo sapiens cDNA clone IMAGE:2958178 3' similar to contains 1.12.1 negative element
11688	24590	38857	2.15	9.0E-05	AA237878.1	EST_HUMAN	HY300.0.1 NCL CGAP_L1 ynd Homo sapiens cDNA clone IMAGE:1082485 3' similar to contains element
12042	19247	32383	3.00	9.0E-05	Q06716	SWISSPROT	PCLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	QTR-SEQ ID NO:	Expression Signal	Most Similar (BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
12521	29518		4.66	9.0E-05	AF129755.1	NT	Human septins MSH56 gene, partial cds; and CTC1, DDAH1, G86, G88, G94, G96, G98, G99, G100, G101, G102, G103, G104, G105, G106, G107, G108, G109, G110, G111, G112, G113, G114, G115, G116, G117, G118, G119, G120, G121, G122, G123, G124, G125, G126, G127, G128, G129, G130, G131, G132, G133, G134, G135, G136, G137, G138, G139, G140, G141, G142, G143, G144, G145, G146, G147, G148, G149, G150, G151, G152, G153, G154, G155, G156, G157, G158, G159, G160, G161, G162, G163, G164, G165, G166, G167, G168, G169, G170, G171, G172, G173, G174, G175, G176, G177, G178, G179, G180, G181, G182, G183, G184, G185, G186, G187, G188, G189, G190, G191, G192, G193, G194, G195, G196, G197, G198, G199, G200, G201, G202, G203, G204, G205, G206, G207, G208, G209, G210, G211, G212, G213, G214, G215, G216, G217, G218, G219, G220, G221, G222, G223, G224, G225, G226, G227, G228, G229, G230, G231, G232, G233, G234, G235, G236, G237, G238, G239, G240, G241, G242, G243, G244, G245, G246, G247, G248, G249, G250, G251, G252, G253, G254, G255, G256, G257, G258, G259, G260, G261, G262, G263, G264, G265, G266, G267, G268, G269, G270, G271, G272, G273, G274, G275, G276, G277, G278, G279, G280, G281, G282, G283, G284, G285, G286, G287, G288, G289, G290, G291, G292, G293, G294, G295, G296, G297, G298, G299, G300, G301, G302, G303, G304, G305, G306, G307, G308, G309, G310, G311, G312, G313, G314, G315, G316, G317, G318, G319, G320, G321, G322, G323, G324, G325, G326, G327, G328, G329, G330, G331, G332, G333, G334, G335, G336, G337, G338, G339, G340, G341, G342, G343, G344, G345, G346, G347, G348, G349, G350, G351, G352, G353, G354, G355, G356, G357, G358, G359, G360, G361, G362, G363, G364, G365, G366, G367, G368, G369, G370, G371, G372, G373, G374, G375, G376, G377, G378, G379, G380, G381, G382, G383, G384, G385, G386, G387, G388, G389, G390, G391, G392, G393, G394, G395, G396, G397, G398, G399, G400, G401, G402, G403, G404, G405, G406, G407, G408, G409, G410, G411, G412, G413, G414, G415, G416, G417, G418, G419, G420, G421, G422, G423, G424, G425, G426, G427, G428, G429, G430, G431, G432, G433, G434, G435, G436, G437, G438, G439, G440, G441, G442, G443, G444, G445, G446, G447, G448, G449, G450, G451, G452, G453, G454, G455, G456, G457, G458, G459, G460, G461, G462, G463, G464, G465, G466, G467, G468, G469, G470, G471, G472, G473, G474, G475, G476, G477, G478, G479, G480, G481, G482, G483, G484, G485, G486, G487, G488, G489, G490, G491, G492, G493, G494, G495, G496, G497, G498, G499, G500, G501, G502, G503, G504, G505, G506, G507, G508, G509, G510, G511, G512, G513, G514, G515, G516, G517, G518, G519, G520, G521, G522, G523, G524, G525, G526, G527, G528, G529, G530, G531, G532, G533, G534, G535, G536, G537, G538, G539, G540, G541, G542, G543, G544, G545, G546, G547, G548, G549, G550, G551, G552, G553, G554, G555, G556, G557, G558, G559, G560, G561, G562, G563, G564, G565, G566, G567, G568, G569, G570, G571, G572, G573, G574, G575, G576, G577, G578, G579, G580, G581, G582, G583, G584, G585, G586, G587, G588, G589, G590, G591, G592, G593, G594, G595, G596, G597, G598, G599, G600, G601, G602, G603, G604, G605, G606, G607, G608, G609, G610, G611, G612, G613, G614, G615, G616, G617, G618, G619, G620, G621, G622, G623, G624, G625, G626, G627, G628, G629, G630, G631, G632, G633, G634, G635, G636, G637, G638, G639, G640, G641, G642, G643, G644, G645, G646, G647, G648, G649, G650, G651, G652, G653, G654, G655, G656, G657, G658, G659, G660, G661, G662, G663, G664, G665, G666, G667, G668, G669, G670, G671, G672, G673, G674, G675, G676, G677, G678, G679, G680, G681, G682, G683, G684, G685, G686, G687, G688, G689, G690, G691, G692, G693, G694, G695, G696, G697, G698, G699, G700, G701, G702, G703, G704, G705, G706, G707, G708, G709, G710, G711, G712, G713, G714, G715, G716, G717, G718, G719, G720, G721, G722, G723, G724, G725, G726, G727, G728, G729, G730, G731, G732, G733, G734, G735, G736, G737, G738, G739, G740, G741, G742, G743, G744, G745, G746, G747, G748, G749, G750, G751, G752, G753, G754, G755, G756, G757, G758, G759, G760, G761, G762, G763, G764, G765, G766, G767, G768, G769, G770, G771, G772, G773, G774, G775, G776, G777, G778, G779, G780, G781, G782, G783, G784, G785, G786, G787, G788, G789, G790, G791, G792, G793, G794, G795, G796, G797, G798, G799, G800, G801, G802, G803, G804, G805, G806, G807, G808, G809, G810, G811, G812, G813, G814, G815, G816, G817, G818, G819, G820, G821, G822, G823, G824, G825, G826, G827, G828, G829, G830, G831, G832, G833, G834, G835, G836, G837, G838, G839, G840, G841, G842, G843, G844, G845, G846, G847, G848, G849, G850, G851, G852, G853, G854, G855, G856, G857, G858, G859, G860, G861, G862, G863, G864, G865, G866, G867, G868, G869, G870, G871, G

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (10p) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5146	18141	30896	0.74	4.0E-05	AF12181.1	NT	Drosophila melanogaster antennal protein (sens) gene, complete cds
7271	20179	33422	0.99	4.0E-05	U01043.1	NT	Human cellular leucocyte antigen (HLA) class II gene 5' region
10553	22659		7.1	4.0E-05	AF20563.1	NT	Homo sapiens PPI200 mRNA, complete cds
10556	23933	36905	0.61	4.0E-05	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN (CONTAINS REVERSE TRANSCRIPTASE);
10891	23778	37202	0.83	4.0E-05	P23780	SWISSPROT	ENDONUCLEASE
11207	24133	37891	4.6	4.0E-05	AIW027946.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
12412	25191	31817	1.36	4.0E-05	AL163562.2	NT	Human MIR repetitive element: 33607 v1
704	13763	26880	0.71	3.0E-05	AI249061.1	EST_HUMAN	Homo sapiens chromosome 21 segment118321032
1088	14130	27085	1.71	3.0E-05	AI273861.1	EST_HUMAN	qR4C10.13 Soares, fetal liver, spleen, INFLS, S1 Homo sapiens cDNA clone IMAGE:1849459 3' similar to contains Alu repetitive element/contains element KKR repeat/ve element;
1158	14150	27135	1.36	3.0E-05	BF037865.1	EST_HUMAN	NC44903 v1 Soares, NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1158	14159	27136	1.36	3.0E-05	BF037865.1	EST_HUMAN	8071461463FT NIH MG66 Homo sapiens cDNA clone IMAGE:3865142 5'
1543	14579	27932	0.99	3.0E-05	BE169211.1	EST_HUMAN	8071461463FT NIH MG66 Homo sapiens cDNA clone IMAGE:3865142 5'
1543	14579	27932	0.99	3.0E-05	BE169211.1	EST_HUMAN	PMH-HT0621-12020-001-e10 RT0621 Homo sapiens cDNA
3335	19331		0.71	3.0E-05	BE169211.1	EST_HUMAN	PMH-HT0621-12020-001-e10 RT0621 Homo sapiens cDNA
4489	17500	30392	0.71	3.0E-05	AI249061.1	EST_HUMAN	qR4C10.13 Soares, NIH/NIH, S1 Homo sapiens cDNA clone IMAGE:1876743 3' similar to TRC08932
4489	17500	30392	0.71	3.0E-05	BE169211.1	EST_HUMAN	OEB332 GLYCINE TYROSINE-RICH HAIR PROTEIN, ;
4578	17590	30417	0.98	3.0E-05	BE169211.1	EST_HUMAN	PMH-HT0621-12020-001-e10 RT0621 Homo sapiens cDNA
4578	17590	30417	0.98	3.0E-05	AA306979.1	EST_HUMAN	EST179998 Plectin1 Homo sapiens cDNA similar to similar to p53-associated protein
4732	17737	30650	0.71	3.0E-05	AF148775.1	EST_HUMAN	EST179998 Plectin1 Homo sapiens cDNA similar to similar to p53-associated protein
4816	17651	30710	0.95	3.0E-05	P07168	SWISSPROT	Homo sapiens NCOU1 protein (NCOU1) gene, exons 1, 2, and 3
4851	17593	26890	0.86	3.0E-05	AI249061.1	EST_HUMAN	CHEKINONE RECEPTOR-LIKE 1 (G-PROTEIN COUPLED RECEPTOR DEZ)
5746	18622	31919	1.71	3.0E-05	11072102	NT	qR4C10.13 Soares, fetal liver, spleen, INFLS, S1 Homo sapiens cDNA clone IMAGE:1849459 3' similar to contains Alu repetitive element/contains element KKR repetitive element;
7052	20396	33519	1.08	3.0E-05	AL225762.1	NT	Human muscular myosin light chain 2, precursor lymphocyte-specific (MYL2b), mRNA
7052	20396	33520	1.08	3.0E-05	AL225762.1	NT	Homo sapiens MYL1 gene, exons 1-8
8178	21400	34117	2.38	3.0E-05	BE237616.1	EST_HUMAN	8071461463FT NIH MG66 Homo sapiens cDNA clone IMAGE:384226 3'
8450	22378	35741	1.95	3.0E-05	AY170362.1	EST_HUMAN	8071461463FT NIH MG66 Homo sapiens cDNA clone IMAGE:300936 3'
9434	23382	36744	1.77	3.0E-05	AY170362.1	EST_HUMAN	8071461463FT NIH MG66 Homo sapiens cDNA clone IMAGE:300936 3'
9438	23396	36746	0.73	3.0E-05	GA5391	EST_HUMAN	8071461463FT NIH MG66 Homo sapiens cDNA clone IMAGE:300936 3'
9753	23601		0.8	3.0E-05	NC02731.1	NT	Human Alu family cluster 15 of alpha1 (gamma) repeat gene

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9690	22778	36161	1.73	3.0E-05	AJ372562.1	EST_HUMAN	EST14478 cDNA adenovirus chimera (V) Homo sapiens cDNA 5' end
10137	23078		3.49	3.0E-05	AF160331.1	EST_HUMAN	AF060121 cDNA 5' end, NSF, P3, OT, P, S1 Homo sapiens cDNA clone IMAGE:2987269.3
11074	23698	37333	0.9	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
11074	23698	37334	0.9	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
12430	25166		1.72	3.0E-05	AF173935.1	EST_HUMAN	Homo sapiens D230403 cDNA 5' end, critical region, cytoplasmic end
12595	25251		1.5	3.0E-05	AJ271735.1	NT	Homo sapiens XJ pseudotumor necrosis factor, segment 173
2046	19354	28337	1.35	2.0E-05	AF169021.1	EST_HUMAN	q96411.1 Scores: NBL, T, CBG, S1 Homo sapiens cDNA clone IMAGE:1855052.3 similar to contains
2320	16618	28511	0.69	2.0E-05	M18792.1	NT	MER332 MER3 tegelline, element
2792	15794		5.86	2.0E-05	AF169592.1	EST_HUMAN	Human adenovirus chemistries (ADA) gene, complete cds
3152	16320	25127	1.91	2.0E-05	BE066036.1	EST_HUMAN	224642.1 r1 Strabagene (NT) neuron (8537233) Homo sapiens cDNA clone IMAGE:382794.5 similar to
3327	16439	20343	0.92	2.0E-05	AF164614.1	EST_HUMAN	contains Alu repetitive element contains element L1 repetitive element ;
3427	16468	20377	0.85	2.0E-05	X65211.1	NT	RC3-RT10318-132020-014-R08 BT19318 Homo sapiens cDNA
3543	15501		0.77	2.0E-05	X05445.1	NT	Homo sapiens P-17 phox (NCF1) gene, complete cds
3875	16004		0.87	2.0E-05	AL039107.1	EST_HUMAN	H-sapiens DNA for endogenous retroviral like element
4803	17804		1.23	2.0E-05	BE378471.1	EST_HUMAN	S.cervinae 12.8 (top fragment of the left arm of chromosome X)
5966	16033	32154	2.01	2.0E-05	AJ011712.1	NT	DNF25090604_r1 956 (synonym: hinc2) Homo sapiens cDNA clone DKF2p5501064.5
6159	15168		0.79	2.0E-05	AF029008.1	NT	DNF23540591 NIH MGSC_44 Homo sapiens cDNA clone IMAGE:3006653.5
6166	16245	32401	2.23	2.0E-05	Q13183	SWISSPROT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
6166	16245	32402	2.23	2.0E-05	Q13183	SWISSPROT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
6308	15146	32517	0.68	2.0E-05	AF140272.1	EST_HUMAN	RENAL SODIUM/DICARBOXYLATE CO-TRANSPORTER (NA+/)DICARBOXYLATE
6475	16520	32996	0.82	2.0E-05	P35585	SWISSPROT	RENAL SODIUM/DICARBOXYLATE CO-TRANSPORTER (NA+/)DICARBOXYLATE
6513	16643	33162	2.19	2.0E-05	AJ714330.1	EST_HUMAN	qp72402.1 Scores: placenta, Biochemicals_2164P8026w Homo sapiens cDNA clone IMAGE:1716114.3
7290	20159	33378	2	2.0E-05	Y06526.1	NT	similar to contains 1.1 L1 repetitive element ;
7292	20181	33390	1.15	2.0E-05	AF029301.1	EST_HUMAN	CALM-BINDING PROTEIN
7292	20181	33390	1.15	2.0E-05	AF029301.1	EST_HUMAN	W00012.1 NT NO CGMP SST Homo sapiens cDNA clone IMAGE:1288519.3
7292	20181	33390	1.15	2.0E-05	AF029301.1	EST_HUMAN	P-1464000 mRNA for ARAPI1 protein, partial
7292	20181	33390	1.15	2.0E-05	AF029301.1	EST_HUMAN	q97106.1 NT CGMP, Adit1 Homo sapiens cDNA clone IMAGE:2030003.3 similar to TR-002711
7292	20181	33390	1.15	2.0E-05	AF029301.1	EST_HUMAN	002711 PRO-TOPOGRAPHASE POLYPROTEIN
7292	20181	33390	1.15	2.0E-05	AF029301.1	EST_HUMAN	W03307.1 Scores: Disaggregase, colon, NPGD Homo sapiens cDNA clone IMAGE:252207.3

Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7514	20493	33738	2.27	2.0E-05 AF224982.1	NT		Heliodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), and HoxA1 (HoxA1) genes, complete cds
7514	20493	33738	2.27	2.0E-05 AF224982.1	NT		Heliodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), and HoxA1 (HoxA1) genes, complete cds
7759	20590		0.95	2.0E-05 AF129547.1	NT		Homo sapiens Indoleamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds
8495	21390	34737	2.20	2.0E-05 AB191010.1	EST_HUMAN		h20705.1 NCI COAP_CLL1 Homo sapiens cDNA clone IMAGE270989.9
8689	22592	35696	0.95	2.0E-05 BE244640.1	EST_HUMAN		TGAP2P-150 Follitriptin pre-B cell acute lymphoblastic leukemia Baylor-HGSC projectTGBA Homo sapiens cDNA clone TGBAP1190
9999	22592	35998	0.95	2.0E-05 BE244640.1	EST_HUMAN		TGAP2P-150 Follitriptin pre-B cell acute lymphoblastic leukemia Baylor-HGSC projectTGBA Homo sapiens cDNA clone TGBAP1190
9907	22713	35958	0.92	2.0E-05 AC45977.1	SWISSPROT		COMPLEMENT DECRY-ACCELERATING FACTOR (CD56)
8507	22713	35958	0.93	2.0E-05 AC45977.1	SWISSPROT		COMPLEMENT DECRY-ACCELERATING FACTOR (CD56)
14344	22923	35741	2.03	2.0E-05 AF163707.2	NT		Homo sapiens chromosome 21 segment HS21007
10624	23520	33954	0.92	2.0E-05 AF059393.1	EST_HUMAN		779999.9 NCI COAP_Bm2c0 Homo sapiens cDNA clone IMAGE334976.5
11002	23946	37263	2.74	2.0E-05 N41751.1	EST_HUMAN		wf1406.1 Soares, placenta, <i>Stibeychia</i> , 21kbpP496W/ Homo sapiens cDNA clone IMAGE299570.5
11029	23946	37264	2.74	2.0E-05 N41751.1	EST_HUMAN		wf1406.1 Soares, placenta, <i>Stibeychia</i> , 21kbpP496W/ Homo sapiens cDNA clone IMAGE299570.5
11030	20131	37544	2.63	2.0E-05 BE17055.1	EST_HUMAN		EBM07.41 Soares, Decidual cells, T1020 Homo sapiens cDNA clone IMAGE252207.3
11899	23950	37424	2.34	2.0E-05 BE17055.1	EST_HUMAN		EG24-T0292-289309P03.15121T0282 Homo sapiens cDNA
							wf1403.41 NCI COAP_HPE2.1
							Q12832.0 VQ00898.HPE2.1
12529	25758		5.85	2.0E-05 BE048200.1	EST_HUMAN		wf1403.3 NCI COAP_Cov11 Homo sapiens cDNA clone IMAGE218353.2 3 similar to T10Q12832 repetitive element
12679	25958		10.30	2.0E-05 AF047404.1	EST_HUMAN		Homo sapiens ABCA1 (ABCA1) gene, complete cds
					NT		AT131613.NT28P93 Homo sapiens cDNA clone NTFR3002707.5
12817	25436	37175	1.49	2.0E-05 AJ131513.1	EST_HUMAN		AB201.41 Soares, testis, N-T Homo sapiens cDNA clone IMAGE1755236.3
13104	22661	37165	2.09	2.0E-05 N320810.1	EST_HUMAN		PUTATIVE SERINE/THREONINE PROTEIN KINASE P78
2296	15244	28932	1.24	1.0E-05 AF272448	SWISSPROT		Homo sapiens chromosome 21 segment HS210382
27445	19963	22731	2.24	1.0E-05 AF163329.2	NT		Drosophila melanogaster strain Larró, 1202 Suppressor of Hairless (Su(H)) gene, partial cds
37419	19700	20038		1.0E-05 AF048273.1	NT		Homo sapiens calcium channel alpha1E (CACNA1E) gene, exons 7-9; and partial cds, alternatively spliced
3981	18910		1.51	1.0E-05 AF22391.1	NT		

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2721	10714	20713	7.86	9.0E-06	AI133811.1	EST_HUMAN	IT2A0X.1 NC1_GCAP_HRC1 Homo sapiens cDNA clone IMAGE:2245385.3
9143	19193	20666	4.34	9.0E-06	AI218983.1	EST_HUMAN	gri143.41 Scars, pleochroa, Schueller, NduP80cV1 Homo sapiens cDNA clone IMAGE:1759191.3'
3074	10707	22068	2.93	9.0E-06	M17183.1	NT	Homo sapiens ribosomal subunit 18S (18S) gene, exons 1 and 2
9123	19182	32317	2.93	9.0E-06	U21416.1	NT	Homo sapiens differentiation antigen CD230 gene, cDNA 5'
7186	20186	33431	1.03	9.0E-06	BE06942.1	EST_HUMAN	RC1-4T0315-11050-017-407 BT0313 Homo sapiens cDNA
7844	20771	34074	0.86	9.0E-06	P0847	SWISSPROT	LINE1 REVERSE TRANSCRIPTASE HOMOLOG
8246	21151	34488	12.95	9.0E-06	AI242470.1	EST_HUMAN	ad0091.41 Scars, fetal liver, scvsmc, INRLS_S1 Homo sapiens cDNA clone IMAGE:1656912.3' similar to contains Alu repetitive element
9039	21062	35322	1.7	9.0E-06	AL163206.2	NT	Homo sapiens chromosome 21 segment H521C05b
9334	22451	35823	3.96	9.0E-06	Q63769	SWISSPROT	SLH1 REPEAT-CONTAINING PROTEIN SRP4 PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9534	22481	35824	3.86	9.0E-06	Q63769	SWISSPROT	SLH1 REPEAT-CONTAINING PROTEIN SRP4 PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9793	22637	35073	3.5	9.0E-06	U93114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
11377	24263	37738	3.33	9.0E-06	AI130239.1	SWISSPROT	POTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2557	19226	28555	1.02	8.0E-06	AI130239.1	EST_HUMAN	RC1-0T026-201190-011-RT C70263 Homo sapiens cDNA
11012	23988	37330	0.78	8.0E-06	P34083	SWISSPROT	FASCDILIN1, PHOSPHATIDYLINOSITOL-LINKED ISOMORPHIC PRECURSOR (FAS 1)
11012	23988	37331	0.78	8.0E-06	P34083	SWISSPROT	FASCDILIN1, PHOSPHATIDYLINOSITOL-LINKED ISOMORPHIC PRECURSOR (FAS 1)
1003	14055		1.82	7.0E-06	AA69729.1	EST_HUMAN	ad0010.41 Stralagene lung (857210) Homo sapiens cDNA clone IMAGE:84281.3' similar to contains MER20.11 MER20 repetitive element
1488	14480	27451	3.05	7.0E-06	7002177	NT	Homo sapiens KIA00555 gene product (KIA00555), mRNA
2918	19039		15.08	7.0E-06	AI398262.1	EST_HUMAN	gri1609.41 NC1_GCAP_U18 Homo sapiens cDNA clone IMAGE:1991268.3' similar to contains Alu repetitive element
3522	19058		0.87	7.0E-06	AA395422.1	EST_HUMAN	EST180268 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
5884	18938		6.3	7.0E-06	AW85314.1	EST_HUMAN	QY2410062-290400-173-001 OT0602 Homo sapiens cDNA
8015	19078	32703	0.34	7.0E-06	NB9463.1	EST_HUMAN	Y55C0771 Scars, multiple_sclerotic_2003-NGSP Homo sapiens cDNA clone IMAGE:378412.3'
9347	22275	35337	1.11	7.0E-06	11420709	NT	Homo sapiens cDNA segment, unknown origin, expressed in testis
10412	22351	35331	0.98	7.0E-06	AI101147	SWISSPROT	CDK10 (CDK10) PRECURSOR (FERROXYDOXIN)
1238	22068	31626	1.98	7.0E-06	BE115072.1	EST_HUMAN	gri161829.1 NH_KCC_87 Homo sapiens cDNA clone IMAGE:4008972.5'
2380	19012	29410	1.59	9.0E-06	BE020189.1	EST_HUMAN	QY2410370-10300-105-411 L110370 Homo sapiens cDNA
3759	19170	29480	1.11	9.0E-06	BE020189.1	EST_HUMAN	QY2410370-10300-105-411 L110370 Homo sapiens cDNA
4883	16035	28088	2.37	9.0E-06	Q01459	SWISSPROT	OVARIN ABUNDANT1 MESSAGE PROTEIN (OVI PROTEIN)

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4874	17873	30737	2.75	6.0E-06/AD/0099.1	EST_HUMAN	EST_HUMAN	αC8602.v1 Scores: fetal_liver_spleen_INTLS_S1 Homo sapiens cDNA clone IMAGE:1957/89.3 similar to contains MERR 12 MERR binding domain
5533	18612	31481	1.37	6.0E-06/AF1674.11	NT	NT	Male musculus E-cadherin binding protein E7 mRNA, complete cds
6594	18670	31549	1.18	6.0E-06/C020.40	SWISSPROT	SWISSPROT	PROTEIN XE7
10370	23259	32370	2.19	6.0E-06/AF091912.1	EST_HUMAN	EST_HUMAN	Human sapiens calcium channel, voltage-dependent, alpha 1L subunit (CACNA1L), mRNA
13081	26587	31740	1.95	6.0E-06/11418167	NT	NT	Homo sapiens chromosome 21 segment H527C0046
6286	19637	32315	1.63	6.0E-06/AL163246.2	NT	NT	
6584	16683	32817	2.11	6.0E-06/U0761.1	NT	NT	Human ABL gene, clone 1b, and human 1b, and putative M8604 M604 Met gene, complete cds
7401	21001	33335	0.67	6.0E-06/BE14771.1	EST_HUMAN	EST_HUMAN	Q102-H10165-101650-025-008 H10169 Homo sapiens cDNA
7603	20338	33827	0.92	6.0E-06/AB07546.1	NT	NT	Homo sapiens gene for LECT12, complete cds
8028	21967	33517	0.86	6.0E-06/AF056972.1	EST_HUMAN	EST_HUMAN	RC1-C10852-123030-013-002 C10852-Homo sapiens cDNA
8028	21967	33517	0.86	6.0E-06/AF056972.1	EST_HUMAN	EST_HUMAN	RC1-C10852-123030-013-002 C10852-Homo sapiens cDNA
10603	23489	33918	0.62	6.0E-06/AF131020.1	EST_HUMAN	EST_HUMAN	EST18486 Colon carcinoma (HCC) cell line Homo sapiens cDNA, 5' end
10603	23489	33918	0.62	6.0E-06/AF131020.1	EST_HUMAN	EST_HUMAN	EST18486 Colon carcinoma (HCC) cell line Homo sapiens cDNA, 5' end
10962	23876	37508	0.68	6.0E-06/P06881	SWISSPROT	SWISSPROT	COMPLEMENT C2 PRECURSOR (C2CS) CONVERSION
12370	25834	31746	4.21	6.0E-06/AD06645.1	EST_HUMAN	EST_HUMAN	H40877 Human fetal liver cDNA library Homo sapiens cDNA
670	13732	28643	4.55	4.5E-06/R16287.1	EST_HUMAN	EST_HUMAN	yeast693 Human Tumor TMB Homo sapiens cDNA, clone IMAGE:53264.5 similar to contains A10 repetitive element (A10), repetitive element
871	18324	28871	4.61	4.5E-06/AF013554.1	EST_HUMAN	EST_HUMAN	AD591241 NCI/CCRP T-1250 Homo sapiens cDNA, clone IMAGE:280678.3 similar to contains A10
1502	14393	27347	3.11	4.5E-06/AF031628.1	EST_HUMAN	EST_HUMAN	930309.1 NCI/CCRP HSC-H Homo sapiens cDNA, clone IMAGE:205168.3
1503	14393	27348	3.11	4.5E-06/AF031628.1	EST_HUMAN	EST_HUMAN	930309.1 NCI/CCRP HSC-H Homo sapiens cDNA, clone IMAGE:205168.3
1503	14393	27348	3.11	4.5E-06/AF031628.1	EST_HUMAN	EST_HUMAN	930309.1 NCI/CCRP HSC-H Homo sapiens cDNA, clone IMAGE:205168.3
1503	14393	27348	3.11	4.5E-06/AF031628.1	EST_HUMAN	EST_HUMAN	930309.1 NCI/CCRP HSC-H Homo sapiens cDNA, clone IMAGE:205168.3
2382	14001	27018	1.85	4.5E-06/AF014011.1	EST_HUMAN	EST_HUMAN	U4-H-BB, cDNA 22990-25030-1 NCI/CCRP S101 Homo sapiens cDNA
2382	14001	27018	1.85	4.5E-06/AF014011.1	EST_HUMAN	EST_HUMAN	U4-H-BB, cDNA 22990-25030-1 NCI/CCRP S101 Homo sapiens cDNA
3111	19201	29058	1.78	4.5E-06/AF105249.1	NT	NT	Salmon salinis Phox2-2 (phox2) mRNA, complete cds
3094	16992	28276	1.26	4.5E-06/AF049263.1	EST_HUMAN	EST_HUMAN	L3-512024.1/152020-24-893 C10274 Homo sapiens cDNA
4021	17921	30734	1.94	4.0E-06/AF069304.1	EST_HUMAN	EST_HUMAN	wide610.1 NCI/CCRP Jm8c8 Homo sapiens cDNA clone IMAGE:243262.3 similar to contains element
9196	21265	36348	0.79	6.0E-06/AF008900.1	SWISSPROT	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9196	21265	36348	0.79	6.0E-06/AF008900.1	SWISSPROT	SWISSPROT	Homo sapiens 1 cell receptor beta locus, TCRB/TSR2 region
9196	21265	36348	0.79	6.0E-06/AF008900.1	SWISSPROT	SWISSPROT	Homo sapiens SPPT2 gene for secreted phosphoprotein 24 precursor, clones 1-8
10290	32523	37291	1.11	4.0E-06/AF127295.1	NT	NT	Homo sapiens mRNA, of ribosome 1 specific transcript KIA0486
11883	23883	37124	4.50	4.0E-06/AB070561.1	NT	NT	23-0408.1 Homo fetal, spleen, INTLS_S1 Homo sapiens cDNA clone IMAGE:434263.3 similar to contains A10.1 repetitive element
2176	15188	28195	1.95	6.0E-06/AA705052.1	EST_HUMAN	EST_HUMAN	

Table 4

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7854	20810	34116	0.59	2.0E-06	A036429.1	EST_HUMAN	ncs006.s1 NCL_GCAP_GCH1 Homo sapiens cDNA clone IMAGE:234060 3' similar to contains L1.8 L1 repetitive element;
8465	21427		1.17	2.0E-06	A1956223.1	EST_HUMAN	MR3-SN007-120400-002-03 SN007 Homo sapiens cDNA
8608	21568	34588	0.78	2.0E-06	U11228.1	EST_HUMAN	A47478.Hs.Homo sapiens cDNA clone A47
8694	22222		0.98	2.0E-06	A472497.1	EST_HUMAN	2427011 at Source: Human sapiens cDNA clone IMAGE:13300 3' similar to H1P-04177401.Hs.Homo sapiens cDNA clone A47
9407	23235	35669	1.62	2.0E-06	A60201.1	EST_HUMAN	ncs006.s1 NCL_GCAP_GCH1 Homo sapiens cDNA clone IMAGE:234060 3' similar to H1P-04177401.Hs.Homo sapiens cDNA clone A47
9707	23531	35035	1.30	2.0E-06	A5303328.1	EST_HUMAN	ncs006.s1 NCL_GCAP_GCH1 Homo sapiens cDNA clone IMAGE:234060 3' similar to H1P-04177401.Hs.Homo sapiens cDNA clone A47
9787	23531	35035	1.30	2.0E-06	A5303328.1	EST_HUMAN	ncs006.s1 NCL_GCAP_GCH1 Homo sapiens cDNA clone IMAGE:234060 3' similar to H1P-04177401.Hs.Homo sapiens cDNA clone A47
9777	23701		0.6	2.0E-06	A473450.1	EST_HUMAN	ncs006.s1 NCL_GCAP_GCH1 Homo sapiens cDNA clone IMAGE:234060 3' similar to H1P-04177401.Hs.Homo sapiens cDNA clone A47
10223	23114	35515	0.82	2.0E-06	N03070.1	EST_HUMAN	y060403.at Source: placenta, Bld/Spleen, 2N6 (P306)W Homo sapiens cDNA clone IMAGE:237212 3'
10400	23319		0.65	2.0E-06	A4735908.1	EST_HUMAN	A4746608.Hs.Homo sapiens cDNA clone NFCA003.5
12652	25609	31967	1.78	2.0E-06	P23249	SWISSPROT	PROTEIN NOV-10
12735	25378		3.99	2.0E-06	B6323232.1	EST_HUMAN	ncs006.s1 NCL_GCAP_GCH1 Homo sapiens cDNA clone IMAGE:234060 3' similar to contains L1.12 L1 repetitive element;
35	13151	26040	1.77	1.0E-06	Q70632	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 9) (HIGH- AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
800	13742	22657	1.51	1.0E-06	A7054384.1	NT	Mus musculus DDMKSE protein (Ddmk5) mRNA, complete cds
1470	14801	27462	2	1.0E-06	P00125	SWISSPROT	MEROZOITE SURFACE PROTEIN CH2-8
1548	14577	27857	1.22	1.0E-06	AL165278.2	NT	Homo sapiens chromosome 21 segment HS21C07/8
1592	14623	27858	1.2	1.0E-06	A0034141.1	EST_HUMAN	ncs006.s1 NCL_GCAP_GCH1 Homo sapiens cDNA clone IMAGE:234060 3' similar to H1P-04177401.Hs.Homo sapiens cDNA clone A47
1592	14623	27858	1.2	1.0E-06	A0034141.1	EST_HUMAN	ncs006.s1 NCL_GCAP_GCH1 Homo sapiens cDNA clone IMAGE:234060 3' similar to H1P-04177401.Hs.Homo sapiens cDNA clone A47
1606	14637		1.18	1.0E-06	P72765	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
2010	15028	28020	6.69	1.0E-06	A184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
2010	15028	28021	6.69	1.0E-06	A184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4476	17457	30346	15.6	1.0E-06	U07091.1	NT	Human ABL gene, exon 1b and intron 1b, and putative N69c4 Met protein (M69c4 Met) gene, complete cds
5246	18233	37082	1.95	1.0E-06	AL16285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5246	18233	37083	1.95	1.0E-06	AL16285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5473	18554	37396	4.81	1.0E-06	B523015.1	EST_HUMAN	MK1-B10000-000700-002-006 B10000 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID No.	Exon SEQ ID No.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) HIT BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2515	15516	28520	2.42	6.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing intron X (introns-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complementary component C4 (C4B) 011, introns (SK24), R0, complement factor B (B) and complement component C2 (C2) genes>
4059	17033		1.96	6.0E-07	P14470	SWISSPROT	HYPOPHOSPHATASE 1, NO PROTEIN IN LIVER, INTERGENIC REGION
6984	22610	33584	1.57	6.0E-07	BF001892.1	EST_HUMAN	7464007.x1 NCL CGAP_C048 Homo sapiens cDNA clone IMAGE:3311448 3' similar to R076820 O76820
12207	25042	39845	3.50	6.0E-07	A762503.1	EST_HUMAN	0837005.05 NCL CGAP_K03 Homo sapiens cDNA clone IMAGE:1644177 5'
12498	25891		2.14	6.0E-07	AF060222.1	EST_HUMAN	CH44NN1029-250000-127-H12 NN1029 Homo sapiens cDNA
346	13435		1.03	6.0E-07	A1831802.1	EST_HUMAN	W16410.x1 NCL CGAP_K011 Homo sapiens cDNA clone IMAGE:2385547 3'
1024	14128		2.50	6.0E-07	AA339050.1	EST_HUMAN	EST12815 Supr cells Homo sapiens cDNA 5' end
3078	16129		0.78	6.0E-07	A1831802.1	EST_HUMAN	W16410.x1 NCL CGAP_K011 Homo sapiens cDNA clone IMAGE:2385547 3'
6359	18408	32573	1.35	6.0E-07	U95057.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
6449	18445	32970	0.44	6.0E-07	AA278183.1	EST_HUMAN	71605.01 NCL CGAP_G031 Homo sapiens cDNA clone IMAGE:712562 5' similar to gb253741.t1a1
7418	20117	33335	1.84	6.0E-07	A1360981.1	EST_HUMAN	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
7418	20117	33354	1.84	6.0E-07	A1360981.1	EST_HUMAN	IG0805.x1 NCL CGAP_C011 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains AU repetitive element;containing element AS1 repetitive element;
7795	20657	33584	15.89	6.0E-07	A1070985.1	EST_HUMAN	IG0805.x1 NCL CGAP_C011 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains AU repetitive element;containing element AS1 repetitive element;
8981	21781	35128	1.11	6.0E-07	Q8WUQ1	SWISSPROT	IG0805.x1 NCL CGAP_C011 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains AU repetitive element;containing element AS1 repetitive element;
9099	21988		1.04	6.0E-07	P09593	SWISSPROT	IG0805.x1 NCL CGAP_C011 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains AU repetitive element;containing element AS1 repetitive element;
10954	23740	37163	7.25	6.0E-07	A108957.1	EST_HUMAN	IG0805.x1 NCL CGAP_C011 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains AU repetitive element;containing element AS1 repetitive element;
11106	24037	37482	1.56	6.0E-07	P09597.1	SWISSPROT	IG0805.x1 NCL CGAP_C011 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains AU repetitive element;containing element AS1 repetitive element;
11947	24791	38289	3.91	6.0E-07	P11057	SWISSPROT	IG0805.x1 NCL CGAP_C011 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains AU repetitive element;containing element AS1 repetitive element;
12012	24854		2.0	6.0E-07	A1271735.1	NT	IG0805.x1 NCL CGAP_C011 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains AU repetitive element;containing element AS1 repetitive element;
12858	13176		3.21	6.0E-07	A108957.1	EST_HUMAN	IG0805.x1 NCL CGAP_C011 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains AU repetitive element;containing element AS1 repetitive element;
7523	24418		0.95	6.0E-07	A108957.1	EST_HUMAN	IG0805.x1 NCL CGAP_C011 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains AU repetitive element;containing element AS1 repetitive element;
7518	20578	33972	0.85	6.0E-07	Q02249	SWISSPROT	IG0805.x1 NCL CGAP_C011 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains AU repetitive element;containing element AS1 repetitive element;
7518	20578	33973	0.85	6.0E-07	Q02249	SWISSPROT	IG0805.x1 NCL CGAP_C011 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains AU repetitive element;containing element AS1 repetitive element;
8511	21432	34773	0.85	6.0E-07	A108957.1	NT	IG0805.x1 NCL CGAP_C011 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains AU repetitive element;containing element AS1 repetitive element;
8504	22630	35937	4.84	6.0E-07	A1116194.1	EST_HUMAN	IG0805.x1 NCL CGAP_C011 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains AU repetitive element;containing element AS1 repetitive element;

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
105-4	28700	37128	0.51	4.0E-07	AF15218.2	NT	homo sapiens chromosome 2, segment HS22018
11376	24252	37186	3.3	4.0E-07	AF08593.1	EST_HUMAN	homo sapiens cDNA clone IMAGE:2269703 3'
11376	24252	37187	3.3	4.0E-07	AF08593.1	EST_HUMAN	homo sapiens cDNA clone IMAGE:2269703 3'
11670	24574		1.78	4.0E-07	BE01628.1	EST_HUMAN	homo sapiens cDNA clone IMAGE:2269703 3'
464	13536	26456	4.44	3.0E-07	U19719.1	NT	homo sapiens cDNA clone IMAGE:2269703 3'
604	13670	24573	1.46	3.0E-07	AF127135.1	NT	homo sapiens cDNA clone IMAGE:2269703 3'
1401	14432	27387	2.03	3.0E-07	ME9149.1	NT	homo sapiens cDNA clone IMAGE:2269703 3'
1649	14686		2.04	3.0E-07	ME94697.1	NT	homo sapiens cDNA clone IMAGE:2269703 3'
2000	15076		1.07	3.0E-07	AA529768.1	EST_HUMAN	homo sapiens cDNA clone IMAGE:2269703 3'
2307	15315	28318	1.77	3.0E-07	ME9149.1	NT	homo sapiens cDNA clone IMAGE:2269703 3'
2402	15494	28404	4.05	3.0E-07	BE003077.1	EST_HUMAN	homo sapiens cDNA clone IMAGE:2269703 3'
2402	15494	28405	4.05	3.0E-07	BE003077.1	EST_HUMAN	homo sapiens cDNA clone IMAGE:2269703 3'
3061	15132	25028	0.84	3.0E-07	TA74794.1	EST_HUMAN	homo sapiens cDNA clone IMAGE:2269703 3'
3202	16260	25146	2.3	3.0E-07	P38739	SWISSPROT	homo sapiens cDNA clone IMAGE:2269703 3'
4840	17841	30710	8.54	3.0E-07	AF050204.1	EST_HUMAN	homo sapiens cDNA clone IMAGE:2269703 3'
4878	17875	30740	0.87	3.0E-07	AF077235.1	EST_HUMAN	homo sapiens cDNA clone IMAGE:2269703 3'
5198	18190	31031	1.7	3.0E-07	U19719.1	EST_HUMAN	homo sapiens cDNA clone IMAGE:2269703 3'
5198	18190	31032	1.7	3.0E-07	U19719.1	EST_HUMAN	homo sapiens cDNA clone IMAGE:2269703 3'
5983	19534	32053	11.51	3.0E-07	OE8907	SWISSPROT	homo sapiens cDNA clone IMAGE:2269703 3'
6202	19498	32405	0.81	3.0E-07	U62290	SWISSPROT	homo sapiens cDNA clone IMAGE:2269703 3'
7000	20027		4.52	3.0E-07	AA816175.1	EST_HUMAN	homo sapiens cDNA clone IMAGE:2269703 3'
7532	20654	34182	4.02	3.0E-07	AF177198.1	EST_HUMAN	homo sapiens cDNA clone IMAGE:2269703 3'
8114	21029		0.75	3.0E-07	AF041055.1	EST_HUMAN	homo sapiens cDNA clone IMAGE:2269703 3'
11951	24776		1.48	3.0E-07	BE439499.1	EST_HUMAN	homo sapiens cDNA clone IMAGE:2269703 3'
12094	24625		2.07	3.0E-07	AF028308.1	NT	homo sapiens cDNA clone IMAGE:2269703 3'
13052	25009		6.32	3.0E-07	AF132352.1	NT	homo sapiens cDNA clone IMAGE:2269703 3'
30	13156	28034	2.82	2.0E-07	AF126386.1	NT	homo sapiens cDNA clone IMAGE:2269703 3'

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
164	13265	26182	6.85	2.0E-07	L77688.1	NT	Homo sapiens D/Gauche syndrome critical region, intronic and
164	13265	26183	0.85	2.0E-07	L77688.1	NT	Homo sapiens D/Gauche syndrome critical region, intronic and
165	13261	26206	33.69	2.0E-07	U38848.1	NT	Fugu ratpax beta-2 cytoplasmic (beta-2) cDNA, complete cds
172	13628	26700	3.24	2.0E-07	AF003830.1	NT	Homo sapiens homodioxin protein (HMOX1) cDNA, complete cds
172	13628	26761	3.24	2.0E-07	AF003830.1	NT	Homo sapiens homodioxin protein (HMOX1) cDNA, complete cds
785	13844		0.86	2.0E-07	P11389	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS REVERSE TRANSCRIPTASE, NUCLEASE]
971	14022	26998	2.78	2.0E-07	AA223260.1	EST_HUMAN	trf0847.v1 Stragapine NT2 neuronal precursor 897230 Homo sapiens cDNA clone IMAGE:650999 3' similar to dbL31800 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element.
972	14023	26997	7.01	2.0E-07	T63042.1	EST_HUMAN	trf1504.v1 Stragapine linc (657270) Homo sapiens cDNA clone IMAGE:60760 3' similar to contains L1 repetitive element.
1023	14259	27188	0.95	2.0E-07	Q36768	SWISSPROT	UB AUTOANTIGEN
3884	16717	27617	2.21	2.0E-07	Q37071	SWISSPROT	HYPOPHYSICAL 7.5 KD PROTEIN C257.10 IN CHROMOSOME 1
3754	16788	26675	0.66	2.0E-07	BF131367.1	EST_HUMAN	trf018.8918T1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:404987 5'
5280	18209		0.78	2.0E-07	AF102219.1	EST_HUMAN	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
6528	18807	31466	1.79	2.0E-07	AF168098.1	EST_HUMAN	QV3-NN1025-200400-168-r111 NN1025 Homo sapiens cDNA
8931	25685	33077	0.89	2.0E-07	AW446888.1	EST_HUMAN	RC3-NN008-300400-021-r11 NN008 Homo sapiens cDNA
8937	18500	33210	1.79	2.0E-07	AI026715.1	EST_HUMAN	UHH-83-site-B-01-C-11 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734008 3'
6971	19968	33228	0.87	2.0E-07	AA572653.1	EST_HUMAN	trf05005.v1 Soares, Iudis, NHT Homo sapiens cDNA clone IMAGE:1809177 3'
8039	21908		4.86	2.0E-07	AV72599.1	EST_HUMAN	trf033405.v1 NCL CGAP_L1p2 Homo sapiens cDNA clone IMAGE:1091938 similar to contains Alu repetitive element.
9230	22171	35335	1.24	2.0E-07	AA031986.1	EST_HUMAN	AV72599 RHC Homo sapiens cDNA clone HTCAE063 5'
10261	23161		1.71	2.0E-07	AL163303.2	NT	452766.v1 Soares, Program, uterus, NHPHU Homo sapiens cDNA clone IMAGE:471898 3'
10720	23048	37076	7.43	2.0E-07	AW825007.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
10967	23481	37275	1.08	2.0E-07	P00751	SWISSPROT	CMH-NN0085-280000-724-v08 NN0085 Homo sapiens cDNA
10967	25691	37276	1.08	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
12331	25528		1.88	2.0E-07	BE193717.1	EST_HUMAN	(GLYONE-RICH BETA GLYCOPROTEIN) (BAG) (PBP2)
12396	23776		2.33	2.0E-07	AF732402.1	EST_HUMAN	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
1128	14171		0.97	1.0E-07	AL162262.2	NT	(GLYONE-RICH BETA GLYCOPROTEIN) (BAG) (PBP2)
							trf06811.v1 Stragapine lung carcinoma 897218 Homo sapiens cDNA clone IMAGE:565029 3' similar to contains 1TRX2 1TRX repetitive element.
							Homo sapiens chromosome 21 segment HS21C092

Table 4
Single Exon Probes Expressed in Adult Liver

Probe Seq ID NO.	Exon Seq ID NO.	QRT-SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1986	15034	27691	1.33	1.0E-07/AL163243.2	NT	EST_HUMAN	Homo sapiens chromosome 2: segment HS21C018
1986	15034	27692	1.33	1.0E-07/AL163243.2	NT	EST_HUMAN	Homo sapiens chromosome 2: segment HS21C018
2408	15411	28414	0.94	1.0E-07/P10283	SWISSPROT	EST_HUMAN	RECYCLING-RELATED GAG POLYPROTEIN (VERSION 1)
2873	14713	27336	2.43	1.0E-07/P62268	SWISSPROT	EST_HUMAN	GLYCOPROTEIN GP
3807	14713	27336	2.43	1.0E-07/P62268	SWISSPROT	EST_HUMAN	Homo sapiens chromosome 2: segment HS21C082
4356	17408	30274	3.07	1.0E-07/AF12682.2	EST_HUMAN	EST_HUMAN	AV1718652 (B) Homo sapiens cDNA clone GLOR194.5'
4356	17408	30275	3.07	1.0E-07/AF12682.2	EST_HUMAN	EST_HUMAN	AV1718652 (B) Homo sapiens cDNA clone GLOR194.5'
6780	16813	33026	1.37	1.0E-07/UK2071.2	NT	EST_HUMAN	Homo sapiens chromosome 22q11.2 melanosomal antigen family A2a (IMAGE42A), melanoma antigen family A12 (IMAGE42), melanoma antigen family A2b (IMAGE42B), melanoma antigen family A3 (IMAGE43), cathectin (CAT), NAUPH dehydrogenase-like protein (NSDHL), and Lipo
7102	20102	33436	5.49	1.0E-07/BE047871.1	EST_HUMAN	EST_HUMAN	1243305.v1 NCL CGAP Bm52 Homo sapiens cDNA clone IMAGE 2291339.5'
7102	20102	33436	5.49	1.0E-07/BE047871.1	EST_HUMAN	EST_HUMAN	1243305.v1 NCL CGAP Bm52 Homo sapiens cDNA clone IMAGE 2291339.5'
7914	20538	34141	8.03	1.0E-07/NE5081.1	EST_HUMAN	EST_HUMAN	W43207.v1 Scores 5447 liver spleen TNL3 Homo sapiens cDNA clone IMAGE 244843.3'
8007	21009	34334	0.98	1.0E-07/BF37690.1	EST_HUMAN	EST_HUMAN	PM4-TN0224-030800-002-505 TN0224 Homo sapiens cDNA
8007	21009	34334	0.98	1.0E-07/BF37690.1	EST_HUMAN	EST_HUMAN	PM4-TN0224-030800-002-505 TN0224 Homo sapiens cDNA
8130	21040	34369	1.32	1.0E-07/AL163261.2	NT	EST_HUMAN	Homo sapiens chromosome 2: segment HS21C081
8344	21259	34509	0.48	1.0E-07/AL163261.2	NT	EST_HUMAN	Homo sapiens chromosome 2: segment HS21C081
8794	21724	35071	2.11	1.0E-07/P97435	SWISSPROT	EST_HUMAN	ENTEROPEPTIDASE [ENTEROKINASE]
8794	21724	35072	2.11	1.0E-07/P97435	SWISSPROT	EST_HUMAN	ENTEROPEPTIDASE [ENTEROKINASE]
9509	22430	35800	3.72	1.0E-07/AA063576.1	EST_HUMAN	EST_HUMAN	261610.v1 Scores 5447 liver spleen TNL3 Homo sapiens cDNA clone IMAGE 434346.3'
9810	22716	36068	1.14	1.0E-07/P97110	SWISSPROT	EST_HUMAN	ADAMTS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
10143	23034	36432	0.89	1.0E-07/BE32764.1	EST_HUMAN	EST_HUMAN	MOTIFS 9 (ADAMTS-8) (ADAM-TS8) (METH-2)
10143	23034	36432	0.89	1.0E-07/BE32764.1	EST_HUMAN	EST_HUMAN	MOTIFS 9 (ADAMTS-8) (ADAM-TS8) (METH-2)
10453	23342	36759	1.26	1.0E-07/AA088311.1	EST_HUMAN	EST_HUMAN	1028105.v1 NCL CGAP Mth5 Homo sapiens cDNA clone IMAGE 3171419.3' similar to contains MER18.43
10943	23828		1.84	1.0E-07/AL163261.2	NT	EST_HUMAN	MER18 repetitive element;
12546	25744	31571	2.88	1.0E-07/BE048770.1	EST_HUMAN	EST_HUMAN	60213771.v1 NCL CGAP Bm52 Homo sapiens cDNA clone IMAGE 427429.5'
7690	20554	33602	0.75	9.0E-06/AF163062.1	EST_HUMAN	EST_HUMAN	EST_HUMAN
13999	23298	36710	2.31	9.0E-06/AF174819.1	EST_HUMAN	EST_HUMAN	103511.v1 NCL CGAP Mth5 Homo sapiens cDNA clone IMAGE 313212.3' similar to TR 046772 046772
1628	24533	38002	2.18	9.0E-06/AB91065.1	EST_HUMAN	EST_HUMAN	W434007.v1 Scores 5447 liver spleen TNL3 Homo sapiens cDNA clone IMAGE 2000165.3'
12053	24634	38441	2.80	9.0E-06/AL163071.2	NT	EST_HUMAN	W434007.v1 NCL CGAP Mth5 Homo sapiens cDNA clone IMAGE 244843.3' similar to contains OFR12
					NT	EST_HUMAN	OFRT repetitive element;

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Probe SEQ ID NO.	Exam SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
12206	24848	38347	1.53	3.0E-08 R82276.1	EST_HUMAN	h12b10.01 Scores: breast 3Hh-Bat Homo sapiens cDNA clone IMAGE:187165 3' similar to g15M4079 FAT	
12247	23070		28.09	3.0E-08 R18420.1	EST_HUMAN	h12b10.01 Scores: infant1 (human) Homo sapiens cDNA clone IMAGE:30048 5' similar to g15M4079 FAT	
219	131849		6.29	2.0E-08 AF193206.1	EST_HUMAN	h12b10.01 Scores: infant1 (human) Homo sapiens cDNA clone IMAGE:30048 5' similar to g15M4079 FAT	
246	133444		8.07	2.0E-08 AA42593.1	EST_HUMAN	h12b10.01 Scores: infant1 (human) Homo sapiens cDNA clone IMAGE:27371 30 3'	
519	137869	29502	2.33	2.0E-08 AF193436.1	NT	zw4807.1 rat_yak1_Nb2HF9_0w Homo sapiens cDNA clone IMAGE:77317 5' similar to contains	
583	137445	29502	8.21	2.0E-08 AF193436.1	NT	Galus gallus Dact2 protein (Dact2) mRNA, complete cds	
583	137445	29502	8.21	2.0E-08 AF193436.1	EST_HUMAN	MIR-010039-242020-001-g88 OT0089 Homo sapiens cDNA	
1017	14047		19.63	2.0E-08 BE28047.1	EST_HUMAN	MIR-010039-242020-001-g88 OT0089 Homo sapiens cDNA	
1371	14493	27387	1.66	2.0E-08 AL163247.2	EST_HUMAN	OT1185321P1 NM_1_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'	
1789	14795		2.44	2.0E-08 BE73487.1	NT	Homo sapiens chromosome 21 segment H82T047	
1879	14900		3.28	2.0E-08 AF170271.1	EST_HUMAN	h1670468F1 NM_1_MGC_21 Homo sapiens cDNA clone IMAGE:3848100 5'	
2374	15573		1.96	2.0E-08 AK00211.1	EST_HUMAN	sp4311.X1 NC1_GGAP_JN11 Homo sapiens cDNA clone IMAGE:2749148 3'	
3283	16301	28206	6.87	2.0E-08 O43280	SWISSPROT	Sheep Hic-RNA-GUG	
3283	16301	28207	6.87	2.0E-08 O43280	SWISSPROT	WNT-74 PROTEIN PRECURSOR	
3926	16854		2.68	2.0E-08 AF181920.1	EST_HUMAN	RGS-370167-161069-012-006 ST01047 Homo sapiens cDNA	
4104	17185	30038	0.73	2.0E-08 J82954.1	NT	Homo sapiens fibro gene, alternatively spliced products, complete cds	
4511	17521		2.16	2.0E-08 GA498040.1	EST_HUMAN	ad36077.N1 NC1_GGAP_OC081 Homo sapiens cDNA clone IMAGE:314380 5' similar to contains L1.12.1	
6072	18069		4.82	2.0E-08 AW57598.1	EST_HUMAN	h17708.2 NC1_GGAP_CML1 Homo sapiens cDNA clone IMAGE:2519327 3' similar to contains Au	
8532	19043	32019	0.37	2.0E-08 GA318204.1	EST_HUMAN	ad36071.1 NC1_GGAP_CML1 Homo sapiens cDNA clone IMAGE:2519327 3' similar to contains Au	
8532	19043	32238	0.37	2.0E-08 AW08264.1	EST_HUMAN	ad36071.1 NC1_GGAP_OC02 Homo sapiens cDNA clone IMAGE:2895942 3' similar to contains MER1833	
8450	21119	34459	0.87	2.0E-08 AF193436.1	EST_HUMAN	ad36071.1 NC1_GGAP_OC02 Homo sapiens cDNA clone IMAGE:2895942 3' similar to contains MER1833	
8450	21119	34461	1.87	2.0E-08 AF193436.1	EST_HUMAN	ad36071.1 NC1_GGAP_OC02 Homo sapiens cDNA clone IMAGE:2895942 3' similar to contains MER1833	
9391	22237		1.1	2.0E-08 AF193436.1	EST_HUMAN	ad36071.1 NC1_GGAP_OC02 Homo sapiens cDNA clone IMAGE:2895942 3' similar to contains MER1833	
10696	23933	37374	0.91	2.0E-08 AF193436.1	EST_HUMAN	ad36071.1 NC1_GGAP_OC02 Homo sapiens cDNA clone IMAGE:2895942 3' similar to contains MER1833	
10999	26926	37315	1.97	2.0E-08 AF193436.1	EST_HUMAN	ad36071.1 NC1_GGAP_OC02 Homo sapiens cDNA clone IMAGE:2895942 3' similar to contains MER1833	
30008	26926		0.71	2.0E-08 AF193436.1	EST_HUMAN	ad36071.1 NC1_GGAP_OC02 Homo sapiens cDNA clone IMAGE:2895942 3' similar to contains MER1833	

Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1528	15603	27519	1.33	1.0E-08	P31792	SWISSPROT	POLY(ADP-RIBOSE) POLYMERASE 1 (PAP1) [HUMAN]
1530	16128	27704	1.79	1.0E-08	AF122348.1	NT	Human PAP1 (PAP1) [HUMAN]
2088	15000		2.52	1.0E-08	BE141896.1	EST_HUMAN	Human PAP1 (PAP1) [HUMAN]
3235	12633	28164	1.16	1.0E-08	BE240844.1	EST_HUMAN	Human PAP1 (PAP1) [HUMAN]
3235	12633	28165	1.16	1.0E-08	BE240844.1	EST_HUMAN	Human PAP1 (PAP1) [HUMAN]
5733	18495	31973	3.35	1.0E-08	AJ017701.1	NT	Human PAP1 (PAP1) [HUMAN]
6238	21143	34478	1.14	1.0E-08	P18474	SWISSPROT	Human PAP1 (PAP1) [HUMAN]
8111	22039	35985	2.16	1.0E-08	AF153043.1	EST_HUMAN	Human PAP1 (PAP1) [HUMAN]
8746	22070	39033	0.75	1.0E-08	BE372572.1	EST_HUMAN	Human PAP1 (PAP1) [HUMAN]
10472	23360	39774	0.95	1.0E-08	P70710	SWISSPROT	Human PAP1 (PAP1) [HUMAN]
11032	23910	37959	0.85	1.0E-08	F98063	SWISSPROT	Human PAP1 (PAP1) [HUMAN]
11700	24501	35149	4.28	1.0E-08	AF040083.1	NT	Human PAP1 (PAP1) [HUMAN]
12622	25307		1.99	1.0E-08	X51755.1	NT	Human PAP1 (PAP1) [HUMAN]
4241	17355	30219	5.3	9.0E-09	AF163279.2	NT	Human PAP1 (PAP1) [HUMAN]
4341	17355	30220	5.3	9.0E-09	AF163279.2	NT	Human PAP1 (PAP1) [HUMAN]
10554	23430		0.59	9.0E-09	BT9450.1	EST_HUMAN	Human PAP1 (PAP1) [HUMAN]
9750	19750		0.87	8.0E-09	AI270915.1	EST_HUMAN	Human PAP1 (PAP1) [HUMAN]
7639	20574	33688	7.89	8.0E-09	AI163500.1	EST_HUMAN	Human PAP1 (PAP1) [HUMAN]
8578	21510	34556	2.58	8.0E-09	AY020169.1	EST_HUMAN	Human PAP1 (PAP1) [HUMAN]
9540	22467		3.37	8.0E-09	AJ038892.1	EST_HUMAN	Human PAP1 (PAP1) [HUMAN]
3670	19703		2.5	7.0E-09	D98942.1	NT	Human PAP1 (PAP1) [HUMAN]
4033	17118		2.93	7.0E-09	U06571.1	NT	Human PAP1 (PAP1) [HUMAN]
9025	21550		0.94	7.0E-09	AJ252203.1	EST_HUMAN	Human PAP1 (PAP1) [HUMAN]
3912	22768	36391	2.88	7.0E-09	U07038.1	NT	Human PAP1 (PAP1) [HUMAN]
10090	20306	30946	1.00	7.0E-09	BE254630.1	EST_HUMAN	Human PAP1 (PAP1) [HUMAN]
10533	23719		1.72	7.0E-09	AJ058628.1	EST_HUMAN	Human PAP1 (PAP1) [HUMAN]

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11117	26047		3.26	7.0E-50	T07690.1	EST_HUMAN	beta42.41 Soares: full liver globin (HbE) Homo sapiens cDNA clone IMAGE:421618.3
5102	10049	30847	8.36	6.0E-50	BE1042.1	EST_HUMAN	PH-1110623-110200-001-505 HT222 Homo sapiens cDNA
2032	18374	31216	1.19	6.0E-50	AA527640.1	EST_HUMAN	HT111-111 NCI COG: H2C1 Homo sapiens cDNA clone IMAGE:194052, similar to contains L12 L1
5955	18633	31521	8.92	6.0E-50	AV159784.1	EST_HUMAN	wt6908.v41 Soares: NHEK-1, 5' end, 5' Homo sapiens cDNA clone IMAGE:2701311.3
9130	22047	35426	1.4	6.0E-50	BF161633.1	EST_HUMAN	NF3-1110446-263300-301-H12 T10443 Homo sapiens cDNA
8718	22843	36024	2.86	6.0E-50		NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, rhizomelic dwarfism) (FGFR3) mRNA
10769	26655		4.23	6.0E-50	AI220529.2	NT	Homo sapiens brain-specific kinase substrate 1 (TSK1) gene, complete cds
11173	24100	37546	1.41	6.0E-50	BF100756.1	EST_HUMAN	704510.v1 Soares: NSF FR_9W_OT_P_A_P.31 Homo sapiens cDNA clone IMAGE:332446.3 similar to contains MER28a2, MER20, and MER21
12122	24053	38466	1.8	6.0E-50	P08547	SWISSPROT	LINE1 REVERSE TRANSCRIPTASE HOMOLOG
12122	24053	38467	1.8	6.0E-50	P08547	SWISSPROT	LINE1 REVERSE TRANSCRIPTASE HOMOLOG
12127	25052	38633	1.49	6.0E-50	C01803.1	EST_HUMAN	HUM950003762 Human adult (K.Osaka)
1439	14499	27425	4.36	5.0E-50	BE146264.1	EST_HUMAN	RC2-1110253-110200-014-H10 HT0252 Homo sapiens cDNA
1877	14868	27852	1.16	5.0E-50	AL162842.1	NT	Homo sapiens chromosome 21 segment HS21C084
6575	19712	32005	3.42	5.0E-50	AA359454.1	EST_HUMAN	EST168746 fetal lung II Homo sapiens cDNA 3' end
							Human germline T-cell receptor beta chain Docanina-beta-hydroxylase-like, TRV1, TRV2, TRV3
							TCRBV2754P, TCRBV2251A2M1, TCRBV951A1T, TCRBV751A1N2T, TCRBV651A1T, TCRBV1533, TCRBV657P, TCRBV753A2T, TCRBV133A2T, TCRBV652A2P1, TCRBV752A1N4T,
							TCRBV133M135>
7105	19435	31340	0.53	5.0E-50	U00096.1	NT	PHU2-DM0053-240300-005-c09 UM0053 Homo sapiens cDNA
10597	25463	59912	3.23	5.0E-50	AV176697.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
644	13513		1.75	4.0E-50	AL163262.2	NT	Homo sapiens chromosome 21 segment HS21C082
691	14041		1.82	4.0E-50	AL163265.2	NT	Homo sapiens chromosome 21 segment HS21C082
1488	14519	27460	1.67	4.0E-50		NT	Homo sapiens hypodermal protein (AF038169), mRNA
2036	16093	28051	1.23	4.0E-50	AF176325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
2036	16093	28052	1.23	4.0E-50	AF176325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
2454	14598	28455	4.22	4.0E-50	AA303978.1	EST_HUMAN	EST158355 Human brain Homo sapiens cDNA 3' end similar to similar to heat shock protein, 90 kDa
8426	21391	37700	0.74	4.0E-50	AA493747.1	EST_HUMAN	wt64076.v1 NCI COG: D2C1 Homo sapiens cDNA clone IMAGE:765209.9
11514	24424	37862	1.38	4.0E-50	AA664901.1	EST_HUMAN	wt64076.v1 NCI COG: D2C1 Homo sapiens cDNA clone IMAGE:765209.9
							25442121 Soares: NHEK1P, 5' Homo sapiens cDNA clone IMAGE:665275 similar to g01.07507
11557	24466		1.82	4.0E-50	AA1165142.1	EST_HUMAN	DYNAMIN-1 (HUMAN)
							pub406.v1 NCI COG: L122 Homo sapiens cDNA clone IMAGE:3195120.3 similar to contains MER18.B
2374	13378	26381	4.46	3.0E-50	BE222239.1	EST_HUMAN	MER1 to repetitive element 1

Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	QRF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2537 15595	2537	2537	1.65	3.0E-09	BE222298.1	EST_HUMAN	h00406.v1 NCL CGAP_Luc2 Homo sapiens cDNA, clone IMAGE31961/20 3' similar to contains MER18.0
2539 15603	2539	2539	1.11	3.0E-09	P22249	SWISSPROT	MER18.0 similar element, 1
3376 19420	3376	29422	1.03	3.0E-09	BE222298.1	EST_HUMAN	h00406.v1 NCL CGAP_Luc2 Homo sapiens cDNA, clone IMAGE31961/20 3' similar to contains MER18.0
3434 16476	3434	29422	0.76	3.0E-09	AA442727.1	EST_HUMAN	MER18.0 similar element, 1
4197 17273	4197	30404	0.84	3.0E-09	X16914.1	NT	h00406.v1 NCL CGAP_Luc2 Homo sapiens cDNA, clone IMAGE31961/20 3' similar to contains MER18.0
4533 17542	4533	30404	0.76	3.0E-09	X16914.1	NT	h00406.v1 NCL CGAP_Luc2 Homo sapiens cDNA, clone IMAGE31961/20 3' similar to contains MER18.0
4533 17559	4533	30402	2.44	3.0E-09	Q93763	SWISSPROT	Homo sapiens adenylylating factor 441 (EIF4A1) gene, partial cds
5327 18311	5327	30402	0.6	3.0E-09	D69842.1	NT	258.1 KDA PROTEIN C21ORF5 (KIA0053)
8490 21411	8490	34748	1.10	3.0E-09	BE487890.1	EST_HUMAN	Homo sapiens DNA for 3-ketolase-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
10741 23627	10741	37057	2.07	3.0E-09	AF168472	NT	h00406.v1 NCL CGAP_Luc2 Homo sapiens cDNA, clone IMAGE31961/20 3' similar to contains MER18.0
11450 24375	11450	37823	4.02	3.0E-09	BF105943.1	EST_HUMAN	h00406.v1 NCL CGAP_Luc2 Homo sapiens cDNA, clone IMAGE31961/20 3' similar to contains MER18.0
11450 24375	11450	37823	4.02	3.0E-09	BF105943.1	EST_HUMAN	h00406.v1 NCL CGAP_Luc2 Homo sapiens cDNA, clone IMAGE31961/20 3' similar to contains MER18.0
1295 14318	1295	27269	6.55	2.0E-09	AL162842	NT	h00406.v1 NCL CGAP_Luc2 Homo sapiens cDNA, clone IMAGE31961/20 3' similar to contains MER18.0
1695 14716	1695	27269	6.07	2.0E-09	AL116573.1	EST_HUMAN	h00406.v1 NCL CGAP_Luc2 Homo sapiens cDNA, clone IMAGE31961/20 3' similar to contains MER18.0
2848 18356	2848	29529	1.41	2.0E-09	Q93763	SWISSPROT	Homo sapiens adenylylating factor 441 (EIF4A1) gene, partial cds
4013 17040	4013	31162	4.32	2.0E-09	Q02041	SWISSPROT	IRFAN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
5098 18350	5098	31162	0.98	2.0E-09	P24623	SWISSPROT	IRFAN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
6921 19498	6921	32107	0.81	2.0E-09	AL004062.1	EST_HUMAN	h00406.v1 NCL CGAP_Luc2 Homo sapiens cDNA, clone IMAGE31961/20 3' similar to contains MER18.0
6920 19499	6920	32107	0.82	2.0E-09	AL163246.2	NT	h00406.v1 NCL CGAP_Luc2 Homo sapiens cDNA, clone IMAGE31961/20 3' similar to contains MER18.0
7097 20293	7097	32107	0.88	2.0E-09	AA357407.1	EST_HUMAN	h00406.v1 NCL CGAP_Luc2 Homo sapiens cDNA, clone IMAGE31961/20 3' similar to contains MER18.0
7695 20732	7695	34085	6.75	2.0E-09	AA467430.1	EST_HUMAN	h00406.v1 NCL CGAP_Luc2 Homo sapiens cDNA, clone IMAGE31961/20 3' similar to contains MER18.0
7947 20809	7947	34181	0.84	2.0E-09	W62894.1	EST_HUMAN	h00406.v1 NCL CGAP_Luc2 Homo sapiens cDNA, clone IMAGE31961/20 3' similar to contains MER18.0
8269 21174	8269	34950	0.46	2.0E-09	AI3732.1	EST_HUMAN	h00406.v1 NCL CGAP_Luc2 Homo sapiens cDNA, clone IMAGE31961/20 3' similar to contains MER18.0
8347 21262	8347	34950	0.83	2.0E-09	AA1862126.1	EST_HUMAN	h00406.v1 NCL CGAP_Luc2 Homo sapiens cDNA, clone IMAGE31961/20 3' similar to contains MER18.0
9271 22199	9271	35557	1.27	2.0E-09	AA27735.1	NT	h00406.v1 NCL CGAP_Luc2 Homo sapiens cDNA, clone IMAGE31961/20 3' similar to contains MER18.0
11712 22814	11712	35950	1.87	2.0E-09	AL163246.2	NT	h00406.v1 NCL CGAP_Luc2 Homo sapiens cDNA, clone IMAGE31961/20 3' similar to contains MER18.0
12701 18422	12701	35950	15.23	2.0E-09	X16914.1	NT	h00406.v1 NCL CGAP_Luc2 Homo sapiens cDNA, clone IMAGE31961/20 3' similar to contains MER18.0
12820 29937	12820	3422076.1	1.74	2.0E-09	AA22076.1	EST_HUMAN	h00406.v1 NCL CGAP_Luc2 Homo sapiens cDNA, clone IMAGE31961/20 3' similar to contains MER18.0

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (E-Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10221	14071		1.95	1.0E-09	W719152.1	EST_HUMAN	zfxD3.61 Soares, test_Hort_NHH16W Homo sapiens cDNA clone IMAGE:346833 similar to gh1.02933 CCAAT-box-binding transcription factor (CBTF) mRNA
11391	14171	27115	1.61	1.0E-09	5031024.NT	EST_HUMAN	Homo sapiens COXAT-box-binding transcription factor (CBTF) mRNA
11391	14171	27116	1.51	1.0E-09	5031024.NT	EST_HUMAN	Homo sapiens COXAT-box-binding transcription factor (CBTF) mRNA
1698	14988		1.91	1.0E-09	AJ290441.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21c22, segment 1/3
23525	15526		1.25	1.0E-09	AJ393066.1	EST_HUMAN	gcy4E1.1X1 NOLCGAP_31005 Homo sapiens cDNA clone IMAGE:20108133 similar to contains MER12.02 MER12 (negative element)
23521	15984	28683	1.74	1.0E-09	U00017.1	NT	Homo sapiens basic transcription factor 2 p-4 (352p-4) gene, partial cds, neuronal apoptosis inhibitory protein (nup) and survival motor neuron protein (smn) genes, complete cds
2968	18020	28517	2.04	1.0E-09	M26968.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPB1) mRNA, complete cds
2968	18020	28518	2.04	1.0E-09	M26968.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPB1) mRNA, complete cds
3043	19136	22032	0.85	1.0E-09	BE035440.1	EST_HUMAN	htf00600F1 NH_P00C_110 Homo sapiens cDNA clone IMAGE:3445177.5
47914	17913		0.65	1.0E-09	AY116297.1	EST_HUMAN	htf00603.1 Soares, pnc1, gland_N34-PG Homo sapiens cDNA clone IMAGE:414029.3 similar to contains Au repetitive element contains element1 MER32 (negative element)
6693	18768	31060	1.1	1.0E-09	AL163263.2	NT	Homo sapiens chromosome 21 segment H52T0083
6043	19102	32235	1.35	1.0E-09	U07990.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
6394	19433	32000	3.04	1.0E-09	D37094.1	SWISSPROT	CRUMPORZOITIE PROTEIN PRECURSOR (CS)
8529	21294	34498	0.95	1.0E-09	AY1726945.1	EST_HUMAN	AY1726945 HTC Homo sapiens cDNA clone HTCC01607.5
8633	21801	35290	0.65	1.0E-09	N688474.1	EST_HUMAN	wt68003.1 Soares, NFL_21_GBC_S31 Homo sapiens cDNA clone IMAGE:3530481.3 similar to contains MERCA11 MERCA3 repetitive element
10051	23689		2.91	1.0E-09	AL163263.2	NT	Homo sapiens chromosome 21 segment H52T0083
12196	26303	33045	1.85	1.0E-09	AL163263.2	NT	Homo sapiens chromosome 21 segment H52T0083
12670	28307	31481	1.52	1.0E-09	U114121.NT	EST_HUMAN	Homo sapiens cDNA clone IMAGE:347158.3
12749	29070	32674	1.61	1.0E-09	U73366.1	EST_HUMAN	h91012A15 Homo sapiens cDNA clone IMAGE:347158.3
13394	32682		2.12	1.0E-09	U250225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete, alternatively spliced
13356	14369	27919	1.0	9.0E-10	AY1967140.1	EST_HUMAN	h91012A15 Homo sapiens cDNA clone IMAGE:347158.3
2851	15936	28641	5.32	9.0E-10	AB170071.1	EST_HUMAN	h91012A15 Homo sapiens cDNA clone IMAGE:347158.3
7147	20235	33507	4.51	9.0E-10	U49392.1	EST_HUMAN	h91012A15 Homo sapiens cDNA clone IMAGE:347158.3
3391	19434	29337	0.83	9.0E-10	U49392.1	EST_HUMAN	h91012A15 Homo sapiens cDNA clone IMAGE:347158.3
43927	17311		4.83	9.0E-10	U437683.1	EST_HUMAN	h91012A15 Homo sapiens cDNA clone IMAGE:347158.3

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10471	23359		3.22	8.0E-10	U0309.2	NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
726	13763	26707	17.98	7.0E-10	T706226	NT	Homo sapiens TPA inducible protein (LOC1186), mRNA
726	13763	26709	17.98	7.0E-10	T706226	NT	Homo sapiens TPA inducible protein (LOC1186), mRNA
1645	14670	27640	2.31	7.0E-10	Q13342	SWISSPROT	LTP100 PROTEIN (LYMPHOD-RESTRICTED HOMOLOG OF SP100)
2694	15562		20.7	7.0E-10	P09547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3137	16167	26076	2.85	7.0E-10	XQ0366.1	NT	H. sapiens DHFR gene, exon 3
8426	16473	32647	4.26	7.0E-10	AA344220.1	EST_HUMAN	EST161247 Gall bladder II Homo sapiens cDNA 5' end
7817	20746	34051	1.39	7.0E-10	P352463.1	EST_HUMAN	LS3-H1019-110700-269-012 H1019 Homo sapiens cDNA
8105	21017		1.81	7.0E-10	P352463.1	EST_HUMAN	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8554	21485	34525	1.44	7.0E-10	A029701.2	SWISSPROT	Homo sapiens preactin-1 gene, exons 1 and 2
8954	21485	34526	1.44	7.0E-10	A029701.2	NT	Homo sapiens preactin-1 gene, exons 1 and 2
12095	24628	38430	1.82	7.0E-10	AW178709.1	EST_HUMAN	h012902.x1 NCL_CGAP_H204 Homo sapiens cDNA clone IMAGE:3037202 3' similar to contains AU repetitive element/contains MER1 3' MER1 repetitive element 1
938	13690	26932	2.8	6.0E-10	AJ40877.1	NT	Homo sapiens ASOL3 gene, CEGP1 gene, C1orf14 gene, C1orf16 gene and C1orf17 gene
2720	19719	28718	1.06	8.0E-10	AI40877.1	EST_HUMAN	h05007.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2096021 3'
4603	17614	30475	0.68	8.0E-10	Q02817	SWISSPROT	MUCH2 PRECURSOR (INTESTINAL MUCIN 2)
4652	17694		3.3	8.0E-10	AY185719.1	EST_HUMAN	RC3-C1025-031099-012-012 C10254 Homo sapiens cDNA
9042	22270	35632	1.03	9.0E-10	P33730	SWISSPROT	IC-SELECTIN PRECURSOR (ENDOHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
9042	22270	35633	1.03	9.0E-10	P33730	SWISSPROT	LEUCOCYTE-ENDOHELIAL CELL ADHESION MOLECULE 2 (LECAM2) (CD62E)
10100	20451	36453	0.7	8.0E-10	P30730	SWISSPROT	SELECTIN PRECURSOR (ENDOHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
799	13942		6.7	8.0E-10	AI40804.1	EST_HUMAN	INTER-OEPININ PRECURSOR (INTEROININASE)
7709	20338		1.39	8.0E-10	AF030116.1	EST_HUMAN	DKEZ424N19.11 AS1 (cDNA from fibro) Homo sapiens cDNA clone DKEZ424N19.1 5'
10095	22641	36371	2.15	8.0E-10	P34678	SWISSPROT	810210261 NH MG-27 (cDNA from fibro) Homo sapiens cDNA clone IMAGE:242413 5'
10095	22641	36372	2.15	8.0E-10	P34678	SWISSPROT	HYPOHEMICAL 67.9 KD PROTEIN Zyx68.3 IN CHROMOSOME II
115	13223		1.09	4.0E-10	AI21063.1	EST_HUMAN	g000001.1 Homo sapiens, subfamily 2, 20kbp/10kbp Homo sapiens cDNA clone IMAGE:1769048 3' similar to contains LTR1.82.1 TR8 repetitive element
2812	19530	28028	1.34	4.0E-10	AW54709.1	EST_HUMAN	h05003.x1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:2069444 3' similar to contains ALU repetitive element
2010	15038	28603	7.51	4.0E-10	AI103303.2	NT	Homo sapiens chromosome 21 segment H21C103
7540	20476	33767	18.76	4.0E-10	AI224696.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) gene, complete cds

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Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10026	23811	37239	0.94	4.0E-10	AI067945.1	EST_HUMAN	23811.11 Stanley Frontal SV 20 Homo sapiens cDNA clone IMAGE:2055693
549	13621	28534	1.42	3.0E-10	N09113.1	EST_HUMAN	13621.01 Homo sapiens intron 21 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
10041	14412		5.1	3.0E-10	AY002159.1	NT	14411.11 Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
4452	17658	30524	1.06	3.0E-10	AI182303.2	NT	Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
4452	17658	30526	1.06	3.0E-10	AI182303.2	NT	Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
5540	17615	31619	0.82	3.0E-10	N01019.1	EST_HUMAN	17615.01 Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
6444	19490	32697	1.99	3.0E-10	P23300	SWISSPROT	19490.01 Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
6609	19659	32834	1.86	3.0E-10	B232970.1	EST_HUMAN	19659.01 Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
8228	21133	34463	1.71	3.0E-10	AY743021	EST_HUMAN	AY743021 CB Homo sapiens cDNA clone CBFBG008 5'
8228	21133	34464	1.71	3.0E-10	AY743021	EST_HUMAN	AY743021 CB Homo sapiens cDNA clone CBFBG008 5'
9289	22217	35579	1.21	3.0E-10	H07208.1	EST_HUMAN	9289.01 Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
6902	22528	35894	1.72	3.0E-10	AY560731.1	EST_HUMAN	6902.01 Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
6902	22528	35895	1.72	3.0E-10	AY560731.1	EST_HUMAN	6902.01 Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
8319	22794		0.86	3.0E-10	AF029503.1	NT	Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
10041	23826		1.4	3.0E-10	T6951.1	EST_HUMAN	10041.01 Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
11005	23849		1.37	3.0E-10	AA76924.1	EST_HUMAN	11005.01 Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
1271	25494	31768	2.23	3.0E-10	BE179517.1	EST_HUMAN	1271.01 Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
37	13103	20042	1.43	2.0E-10	P49908	SWISSPROT	37.01 Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
37	13103	20043	1.43	2.0E-10	P49908	SWISSPROT	37.01 Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
1915	14638		2.21	2.0E-10	U00017.1	NT	1915.01 Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
3028	10089		0.85	2.0E-10	BF67047.1	EST_HUMAN	3028.01 Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
5392	18344	31189	1.82	2.0E-10	P11227	SWISSPROT	5392.01 Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
5914	10077		2.81	2.0E-10	Q38640	SWISSPROT	5914.01 Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
6469	18543	32719	1.92	2.0E-10	AF260167.1	NT	6469.01 Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
7772	2702	34001	8.3	2.0E-10	BE751082.1	EST_HUMAN	7772.01 Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
8592	21023	34567	0.7	2.0E-10	P23508	SWISSPROT	8592.01 Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains
8592	21023	34568	0.7	2.0E-10	P23508	SWISSPROT	8592.01 Homo sapiens intron 11 Homo sapiens cDNA clone IMAGE:272063 3' similar to contains

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mod Similar (Top) HL E/ASIE Value	Top HL Accession No.	Top HL Database Source	Top HL Descriptor
9842	2747		1.18	2.0E-10	BF434965.1	EST_HUMAN	767683.1 NCL CGAP_c0rt1 Homo sapiens cDNA clone IMAGE3542303 3' similar to contains L1.13 L1 repetitive element;
1028	14559		1.5	1.0E-10	AW967797.1	EST_HUMAN	MF03400523-26030500-401 SN0383 Homo sapiens cDNA
1628	14559	27622	3.22	1.0E-10	AW967253.1	EST_HUMAN	AY552123 GLO Homo sapiens cDNA clone GLCOX11 3'
2819	19317		1.64	1.0E-10	AW952001.1	EST_HUMAN	U037010225-197109-038-408 CT0228 Homo sapiens cDNA
3558	16395	29468	0.95	1.0E-10	AW932912.1	EST_HUMAN	U037110003-197109-038-408 CT0228 Homo sapiens cDNA
3800	16337		0.74	1.0E-10	AL041655.1	EST_HUMAN	DK-224544N1317.1 431 (genonym: Ilb25) Homo sapiens cDNA clone DK224544N1317 5'
3873	16337		0.50	1.0E-10	AL041655.1	EST_HUMAN	DK-224544N1317.1 431 (genonym: Ilb25) Homo sapiens cDNA clone DK224544N1317 5'
4101	17126		8.43	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4225	17241	30108	7.39	1.0E-10	U02111.2	NT	Homo sapiens Y28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), discoidal protein L1 (a RPL19a), Cdc2/Cdk5-inhibitor dependent protein kinase 1 (CAK1), creatine transporter (CTR), CDM protein (CDM), edematous/edematous protein >
4225	17241	30109	7.39	1.0E-10	U02111.2	NT	Homo sapiens Y28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), discoidal protein L1 (a RPL19a), Cdc2/Cdk5-inhibitor dependent protein kinase 1 (CAK1), creatine transporter (CTR), CDM protein (CDM), edematous/edematous protein >
4233	17246	30118	2.13	1.0E-10	AE031055.1	NT	CDM protein (CDM), edematous/edematous protein >
4266	17262		2.63	1.0E-10	N300263.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5316	18300		1.02	1.0E-10	AF197746.1	EST_HUMAN	web204.14 Source: NPL_1 GBC_S1 Homo sapiens cDNA clone IMAGE2347615 3' similar to contains
7014	20041	33276	0.43	1.0E-10	AA033235.1	EST_HUMAN	MEK31.11 MEK31 repetitive element;
7130	20334	33598	0.46	1.0E-10	AF003528.1	NT	MEK31.11 MEK31 repetitive element;
7895	20321		0.73	1.0E-10	U00848.4	SWISSPROT	regions
8136	21045	34375	0.95	1.0E-10	U12964.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8816	21746	35504	1.48	1.0E-10	AW409990.1	EST_HUMAN	ALU28934NT28P2 Homo sapiens cDNA clone NT28P209781 5'
9213	22141		1.27	1.0E-10	AF093240.1	EST_HUMAN	IB_044 Fetal brain library Homo sapiens cDNA
10658	23594		8.22	1.0E-10	AA081808.1	EST_HUMAN	emb01610.31 NCL CGAP_Lus Homo sapiens cDNA clone IMAGE:1898974 3' similar to contains L1.11 L1 repetitive element;
11352	24270	37712	2.06	1.0E-10	AA039601.1	EST_HUMAN	mc3509.11 Shiga toxin neoplasia NTP9AM 57234 Homo sapiens cDNA clone IMAGE:548314 5'
281	13375	26500	0.82	9.0E-11	BE145903.1	EST_HUMAN	g60903.11 Shiga toxin, liver system, INFLS_S1 Homo sapiens cDNA clone IMAGE:1672601 3'
1161	19129	28134	8.04	9.0E-11	AL134393.1	EST_HUMAN	IL24H10203-197109-038-408 CT0228 Homo sapiens cDNA
2116	19129	28136	9.04	9.0E-11	AL134393.1	EST_HUMAN	DK224544N1317.1 441 (genonym: Ilb2) Homo sapiens cDNA clone DK224544N1317 5'

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mod Similar (Top) hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2638	15827	28823	11.8	4.0E-11	BE265000.1	EST_HUMAN	D0750731F1 NH ₂ MGCC_71 Homo sapiens cDNA clone IMAGE300526 6
3010	15502	29566	1.57	4.0E-11	AL16343.7	NT	Homo sapiens chromosome 21 segment HS21C047
4731	17736	31968	0.86	4.0E-11	AL144966.1	EST_HUMAN	HUMSP10709 Homo brain cDNA Homo sapiens cDNA clone 04g
6750	19764	32597	2.07	4.0E-11	P23066	SWISSPROT	PRE-RNA SPLICING FACTOR RNA HELICASE PRP2
7345	23341	35007	1.10	4.0E-11	AA442930.1	EST_HUMAN	G2691071 Soares, Iselle, NHT Homo sapiens cDNA clone IMAGE779093 6 similar to TR 01465620 G106520 PHOTONOME RECEPTOR VN4.1 Homo sapiens macrophage, Iselle A, lysosome (MAMBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBC23) genes, complete cds
7707	22637		4.08	4.0E-11	A1524668.1	NT	PC-141702-121030415-405 HT10253 Homo sapiens cDNA
9631	22836		1.91	4.0E-11	AF124423.1	EST_HUMAN	PC-141702-121030415-405 HT10253 Homo sapiens cDNA
10156	23079	36479	1.07	4.0E-11	A1639793.1	EST_HUMAN	SE30395 NC_100472_2 Homo sapiens cDNA clone IMAGE210830 3 similar to WIP-ZK583.1
12782	26419	31701	4.36	4.0E-11	U1545732.1	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
16101	34461	27593	0.92	3.0E-11	A1516933.1	EST_HUMAN	SH3 domain expressed in non-neuronic cells 2, protein (NU23B) (Nm23)
2643	16556		0.22	3.0E-11	A1516933.1	EST_HUMAN	SH3 domain expressed in non-neuronic cells 2, protein (NU23B) (Nm23)
4374	17986		1.42	3.0E-11	AA309243.1	EST_HUMAN	SH3 domain expressed in non-neuronic cells 2, protein (NU23B) (Nm23)
896	14037	20980	1.31	2.0E-11	A1159052.1	EST_HUMAN	SH3 domain expressed in non-neuronic cells 2, protein (NU23B) (Nm23)
1213	12421	27193	4.27	2.0E-11	D24907.1	EST_HUMAN	SH3 domain expressed in non-neuronic cells 2, protein (NU23B) (Nm23)
1213	12421	27194	4.27	2.0E-11	D24907.1	EST_HUMAN	SH3 domain expressed in non-neuronic cells 2, protein (NU23B) (Nm23)
1636	14036	27628	3	2.0E-11	U17432.1	NT	SH3 domain expressed in non-neuronic cells 2, protein (NU23B) (Nm23)
1538	14266	27629	3	2.0E-11	U17432.1	NT	SH3 domain expressed in non-neuronic cells 2, protein (NU23B) (Nm23)
2815	15504	28802	1.26	2.0E-11	A1437673.1	NT	SH3 domain expressed in non-neuronic cells 2, protein (NU23B) (Nm23)
3201	10288	28812	8.71	2.0E-11	P170303	SWISSPROT	SH3 domain expressed in non-neuronic cells 2, protein (NU23B) (Nm23)
3731	19415	28816	0.8	2.0E-11	A1478717.1	EST_HUMAN	SH3 domain expressed in non-neuronic cells 2, protein (NU23B) (Nm23)
4533	17521		0.82	2.0E-11	BE005337.1	EST_HUMAN	SH3 domain expressed in non-neuronic cells 2, protein (NU23B) (Nm23)
4716	17721		0.73	2.0E-11	BE005337.2	EST_HUMAN	SH3 domain expressed in non-neuronic cells 2, protein (NU23B) (Nm23)
5125	18121	30963	1.02	2.0E-11	AL162792.2	NT	SH3 domain expressed in non-neuronic cells 2, protein (NU23B) (Nm23)
5125	18121	30963	1.02	2.0E-11	AL162792.2	NT	SH3 domain expressed in non-neuronic cells 2, protein (NU23B) (Nm23)
8195	31002		2.36	2.0E-11	AA307331.1	EST_HUMAN	SH3 domain expressed in non-neuronic cells 2, protein (NU23B) (Nm23)
8376	19424	32960	1.28	2.0E-11	A16747693.1	EST_HUMAN	SH3 domain expressed in non-neuronic cells 2, protein (NU23B) (Nm23)
8376	19424	32960	1.28	2.0E-11	A16747693.1	EST_HUMAN	SH3 domain expressed in non-neuronic cells 2, protein (NU23B) (Nm23)

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Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4723	17739	30500	0.75	4.0E-12	A189564.1	EST_HUMAN	TCORP5.1 NC1 CGAP L244 Homo sapiens cDNA clone IMAGE:270743.3 similar to TRC13539 Q13539
8007	20590		0.83	4.0E-12	BF44140.1	EST_HUMAN	MARNER TRANSCRIPTIONAL REPRESSOR 1 (MARNER1) HOMO SAPIENS cDNA clone IMAGE:336877.3 similar to contains MIER7.02
8816	21746		3.74	4.0E-12	AF103607.1	NT	Homo sapiens S164 gene, perial cdx, PS and hypochloral protein genes, complete cds, and S.71 gene, perial cdx
8245	22173	35527	0.95	4.0E-12	AB042815.1	NT	Box locus M122 mRNA for mitochondrial carrier homolog 2, complete cds
11521	24431	37869	4.88	4.0E-12	A122645.1	NT	Homo sapiens 559 kb contig between AML1 and CBR1 on chromosome 2, q22, segment 3.3
639	13700	26006	2.95	3.0E-12	AF134893.1	EST_HUMAN	Hd1301.v1 Source_NFL_I_QBC_S11 Homo sapiens cDNA clone IMAGE:200377.3 similar to TRC14517
639	13700	26007	2.95	3.0E-12	AF134893.1	EST_HUMAN	Hd1301.v1 Source_NFL_I_QBC_S11 Homo sapiens cDNA clone IMAGE:200377.3 similar to TRC14517
8315	19399	31151	0.72	3.0E-12	AF162968.1	NT	Homo sapiens chromosome 21 segment HS21C083
8317	19713	31814	1.35	3.0E-12	AF111688.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds, and unknown genes
7371	20365	33634	0.47	3.0E-12	BEE14962.1	EST_HUMAN	RC1-H10256-200300-017-c09 HT0256 Homo sapiens cDNA
7629	20798		0.80	3.0E-12	AB042297.1	NT	Homo sapiens P15 gene for 6-phydroxyhydroxyphenyl synthase, complete cds
8221	21128		0.45	3.0E-12	AF184523.1	EST_HUMAN	RC3-OT0255-09109-011-H02 Q10255 Homo sapiens cDNA
9551	22577	35546	0.73	3.0E-12	OS5453	SWISSPROT	SERINE PROTEASE HEPNIN
11039	24030	37474	3.17	3.0E-12	U97972.1	NT	Human prolactin specific antigen gene, 3' flanking region
11060	24030	37475	3.17	3.0E-12	U97972.1	NT	Human prolactin specific antigen gene, 3' flanking region
10880	14710	27872	1.83	2.0E-12	AF182131.1	EST_HUMAN	ILCUM0071-120400-095-405 UN0071 Homo sapiens cDNA
3527	10325	29409	0.83	2.0E-12	6754495	NT	Male muscular keratin-associated protein C2 (Kifc2-2), mRNA
4208	17225	30092	1.22	2.0E-12	J01844.1	NT	Ref. USA small nuclear RNA
4208	17225	30093	1.22	2.0E-12	J01844.1	NT	Ref. USA small nuclear RNA
4828	17357	30651	2.47	2.0E-12	BC05906.1	EST_HUMAN	CMR310261-031165-067-063 B10261 Homo sapiens cDNA
5006	18034	30661	0.85	2.0E-12	U07036	SWISSPROT	TRK15 PROTEIN (TRK PROTEIN 15)
5006	18034	30662	0.85	2.0E-12	U07036	SWISSPROT	TRK15 PROTEIN (TRK PROTEIN 15)
5400	18512	31235	0.91	2.0E-12	J011989	SWISSPROT	RETINOIC-ACID-INDUCED POLY (P) PROTEIN (CONTAINS REVERSE TRANSCRIPTASE);
7536	20178	33765	3.21	2.0E-12	U09187.1	EST_HUMAN	EST109048 IMAGE
7536	20178	33766	3.21	2.0E-12	U09187.1	EST_HUMAN	EST109048 IMAGE
7700	20032	33205	1.46	2.0E-12	BE170051.1	EST_HUMAN	MR0-110569-200400-015-c04 HT0569 Homo sapiens cDNA clone HBBA13.6 and
7590	20892		0.99	2.0E-12	AF184298.1	EST_HUMAN	MR0-110569-200400-015-c04 HT0569 Homo sapiens cDNA
8110	21022	34248	2.4	2.0E-12	11422226	NT	MR0-110569-200400-015-c04 HT0569 Homo sapiens cDNA

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9285	22213	35571	0.55	2.0E-12	U14973	SWISSPROT	POLY(ADP-RIBOSE) POLY(ADP-RIBOSE) TRANSFERASE (PROTEIN) DP
9448	22553		1.26	2.0E-12	AF105864.1	NT	ACETYL GALACTOSAMINYL TRANSFERASE (UDP-GALACTOSE 4-EPIMERASE)
10491	20378		1.26	2.0E-12	BE105864.1	EST_HUMAN	ACETYL GALACTOSAMINYL TRANSFERASE (UDP-GALACTOSE 4-EPIMERASE)
10994	20878	37208	0.86	2.0E-12	A1834130.1	EST_HUMAN	Homo sapiens putative BPS syndrome brain protein region protein gene, complete cds
12355	25193		2.32	2.0E-12	A183263.2	NT	MR3-T10447-12020-115-p01 H10487 Homo sapiens cDNA clone IMAGE:181835 5' similar to TR-O13338
127	13232	25145	2.72	1.0E-12	AF162764.1	EST_HUMAN	Homo sapiens chromosome 21 segment H521063
2004	18022		1.26	1.0E-12	A1871726.1	EST_HUMAN	h10406.1 NQ1 CGAP_GUT Homo sapiens cDNA clone IMAGE:2870040 3' similar to contains MERV18.1
3118	19159	26063	0.84	1.0E-12	AF000097.1	NT	Wnt5107.x1 NQ1 CGAP_GUT Homo sapiens cDNA clone IMAGE:2439490 3' similar to contains L1.133 L1
3118	19159	26064	0.84	1.0E-12	AF000097.1	NT	Homo sapiens testis-specific Testis Transcript Y.2 (TTY2) mRNA, partial cds
3943	19971	29953	46.33	1.0E-12	AU132246.1	EST_HUMAN	Homo sapiens testis-specific Testis Transcript Y.2 (TTY2) mRNA, partial cds
3943	19971	29954	46.33	1.0E-12	AU132246.1	EST_HUMAN	AL132248 NT28P3 Homo sapiens cDNA clone NT28P3004070 5'
6194	19250		1.05	1.0E-12	U132248.1	EST_HUMAN	AL132248 NT28P3 Homo sapiens cDNA clone NT28P3004070 5'
6270	19327		1.95	1.0E-12	U132248.1	NT	Homo sapiens adult telomeric telomeric (ATM) gene, complete cds
6394	19442	32310	0.82	1.0E-12	BF42800.1	EST_HUMAN	HYPOPHOSPHATASE 1 (HPP1) HUMAN
6394	19442	32311	0.82	1.0E-12	BF42800.1	EST_HUMAN	EST00008 Scoring_NRL_T_GBC ST Homo sapiens cDNA clone IMAGE:1847980 5'
6811	19844	33054	0.82	1.0E-12	AF123864.1	NT	EST00008 Scoring_NRL_T_GBC ST Homo sapiens cDNA clone IMAGE:1847980 5'
7475	20415	33053	1.19	1.0E-12	AF105864.1	NT	Mus musculus WNT-2 gene, partial cds; putative enolpyruvate-dependent protein and cyclic fibroblast transmembrane
7511	20450	33734	13	1.0E-12	A1248333.1	EST_HUMAN	conductance regulator (CFTR) gene, section 1 of 2 of the complete cds; and unknown gene
7511	20450	33735	13	1.0E-12	A1248333.1	EST_HUMAN	Homo sapiens putative BPS syndrome brain protein region protein gene, complete cds
8038	21937	35341	0.65	1.0E-12	U66032.1	NT	Homo sapiens LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN) contains MER10.1 MER10

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3457	15498		1.0	5.0E-13	AA435723.1	EST_HUMAN	z77412.2 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:728350.3 similar to contains A1u
7232	20203	33417	0.56	5.0E-13	P09693	SWISSPROT	SWISSPROT: A1U022
11294	24214	37063	2.59	5.0E-13	P07213	SWISSPROT	GAP JUNCTION REPAIR PROTEIN (CONNEXIN 39) (CX39)
1800	14611		2.05	4.0E-13	AY137814.1	EST_HUMAN	PK2-110224.2-21094001-111110224 Homo sapiens cDNA
2444	15496		3.04	4.0E-13	AF703029.1	NT	Homo sapiens dyx1c3.3 (GPC3) gene, partial cds and flanking repeat regions
4691	17693		1.15	4.0E-13	AA45024.1	EST_HUMAN	z66407.1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:786459.5
5790	18852	31957	5.23	4.0E-13	BE169131.1	EST_HUMAN	PK4-110526-290200-002-098110520 Homo sapiens cDNA
1572	20508	33766	1.3	4.0E-13	AB037160.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
5056	20699	34265	0.63	4.0E-13	AA431529.1	EST_HUMAN	z67512.1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:782162.5 similar to TRC432763
8192	21069		1.8	4.0E-13	NJ41291.1	EST_HUMAN	Y63905.1 Soares melanocyte 2N8-AM Homo sapiens cDNA clone IMAGE:729350.5 similar to PRA32695
9400	22326	35900	1.27	4.0E-13	AL043510.1	EST_HUMAN	A32995.1 complex identity protein - mouse
10523	23410	36622	4.84	4.0E-13	AL269831.1	EST_HUMAN	DFZF244A0128_11_424 (synonym: Hhes3) Homo sapiens cDNA clone DKFZ:934A0128.5
11608	24515	37865	1.95	4.0E-13	AA43516.1	EST_HUMAN	q1332603.1 NC_CGAP J445 Homo sapiens cDNA clone IMAGE:1869043.5 similar to contains A1u
11618	24518	37866	1.95	4.0E-13	AA43516.1	EST_HUMAN	z178710.21 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:728514.3
12658	26354		5.02	4.0E-13	BE530323.1	EST_HUMAN	h262603.1 NC_CGAP J421 Homo sapiens cDNA clone IMAGE:3274499.5 similar to contains MER311H
191	13269		2.04	3.0E-13	AF005028.1	NT	MER31 repetitive element
600	13643		2.39	3.0E-13	AA433010.1	EST_HUMAN	Homo sapiens X-linked artificial cdc, ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2303	15568	28402	2.22	3.0E-13	AJ27726.1	NT	z63681.1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:79406.5
2601	15603		3.07	3.0E-13	AL163760.2	NT	Homo sapiens X1 pseudautosomal region, segment 22
2713	15707	28702	3.37	3.0E-13	BF37260.2	EST_HUMAN	Homo sapiens chromosome 21 segment H21C010
3290	19278		2.57	3.0E-13	AA748844.1	EST_HUMAN	CH3-F10103-140100-942408 F10100 Homo sapiens cDNA
4004	19278	38472	6.13	3.0E-13	AA433101.1	EST_HUMAN	q618602.1 NC_CGAP J465 Homo sapiens cDNA clone IMAGE:1324055.9
4226	19215	31061	0.66	3.0E-13	BF37260.2	EST_HUMAN	z63681.1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:79406.5
5730	18603	31695	0.78	3.0E-13	AA4134017.1	EST_HUMAN	CH3-F10103-140100-942408 F10100 Homo sapiens cDNA
5730	18603	31697	0.78	3.0E-13	AA4134017.1	EST_HUMAN	z63681.1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:565316.5 similar to
							z63681.1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:565316.5 similar to
							contains THRLE THR, separate domain;

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6228	16278	32432	0.71	3.0E-13	AI006099.1	EST_HUMAN	W68492.1 NT COLP Br-25 Homo sapiens cDNA clone IMAGE:255890.3 similar to TR-075-59 O75159 (MAG44) PROTEIN, 1
8403	21384	34733	7.8	3.0E-13	U02111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), atrodoxylolipoly protein, >
8654	21585	34620	0.78	3.0E-13	AAS52487.1	EST_HUMAN	EST10487 Activated T-cells XX Homo sapiens cDNA 5 and similar to similar to active protease P100, Ras reactive factor
8654	21585	34021	0.78	3.0E-13	AAS32487.1	EST_HUMAN	EST10487 Activated T-cells XX Homo sapiens cDNA 5 and similar to similar to active protease P100, Ras reactive factor
10604	22680	37010	0.7	3.0E-13	AV7635487.1	EST_HUMAN	RC2-DT0007-1.10100-014-p10 D10007 Homo sapiens cDNA
11119	24C49		3.46	3.0E-13	AI024785.1	EST_HUMAN	HAC0355 Human fetal liver cDNA library Homo sapiens cDNA
11482	24396	37845	3.05	3.0E-13	BE03509.1	EST_HUMAN	CD4-B10281-031169-087-403 B10281 Homo sapiens cDNA
12028	24670	38373	1.87	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C043
160	13200	26178	2.22	2.0E-13	U02111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), atrodoxylolipoly protein, >
258	13305	26271	1	2.0E-13	U23838.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1287	14330	27276	5.89	2.0E-13	AF238710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exon 1 through 1' and complete cds
3049	16101	29004	0.79	2.0E-13	86224119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3049	16101	29005	0.79	2.0E-13	86224119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3325	16371	29272	1.02	2.0E-13	BF431806.1	EST_HUMAN	h427605.L1 Source NSF FR 9W OT FA P 3T Homo sapiens cDNA clone IMAGE 3'
3604	16601	26505	1.04	2.0E-13	AF106067.1	NT	Homo sapiens S164 gene, partial cds; YSI and hypothetical protein genes, complete cds; and S171 gene, partial cds
4203	17221		1.7	2.0E-13	AL162782	NT	Homo sapiens chromosome 21 segment HS21C078
5378	19360	31169	1.02	2.0E-13	M06318.1	NT	Homo sapiens all genes
5378	19360	31200	1.02	2.0E-13	M06318.1	NT	Homo sapiens all genes
6302	16411	32516	4.77	2.0E-13	Q08382	SWISSPROT	GELL SURFACE GLYCOPROTEIN 1 PRO-CURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN B) (S-LAYER PROTEIN B)
6403	16494		0.44	2.0E-13	X19471.1	NT	Scorpaenidae 12 mRNA for ribosomal protein S12
7125	20103	33362	0.88	2.0E-13	X18121.1	NT	Human PRL gene for beta-type 5 and 6 phosphatases (EC 2.7.1.1) exon 2
7407	20108	33340	0.93	2.0E-13	U054072.1	NT	Homo sapiens Nucleophosmin 1 (NUP133) mRNA
7407	20108	33341	0.93	2.0E-13	U054072.1	NT	Homo sapiens Nucleophosmin 1 (NUP133) mRNA
10907	20982	37240	1.25	2.0E-13	5001805	NT	Homo sapiens mab-21 (C. elegans) like 1 (MAB21L1) mRNA

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
12403	26208		28.46	2.0E-13	U1602185.1	EST_HUMAN	CHD10001-10000-274-41 1 N10001 Homo sapiens cDNA
311	13083	26320	3.94	1.0E-13	S117263.1	NT	FGF-10-related protein 1 (human, 2009; Genbank, 5/2/01, segment 2 of 2)
873	13065	26012	6.04	1.0E-13	AJ007973.1	NT	Homo sapiens LMO238 gene
1364	14326	27350	1.76	1.0E-13	X87344.1	NT	Homo sapiens DNA, DME, HLA-Z1, PP2, LIP2, 1AP1, LIP7, TAP2, DOB, DOB2 and FIN08, 6, 13 and 14 gene
2035	16002	28050	2.8	1.0E-13	AA72954.1	EST_HUMAN	nc21902.s1 NCL CGAP CG50 Homo sapiens cDNA clone IMAGE:1241193 3' similar to contains 1HR29
4704	17706	30672	1.95	1.0E-13	BP340682.1	EST_HUMAN	THR1 repetitive element
6713	18746	32953	0.47	1.0E-13	AA080732.1	EST_HUMAN	00208000F1 NCL CGAP Bn641 Homo sapiens cDNA clone IMAGE:4163659 5'
8489	21420	34757	1.03	1.0E-13	AA577812.1	EST_HUMAN	Y1333.seq F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
8489	21420	34758	1.03	1.0E-13	AA577812.1	EST_HUMAN	nc24001.s1 NCL CGAP Gact1 Homo sapiens cDNA clone IMAGE:1094001 3' similar to contains Alu
10552	23478		0.03	1.0E-13	O15481	SWISSPROT	repetitive element; contains element MER24 repetitive element;
10790	23579	37100	0.57	1.0E-13	AF300701.1	NT	Melanoma-associated antigen B4 (IMAGE-84 ANTIGEN)
11818	24739	38230	11.71	1.0E-13	BF016561.1	EST_HUMAN	746y10.x1 Soares, NSF_F8_SW_OT_PA_P_311 Homo sapiens cDNA clone IMAGE:3524443 3' similar to
12252	25103		1.6	1.0E-13	AV710377.1	EST_HUMAN	contains MER29 b2 MER29 repetitive element;
12892	25462		2.87	1.0E-13	AJ277561.1	NT	AV710377 DCB Homo sapiens cDNA clone DCBAIE03 5'
333	13440	20353	2.13	9.0E-14	AA761169.1	EST_HUMAN	Homo sapiens Xq pseudofunctional region; segment 1/2
354	13441	26354	2.16	9.0E-14	AA761169.1	EST_HUMAN	g29401.s1 Soares, testis, NNT Homo sapiens cDNA clone 1361232 3' similar to contains MER19.11 MER19
2523	15524		6.16	9.0E-14	AV861667.1	EST_HUMAN	g29401.s1 Soares, testis, NNT Homo sapiens cDNA clone 1361232 3' similar to contains MER19.11 MER19
2632	15530	28624	1.41	9.0E-14	AJ133127.1	NT	RC4-C10322-000100-015-405 C10322 Homo sapiens cDNA
2632	15530	28625	1.41	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2632	15530	28626	1.41	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2632	15530	28627	1.41	9.0E-14	AJ133127.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
3157	15207	29057	6.48	9.0E-14	AV613398.1	EST_HUMAN	nc24001.s1 NCL CGAP UH1 Homo sapiens cDNA clone IMAGE:2707633 3'
3284	13140	20353	1.01	9.0E-14	AA761169.1	EST_HUMAN	g29401.s1 Soares, testis, NNT Homo sapiens cDNA clone 1361232 3' similar to contains MER19.11 MER19
3652	19381		6.91	9.0E-14	DT43577.1	NT	repetitive element;
4670	17070	30734	1.84	9.0E-14	AJ002113.1	NT	Human DNA, SINE repetitive element
3558	19383		1.27	9.0E-14	BE436263.1	EST_HUMAN	nc24001.s1 NCL CGAP UH1 Homo sapiens cDNA clone IMAGE:2707633 3'
4639	17059		4.12	8.0E-14	AT62681.1	EST_HUMAN	AF746031 Soares placenta N234 Homo sapiens cDNA clone IMAGE:144786 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Ht BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9080	21338	34674	50.26	8.0E-14	X69211.1	NT	H sapiens DNA for endogenous ribosomal like element
10780	21339	34675	3.47	8.0E-14	X721011.1	EST_HUMAN	AF170411.1 Spliceosome protein 1977253 Homo sapiens cDNA clone IMAGE:556070.3
11835	24755	34676	3.47	8.0E-14	BE056558.1	EST_HUMAN	U03370525.258102041.401 BT02559 Homo sapiens cDNA clone IMAGE:556070.3
12041	25250	31822	3.19	8.0E-14	A138118.1	EST_HUMAN	H sapiens cDNA
1652	15908		6.71	7.0E-14	AW15973.1	EST_HUMAN	AF041031.1 NCI CGAP CGAP Homo sapiens cDNA clone IMAGE:232814.3
2476	22404		0.14	7.0E-14	AL103285.2	NT	AF041031.1 NCI CGAP CGAP Homo sapiens cDNA clone IMAGE:232814.3 similar to contains MER10.2 MER10 repetitive element
368	13472	20590	6.8	6.0E-14	AF020503.1	NT	Homo sapiens chromosome 21 segment HS21C085
10337	23226	36641	2.86	6.0E-14	AF020503.1	NT	Homo sapiens FRAB3 common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
10337	23226	36642	2.86	6.0E-14	AF020503.1	NT	Homo sapiens FRAB3 common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
841	13702	28809	6.79	5.0E-14	Q6120	SWISSPROT	Homo sapiens FRAB3 common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
9180	18178	31024	1.07	5.0E-14	AW073791.1	EST_HUMAN	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
9723	19798	31893	6.15	5.0E-14	P08547	SWISSPROT	AF038051.1 NCI CGAP CGAP Homo sapiens cDNA clone IMAGE:2575185.3 similar to contains L112.L1 repetitive element
1190	15993		1.84	4.0E-14	P04628	SWISSPROT	AF038051.1 NCI CGAP CGAP Homo sapiens cDNA clone IMAGE:2575185.3 similar to contains L112.L1 repetitive element
1000	14921	27807	6.26	4.0E-14	AA007975.1	NT	LINE-7 REVERSE TRANSCRIPTASE HOMOLOG
3815	18846		0.82	4.0E-14	AA004802.1	EST_HUMAN	Homo sapiens LGH4298 gene
4304	17407	30273	1.05	4.0E-14	N46328.1	EST_HUMAN	AF07605.1 Soares progenitor, uterus, NS-IPU Homo sapiens cDNA clone IMAGE:497529.5
8536	21467		0.73	4.0E-14	X87344.1	NT	AF07605.1 Soares, multiple, telodome, 2NSHNSP Homo sapiens cDNA clone IMAGE:279190.3 similar to contains L1.12.L1 repetitive element
12948	23659		6.5	4.0E-14	AI86224.1	EST_HUMAN	H sapiens DNA, DM8, HLA-21, PP2, LM2, YAP1, LM7, TAP2, DOB, DOB2 and RING9, 9, 13 and 14 genes
877	14128	28570	1.22	3.0E-14	X05460.1	NT	AF07605.1 Soares, multiple, telodome, 2NSHNSP Homo sapiens cDNA clone IMAGE:279190.3 similar to contains L1.12.L1 repetitive element
5036	18033	30890	0.82	3.0E-14	AW125554.1	EST_HUMAN	AF07605.1 Soares, multiple, telodome, 2NSHNSP Homo sapiens cDNA clone IMAGE:279190.3 similar to contains L1.12.L1 repetitive element
7038	20064	33297	1.03	3.0E-14	AA020766.1	EST_HUMAN	AF07605.1 Soares, multiple, telodome, 2NSHNSP Homo sapiens cDNA clone IMAGE:279190.3 similar to contains L1.12.L1 repetitive element
7038	20064	33298	1.03	3.0E-14	AA020766.1	EST_HUMAN	AF07605.1 Soares, multiple, telodome, 2NSHNSP Homo sapiens cDNA clone IMAGE:279190.3 similar to contains L1.12.L1 repetitive element

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top-Hit Accession No.	Top-Hit Database Source	Top-Hit Descriptor
7160	26566		0.96	3.0E-14	AL163249.2	NT	Homo sapiens chromosome 21 segment H821C048
7379	20373	35642	0.98	3.0E-14	U03631.1	EST_HUMAN	EST108951 Homo sapiens cDNA
8845	22273	36635	1.04	3.0E-14	N42163.1	EST_HUMAN	Y73070.1 Saccharomyces cerevisiae cDNA
11684	49333	30860	6.35	3.0E-14	AW26154.1	EST_HUMAN	Y73070.1 Saccharomyces cerevisiae cDNA
12827	30538	26944	2.39	3.0E-14	AL163249.2	NT	Homo sapiens chromosome 21 segment H821C048
411	13264	26404	2.32	2.0E-14	A127176.1	NT	Homo sapiens Xq pseudautosomal region, segment 22
414	13264	26405	2.32	2.0E-14	A127176.1	NT	Homo sapiens Xq pseudautosomal region, segment 22
714	13861	26921	6.69	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment H821C048
2411	18416		1.73	2.0E-14	AW372898.1	EST_HUMAN	RC5-H1037-097289-031-012 H10377 Homo sapiens cDNA
2488	18420		1.22	2.0E-14	AW372898.1	EST_HUMAN	Homo sapiens fibroblast tumor deletion region protein 1 (RTUR1), mRNA
2653	19533	28550	3.65	2.0E-14	AL163249.2	NT	Homo sapiens chromosome 21 segment H821C048
2771	19539		1.43	2.0E-14	BE22452.1	EST_HUMAN	hVdG10.1 NCI CGAP Lu21 Homo sapiens cDNA clone IMAGE3180738 8 similar to contains Alu
6714	19797	31718	0.98	2.0E-14	BF360861.1	EST_HUMAN	replicative element/contains ORF.1 ORF1 repetitive element
5815	19897	31699	0.89	2.0E-14	A131235.1	EST_HUMAN	1478901.1 X2 NCI CGAP_HSC2 Homo sapiens cDNA clone IMAGE2093225 3' similar to contains L1; 13 L1
5622	19899	32708	2.09	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
7210	20210		0.89	2.0E-14	BE00550.1	EST_HUMAN	RC3-BN0072-240200-011-a06 BN0072 Homo sapiens cDNA
7054	20258	33997	1.09	2.0E-14	F64163	SWISSPROT	ZINC-FINGER PROTEIN NURO-D4
7490	20852	34159	20.73	2.0E-14	BE158701.1	EST_HUMAN	L32-H10397-071299-024-D04-H10397 Homo sapiens cDNA
7240	20862	34180	20.73	2.0E-14	BE158701.1	EST_HUMAN	L32-H10397-071299-024-D04-H10397 Homo sapiens cDNA
10428	23317	39795	0.92	2.0E-14	A1916795.1	EST_HUMAN	w38g10.1 NCI CGAP_U1 Homo sapiens cDNA clone IMAGE2492034 3' similar to contains Alu repetitive element
10900	23795	37211	0.61	2.0E-14	AV741648.1	EST_HUMAN	AV741648 CB Homo sapiens cDNA clone CBF-BF04 6'
11219	24145	37590	4.36	2.0E-14	AW139800.1	EST_HUMAN	UHH-BH-sew-a-10-QUL1.1 NCI CGAP_S103 Homo sapiens cDNA clone IMAGE271524 3'
11652	19899	32708	2.09	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
12854	28841		2.34	2.0E-14	AF008191.1	NT	Homo sapiens putative G1 protein (G1G) gene, complete cds
13071	15460		1.86	2.0E-14	7697529	NT	Homo sapiens fibroblast tumor deletion region protein 1 (RTUR1), mRNA
1094	14137	27074	1.15	1.0E-14	AL163249.2	NT	Homo sapiens chromosome 21 segment H821C048
1431	14602	27414	7.47	1.0E-14	AL163249.2	NT	Homo sapiens chromosome 21 segment H821C048
1431	14602	27415	7.47	1.0E-14	AL163249.2	NT	Homo sapiens chromosome X region from human (TUN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
2017	18335	28020	7.34	1.0E-14	L44140.1	NT	

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Probe SEQ ID No.	Exon SEQ ID No.	ORF SEQ ID NO.	Exon Signal	Mod Shift BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2300	15211	28213	4.94	1.0E-14 IL63303.2	NT	Homo sapiens chromosome 21 segment HSZC103	
2303	14437	28437	3.4	1.0E-14 IL63303.1	NT	Homo sapiens chromosome 21 segment HSZC103	
2406	16038	28942	1.58	1.0E-14 P05227	SWISSPROT	HISTONE-RICH PROTEIN PRECURSOR (CLONE PHRP-J)	
3200	16257	29155	5.6	1.0E-14 BQ35227.1	EST_HUMAN	RG2-C70432.3 07090-D13-e09_1 C10432 Homo sapiens cDNA	
3204	16257	29155	5.6	1.0E-14 BQ35227.1	EST_HUMAN	RG2-C70432.3 07090-D13-e09_1 C10432 Homo sapiens cDNA	
3209	16257	29155	5.6	1.0E-14 BQ35227.1	EST_HUMAN	Sg380-12.11 Stragene scRNA brain S11 Homo sapiens cDNA clone IMAGE:571350_3	
3255	16653	29607	2.70	1.0E-14 AF64904.1	EST_HUMAN	Sg380-12.11 Stragene scRNA brain S11 Homo sapiens cDNA clone IMAGE:571350_3	
4585	17564	30432	1.94	1.0E-14 AV219582.1	EST_HUMAN	Bac taurus xenobiotic/metabolism-chaperone fatty acid-CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds	
4902	19062	32208	2.03	1.0E-14 NF126145	NT	Homo sapiens proteasome (mouse)-like 1 [PMOJL], mRNA	
5070	20500	33228	11.73	1.0E-14 I1437150	NT	Homo sapiens promitin (mouse)-like 1 [PMOJL], mRNA	
5070	20500	33227	11.73	1.0E-14 I1437150	NT	Homo sapiens promitin (mouse)-like 1 [PMOJL], mRNA	
1608	14620	27588	1.14	9.0E-15 7427932	NT	Homo sapiens protein tyrosine phosphatases receptor type, T (PTPRT), mRNA	
2185	15187		1.42	9.0E-15 AF496778.1	NT	Homo sapiens transcription factor KHM enhancer 3, JM11 protein, JAM protein, JEA protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 5, and synapophycin genes, complete cds, and 1-type calcium channel alpha	
7617	20541	34143	3.98	9.0E-15 P21416	EST_HUMAN	SWISSPROT GAG POLY(PEPTIDE CONTAINS: CORE PROTEINS P16, P12, P30, P16)	
8595	21628	34870	1.34	9.0E-15 BC033093.1	EST_HUMAN	G04677750F1.NM.MGC_21 Homo sapiens cDNA clone IMAGE:3900156_9	
10302	25825		1.70	9.0E-15 AL1603347.2	NT	Homo sapiens chromosome 21 segment HSZC1047	
13855	13573		0.94	8.0E-15 BE361482.1	EST_HUMAN	BT144693P1.NM.MGC_19 Homo sapiens cDNA clone IMAGE:314203_9	
7545	20483	33772	1.41	7.0E-15 P053527.1	EST_HUMAN	BT144693P1.NM.MGC_19 Homo sapiens cDNA clone IMAGE:3982086_9	
10916	25801		3.03	7.0E-15 AV241958.1	EST_HUMAN	wf74052.1 Source NPL_T_G00_S11 Homo sapiens cDNA clone IMAGE:2700493_3 similar to contains Thr-Leu THR repetitive element:	
12349	25141		2.12	7.0E-15 AV241958.1	EST_HUMAN	253008r1.NM.CCAP_C0341 Homo sapiens cDNA clone IMAGE:701683_5 similar to g01.21634 STENOL	
14201	14700	27013	5.95	5.0E-15 AJ237105.1	NT	CACATransferase PARACADO (HUMAN) contains L1/L11 repeat element,	
6142	16201	32337	1.26	5.0E-15 Q34652.1	NT	Homo sapiens XPA repair endonuclease (human) segment 22	
8142	16201	32338	1.26	5.0E-15 Q34652.1	NT	O rna1 mRNA for yeast homologous protein	
13103	20615	33300	2.70	5.0E-15 AV219582.1	EST_HUMAN	p343112.21 NCBI Sequence NSF F3_9W OT PA_P 311 Homo sapiens cDNA clone IMAGE: 3'	
435	13304	28428	9.56	5.0E-15 IL63308.2	NT	Homo sapiens chromosome 21 segment HSZC1008	
2511	15500	29709	1.6	5.0E-15 BH428.1	NT	Human bivalve hemochromalysin region, haloxen 2k-like protein gene, hereditary haemochromatosis [HLA-H] gene, Rheset gene, and sodium phosphate transporter (NPT3) gene, complete cds	
3559	16559	30677	2.05	5.0E-15 AV219582.1	EST_HUMAN	UHH-BW10-96-p10-U1.1 NCBI CCAP_S049 Homo sapiens cDNA clone IMAGE:2731219_3'	
4050	13117	29003	1.68	4.0E-15 AL1603303.2	NT	Homo sapiens chromosome 21 segment HSZC1003	

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Probe SE ID NO.	Exon SE ID NO.	ORF SEQ ID*NO.	Exon Signal	Mod Similar (Top) Hit BLAST E Value	Top Hit Annotation No.	Top Hit Database Source	Top Hit Description
6423	19470	32644	0.99	2.0E-16	BE632352.1	EST_HUMAN	BT334425IF1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:377289.5
6423	16170	32646	0.99	2.0E-15	BE632352.1	EST_HUMAN	BT334425IF1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:377289.5
7473	20581	33878	2.18	2.0E-16	AJ008717.1	NT	Homo sapiens ASD3 gene, C6orf1 gene, C11orf1 gene, C11orf17 gene
7783	27222	34028	5.1	2.0E-16	W06004.1	EST_HUMAN	277603.at Soares_filed_liver_spleen_TNFSF.51 Homo sapiens cDNA clone IMAGE:460924.3
8334	21298	34571	0.87	2.0E-16	D13347.2	NT	WPF44F4.8 C602227 TRANSPOSASE.1
8493	22783	35783	2.89	2.0E-10	D13447.1	NT	Homo sapiens drosophila 21 segment H5210A7
8622	22848	35918	0.87	2.0E-10	D13447.1	EST_HUMAN	Human DNA, SINE repetitive element
9522	22548	35919	0.87	2.0E-10	D13397758.1	EST_HUMAN	277603.at Soares_filed_liver_spleen_TNFSF.51 Homo sapiens cDNA clone IMAGE:728414.5
9523	22548	35923	0.87	2.0E-10	D13397758.1	EST_HUMAN	277603.at Soares_filed_liver_spleen_TNFSF.51 Homo sapiens cDNA clone IMAGE:728414.5
9599	22841	36234	1.88	2.0E-16	D1377358.1	EST_HUMAN	277603.at Soares_filed_liver_spleen_TNFSF.51 Homo sapiens cDNA clone IMAGE:728414.5
9624	22841	36234	5.05	2.0E-16	D1377358.1	EST_HUMAN	277603.at Soares_filed_liver_spleen_TNFSF.51 Homo sapiens cDNA clone IMAGE:728414.5
11276	24198					NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-9; and partial cds, alternatively spliced
12075	16905	29503	2.6	2.0E-16	F223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-9; and partial cds, alternatively spliced
12075	16905	29509	2.5	2.0E-16	F223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-9; and partial cds, alternatively spliced
2824	19313		3.57	1.0E-16	A1696984.1	EST_HUMAN	W268937.NC1 CGAP_L242 Homo sapiens cDNA clone IMAGE:2270745.5 similar to TRC10359.9/13539.9 MARINER TRANSPOSASE.1
30353	19108	29014	1.18	1.0E-16	BC034384.1	EST_HUMAN	H40C271.NC1 CGAP_OY44 Homo sapiens cDNA clone IMAGE:2399182.5
31065	16235	29130	1.3	1.0E-15	BC034384.1	SWISSPROT	H40C271.NC1 CGAP_OY44 Homo sapiens cDNA clone IMAGE:2399182.5
9372	18344	31194	0.71	1.0E-15	676309.9	NT	W268937.NC1 CGAP_OY44 Homo sapiens cDNA clone IMAGE:2399182.5
9532	16672	32688	1.54	1.0E-15	BE07673.1	EST_HUMAN	ye-B0r0.01 Soares_filed_liver spleen TNFSF.51 Homo sapiens cDNA clone IMAGE:732924.3 similar to containe
7383	20349		1.92	1.0E-15	D07047.1	EST_HUMAN	ye-B0r0.01 Soares_filed_liver spleen TNFSF.51 Homo sapiens cDNA clone IMAGE:732924.3 similar to containe
7390	20349	35324	0.76	1.0E-15	F34367	SWISSPROT	ye-B0r0.01 Soares_filed_liver spleen TNFSF.51 Homo sapiens cDNA clone IMAGE:732924.3 similar to containe
8510	21760	35359	0.86	1.0E-15	A163980.2	NT	ye-B0r0.01 Soares_filed_liver spleen TNFSF.51 Homo sapiens cDNA clone IMAGE:732924.3 similar to containe
8591	21620	35375	5.15	1.0E-15	A2034976.1	EST_HUMAN	ye-B0r0.01 Soares_filed_liver spleen TNFSF.51 Homo sapiens cDNA clone IMAGE:732924.3 similar to containe
8601	21620	35378	0.18	1.0E-15	A2034976.1	EST_HUMAN	ye-B0r0.01 Soares_filed_liver spleen TNFSF.51 Homo sapiens cDNA clone IMAGE:732924.3 similar to containe
8621	21620	35379	0.37	1.0E-15	A2034976.1	EST_HUMAN	ye-B0r0.01 Soares_filed_liver spleen TNFSF.51 Homo sapiens cDNA clone IMAGE:732924.3 similar to containe
8622	21620	35381	0.37	1.0E-15	A2034976.1	EST_HUMAN	ye-B0r0.01 Soares_filed_liver spleen TNFSF.51 Homo sapiens cDNA clone IMAGE:732924.3 similar to containe
9259	22263	36436	1.91	1.0E-15	208478	SWISSPROT	ye-B0r0.01 Soares_filed_liver spleen TNFSF.51 Homo sapiens cDNA clone IMAGE:732924.3 similar to containe

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Single Exon Probes Expressed In Adult Liver

Probe Seq ID Seq ID NC	Exon Seq ID Seq ID NC	ORF Seq ID NO:	Expression Signal	Most Similar (Top) Hit E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
11159	23048	36448	0.98	1.0E-16	A0464653.1	EST_HUMAN	ab37603.1 NC1 CGAP_H4b Homo sapiens cDNA clone IMAGE:1459972.3 similar to contains L1.18 L1 repetitive element;
10129	23418	37651	0.71	3.0E-15	AF044083.1	NT	Homo sapiens major histocompatibility locus class II region
13036	26717	31666	0.74	1.0E-15	A793944.1	EST_HUMAN	131-03.01 NC1 CGAP_Ox23 Homo sapiens cDNA clone IMAGE:227912.3 similar to contains Alu repetitive element;
4431	4431	17442	1.03	9.0E-16	BF04687.1	EST_HUMAN	6921201927 NH_M0C_56 Homo sapiens cDNA clone IMAGE:4277422.9
4625	17631	30405	1.33	8.0E-16	AF00487.1	EST_HUMAN	YAC827121 Stragelung lung (65372)20 Homo sapiens cDNA clone IMAGE:19092.5
11431	24347	37792	1.85	9.0E-16	F06868.1	EST_HUMAN	Homo sapiens out (Ornithine)-like 1 (OCAT displacement protein) (CUT1.1) mRNA
3424	10493	29372	0.73	7.0E-16	U10198.1	NT	HSC23P051 normalized infant brain cDNA Homo sapiens cDNA clone c23005
5600	16939	32087	0.71	7.0E-16	4685120	NT	Homo sapiens PHEX gene
7727	20659	33952	1.44	7.0E-16	008897	SWISSPROT	Homo sapiens chondroline (C-C mol) receptor 3 (C59B) mRNA
7727	20659	33957	1.44	7.0E-16	008897	SWISSPROT	PROTEIN:ARGININE DEMINASE TYPE IV (PEPTIDYLARGININE DEMINASE IV) (PAD-R4)
12964	25798	24039	1.44	7.0E-16	008897	SWISSPROT	PEPTIDYLARGININE DEMINASE TYPE ALPHA
2156	18167	36722	0.98	4.0E-16	AF107261.1	EST_HUMAN	PEPTIDYLARGININE DEMINASE TYPE IV (PAD-R4)
3942	16930	29043	1.06	8.0E-16	AF124960.1	NT	US234722 Homo sapiens cDNA clone IMAGE:1104120.5
2828	28716	29043	1.06	8.0E-16	AF124960.1	NT	US234722 Homo sapiens cDNA clone IMAGE:1104120.5
1936	21073	36336	1.26	5.0E-16	BF177968.1	EST_HUMAN	US234722 Homo sapiens cDNA clone IMAGE:1104120.5
13036	26717	31666	0.74	1.0E-16	A793944.1	EST_HUMAN	US234722 Homo sapiens cDNA clone IMAGE:1104120.5
2402	14557	28410	1.24	4.0E-16	AF107168.1	EST_HUMAN	US234722 Homo sapiens cDNA clone IMAGE:1104120.5
2402	14557	28411	1.43	4.0E-16	AF107168.1	EST_HUMAN	US234722 Homo sapiens cDNA clone IMAGE:1104120.5
3617	16555	29456	0.72	4.0E-16	C10693	SWISSPROT	US234722 Homo sapiens cDNA clone IMAGE:1104120.5
4240	17266	30122	8.21	4.0E-16	BE038765.1	EST_HUMAN	US234722 Homo sapiens cDNA clone IMAGE:1104120.5
4240	17266	30123	8.21	4.0E-16	BE038765.1	EST_HUMAN	US234722 Homo sapiens cDNA clone IMAGE:1104120.5
5263	18063	31023	1.07	4.0E-16	AF107353.1	EST_HUMAN	US234722 Homo sapiens cDNA clone IMAGE:1104120.5
5263	18063	31023	1.07	4.0E-16	AF107353.1	EST_HUMAN	US234722 Homo sapiens cDNA clone IMAGE:1104120.5
8269	18278	31128	1.11	4.0E-16	P06846	SWISSPROT	US234722 Homo sapiens cDNA clone IMAGE:1104120.5
8172	21070	34409	38.21	4.0E-16	AF103264.2	NT	US234722 Homo sapiens cDNA clone IMAGE:1104120.5
9835	22741	361722	0.96	4.0E-16	AF103264.2	NT	US234722 Homo sapiens cDNA clone IMAGE:1104120.5
11698	24572	39048	1.66	4.0E-16	AF107030.1	EST_HUMAN	US234722 Homo sapiens cDNA clone IMAGE:1104120.5
12447	25200	40941	12.86	4.0E-16	C03947.1	EST_HUMAN	US234722 Homo sapiens cDNA clone IMAGE:1104120.5

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Probe SEQ ID No.	Exon SEQ ID No.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12457	26226	31851	1.82	4.0E-16	6012469	NT	Homo sapiens GAB2 associated binder 2 (GAB2GB2), mRNA
1327	13229	26159	1.41	3.0E-16	AF102282.1	EST_HUMAN	455001 v1 Human Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376.5
137	13229	26159	1.41	3.0E-16	AF102282.1	EST_HUMAN	455001 v1 Human Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376.5
498	13559		1.2	3.0E-16	AF104445.1	EST_HUMAN	DKFZ549P07.1T 434 (synonym: Nac3) Homo sapiens cDNA clone DKFZ549P07.1
498	13559		2.08	3.0E-16	AF134445.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1471	14502	27463	1.15	3.0E-16	Q25853	SWISSPROT	ZONADHESIN PRECURSOR
3017	18659	29870	4.45	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) [MA] CONTAINS GLYCOPROTEIN GP220
4008	17635	29825	0.74	3.0E-16	T03168.1	EST_HUMAN	EST109500 Infant Brain, Bonto Source Homo sapiens cDNA clone HBBA13.5 and
4041	17098		0.65	3.0E-16	AF020503.1	NT	Homo sapiens FRAS3 common fragile region, diadenosine triphosphate hydrolase (PHT) gene, exon 5
4042	17098		1.07	3.0E-16	U03887.1	NT	Human BXP20 gene
5058	18039	30006	1.12	3.0E-16	AF1061363.1	EST_HUMAN	AV191333 G1C Homo sapiens cDNA clone G1C5A07.3
5400	18541		0.97	3.0E-16	AA07225.1	EST_HUMAN	H10P02 Chromosome 7 Fetal Brain cDNA Library/Homo sapiens cDNA clone 7510P02
8511	18883	31962	1.49	3.0E-16	AF03529.1	NT	Homo sapiens glycine 3 (GPC3) gene, partial cds and flanking repeat regions
9218	22144	35498	3.69	3.0E-16	AF002834.1	EST_HUMAN	enc8505.t1 Sindigene schizos leish S11 Homo sapiens cDNA clone IMAGE:1684185.3 similar to contains THR12 THR repetitive element
10402	23281		0.81	3.0E-16	BF66597.1	EST_HUMAN	002246538PT NIH_MGC_62 Homo sapiens cDNA clone IMAGE:433232.3
10019	23505	36036	4.38	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
13086	29509	31374	2.1	3.0E-16	AF10268.2	EST_HUMAN	DKFZ544L1825.1T 434 (synonym: hnc5) Homo sapiens cDNA clone DKFZ544L1825.1
698	14048		1.41	2.0E-16	AF103279.2	NT	Homo sapiens chromosome 21 segment HS21C079
2405	15413		1.01	2.0E-16	AA021761.1	EST_HUMAN	460044.31 Soares, Jodi, NHT Homo sapiens cDNA clone IMAGE:1038603.3
2739	15752		1.15	2.0E-16	U03061.1	NT	Human S5A-V-related endogenous retroviral LTR-like element
4274	17288	30165	1.36	2.0E-16	U06271.1	NT	H-sapiens DNA for endogenous retroviral insertion
4594	17602	30458	1.32	2.0E-16	AF049733.1	EST_HUMAN	MEK3B repetitive element
7643	20071	33505	0.9	2.0E-16	Q31125	SWISSPROT	MER23 repetitive element
8176	21083	34415	0.85	2.0E-16	AF07723.1	EST_HUMAN	(1) Ref.1:1 NCL CGAP, Genet Homo sapiens cDNA clone IMAGE:214708.3 similar to contains element MER23 repetitive element
8545	21478	34516	2.1	2.0E-16	AF172837.1	EST_HUMAN	467905.45 NCL CGAP P419 Homo sapiens cDNA clone IMAGE:120547 similar to TR05646 054649
8730	21690	35011	0.73	2.0E-16	BE33583.1	EST_HUMAN	HYPOPHOSPHATASE 2 (HPP2) PROTEIN [2] TR05646 054649
8730	21690	35012	0.73	2.0E-16	BE33583.1	EST_HUMAN	HYPOPHOSPHATASE 2 (HPP2) PROTEIN [2] TR05646 054649
8730	21690	35012	0.73	2.0E-16	BE33583.1	EST_HUMAN	HYPOPHOSPHATASE 2 (HPP2) PROTEIN [2] TR05646 054649

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5001	20230	35376	0.07	2.0E-16	AW187244.1	EST_HUMAN	GM4-PT0034-100200-50a-a01 PT0034 Homo sapiens cDNA
5001	22200	35377	0.07	2.0E-16	AW187244.1	EST_HUMAN	GM4-PT0034-100200-50a-a01 PT0034 Homo sapiens cDNA
196	1524	26207	1.57	1.0E-16	AF220718.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
403	13516		26.26	1.0E-10	AA230923.1	EST_HUMAN	AF569115 Swine, fetal, brain, B26H9, 9w Homo sapiens cDNA, clone IMAGE:1034004.3 similar to
1907	15005	27903	3.12	1.0E-16	B0327942.1	EST_HUMAN	considered ORF.2 ORF, repetitive element 1
5023	18500	32108	0.86	1.0E-16	AF153644.1	EST_HUMAN	QV0-BN014840-700-355a-10 BN0148 Homo sapiens cDNA
5703	19759		21.98	1.0E-16	U45683.1	NT	Homo sapiens CCR8 chemokine receptor (CCR8) gene, complete cds, alternatively spliced
6856	19588	33102	3.03	1.0E-16	Q42779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
7695	19729		6.4	1.0E-16	U45683.1	NT	Homo sapiens CCR8 chemokine receptor (CCR8) gene, complete cds
8628	22720	36111	1.05	1.0E-16	AW187665.1	EST_HUMAN	QV2-PT0012-004000-12a-a03 PT0012 Homo sapiens cDNA
3802	16833	29710	3.35	6.0E-17	AW190004.1	EST_HUMAN	CM1-ANT008-200500-163-a01 NT0038 Homo sapiens cDNA
7025	20051		1.85	9.0E-17	AB392964.1	EST_HUMAN	1q22q11.31 NCI_CGAP_CCL1 Homo sapiens cDNA, clone IMAGE:2109524.3 similar to contains MER28.2 MER28 repetitive element 1
8696	21617		3.72	8.0E-17	AW190267.1	EST_HUMAN	1q14q12.11 NCI_CGAP_UH1 Homo sapiens cDNA, clone IMAGE:2303950.3 similar to contains ORF.2 ORF repetitive element 1
10720	29038		2.59	9.0E-17	AF220718.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1045	14069		1.76	6.0E-17	AW185070.1	EST_HUMAN	QV0-OT0033-2403000-115-b01 OT0033 Homo sapiens cDNA
3662	18900		0.81	8.0E-17	AL163360.2	NT	Homo sapiens chromosome 21 segment HS210880
8778	26302	31091	3.89	8.0E-17	BE172091.1	EST_HUMAN	MR0-HT0559-060000-003-a04 HT0559 Homo sapiens cDNA
7651	20655		1.75	8.0E-17	AW750759.1	EST_HUMAN	AW750759 HTF Homo sapiens cDNA, clone HTF-C1987.9
8210	21115	34445	0.47	8.0E-17	6750981	NT	Mass muscular dystrophin, acute, heavy chain 11 (Dnact11), mRNA
1477	14008		2.48	7.0E-17	6750927	NT	Mass muscular dystrophin B coding complex 2 (Apthec2), mRNA
5506	18955		3.34	7.0E-17	AF120950.1	NT	Homo sapiens putative MTPAP (MTPAP) mRNA, partial cds, alternatively spliced
6964	20111	33243	6.88	7.0E-17	AF729843.1	NT	Mass muscular WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) variant, section 1 of 2 of the complete cds, and unknown gene
216	13315	26233	7.16	6.0E-17	AW190360.1	EST_HUMAN	RC-H-TN0035-220300-002-504 TN0035 Homo sapiens cDNA
6508	19009	32794	2.28	6.0E-17	AW162272.1	EST_HUMAN	1q44q41.31 Swine, adult, brain, N1_CGAP_31 Homo sapiens cDNA, clone IMAGE:2976995.3 similar to contains L1.2 repetitive element 1
444	13111	23897	3.31	8.0E-17	104110.1	EST_HUMAN	QV009-000000-000-000-000 Homo sapiens cDNA, clone IMAGE:79939.5
5024	20640	34265	3.01	8.0E-17	674043.1	EST_HUMAN	QV009-000000-000-000-000 Homo sapiens cDNA, clone IMAGE:79939.5
3703	19759	26229	1.47	4.0E-17	AB392964.1	EST_HUMAN	1q22q11.31 NCI_CGAP_CCL1 Homo sapiens cDNA, clone IMAGE:106327.6

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expressin Signal	Model Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9600	2898	36272	1.16	4.0E-17	AF162485.1	EST_HUMAN	K236c4.1 NCI_CGAP_548 Homo sapiens cDNA, clone IMAGE:261862.3 similar to contains Alu repetitive element contains MER18.13 MER19 repetitive element; HSF2 CG47
11824	24708	38206	2.06	4.0E-17	AF162472.2	NT	Homo sapiens cDNA, clone IMAGE:261862.3 similar to contains Alu repetitive element; HSF2 CG47
12381	25161		2.18	4.0E-17	AF073568.1	EST_HUMAN	Q16300 PAK3 mRNA, complete MER10.12 MER10 repetitive element; HSF2 CG47
2410	16120	28127	1.14	3.0E-17	AF161823.1	EST_HUMAN	W60900 c1.1 Score: 1.1 SRC S1 Homo sapiens cDNA clone IMAGE:2004784.3
3257	16295	20681	1.46	3.0E-17	AF034392.1	SWISSPROT	MAS-RELATED G-PROTEIN COUPLED RECEPTOR URG
3710	16762	20681	1.46	3.0E-17	BE324922.1	EST_HUMAN	W60900 c1.1 NCI_CGAP_Luc4 Homo sapiens cDNA clone IMAGE:3181669.3
3710	16762	20682	1.49	3.0E-17	BE324922.1	EST_HUMAN	W60900 c1.1 NCI_CGAP_Luc4 Homo sapiens cDNA clone IMAGE:3181669.3
8644	21774	36121	1.35	3.0E-17	N68451.1	EST_HUMAN	cat1402 c1.1 Score: full liver spleen NF1.3 Homo sapiens cDNA clone IMAGE:262497.3 similar to contains PTR18.1 PTR5 repetitive element;
10224	23115	30516	6.18	3.0E-17	A826888.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
10658	23794	37180	0.71	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-a7 BN0047 Homo sapiens cDNA
10658	23794	37181	0.71	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-a7 BN0047 Homo sapiens cDNA
12348	25140		3.48	3.0E-17	11417596	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
373	13480	26375	2.95	2.0E-17	AF070060.1	EST_HUMAN	q183a05.x1 NCI_CGAP_Ezad Homo sapiens cDNA clone IMAGE:166922.3 similar to contains Alu repetitive element;
374	13480	26375	2.05	2.0E-17	AF070060.1	EST_HUMAN	q183a05.x1 NCI_CGAP_Ezad Homo sapiens cDNA clone IMAGE:166922.3 similar to contains Alu repetitive element;
1018	14005		1.18	2.0E-17	AAT72932.1	EST_HUMAN	repetitive element;
2471	15474	28478	2.23	2.0E-17	Q26843	SWISSPROT	ZONADHESIN PRECURSOR
2471	15474	28474	2.23	2.0E-17	Q26843	SWISSPROT	ZONADHESIN PRECURSOR
2972	16024	28924	8.93	2.0E-17	PI12068	SWISSPROT	NEUROFILAMENT TRIPHETH PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5551	18528	31506	1.75	2.0E-17	M77685.1	NT	Mus musculus ultra high salt fraction gene, complete cds
5551	18528	31507	1.75	2.0E-17	M77685.1	NT	Mus musculus ultra high salt fraction gene, complete cds
6516	19540		1.76	2.0E-17	AF030966.1	EST_HUMAN	Homo sapiens MHC class I region
6766	19600		1.57	2.0E-17	AF134086.1	EST_HUMAN	DNF2702000J011102 (exon1: 1mm2) Homo sapiens cDNA clone DNF2702000J011102
8396	21281	34396	0.73	2.0E-17	AF007839.1	NT	Homo sapiens protein for KIAA1418 protein, complete cds
8652	21563	34932	1.39	2.0E-17	Q05155	SWISSPROT	CELL FACTORY RECEPTOR FOR PROTEIN (CFR)
9005	21954	36812	1.13	2.0E-17	AF030940.1	EST_HUMAN	EST1336c4.1 NCI_CGAP_Ezad Homo sapiens cDNA, 5' similar to polyoma
10382	23271	39984	1.93	2.1E-17	BE230668.1	EST_HUMAN	EST1336c4.1 NCI_CGAP_Ezad Homo sapiens cDNA, 5' similar to polyoma
10415	23304	36721	3.26	2.0E-17	AF162472.2	NT	Homo sapiens antraxinone 21, fragment HSF2 CG47

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
12618	124156	29270	6.36	7.0E-18	AW316976.1	EST_HUMAN	LOC104111 NOL_CGAP_Prat Homo sapiens cDNA, clone IMAGE-2837071 3' similar to gb:U36868.60S PROSOAL, partial Cdkp-1, gene for dca-derived neuroprotection protein, enhancer region
3338	16334	29269	1.27	6.0E-18	X71791.2	NT	Scara proteinase particle CD44P-1, gene for dca-derived neuroprotection protein, enhancer region
4890	17362		4.82	6.0E-18	P52181	SWISSPROT	PROTEIN:GLUTAMINE GAMMA-GLUTAMYL TRANSFERASE (TISSUE TRANSOLUTAMINASE) (TGASE C) (TOP)
8829	21755		2.35	6.0E-18			Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H1 sapiens) (LOC83446). mRNA
8822	21832	35207	0.77	6.0E-18	AL16310.2	NT	Homo sapiens chromosome 21, segment H331C010
8635	22651	35336	0.59	6.0E-18	AI003253.2	EST_HUMAN	RC-BT168-020459-074 BT168 Homo sapiens cDNA
8635	22651	35331	0.50	6.0E-18	AI003253.1	EST_HUMAN	RC-BT168-020459-074 BT168 Homo sapiens cDNA
11772	24672	38160	1.59	6.0E-18	X87344.1	NT	H. sapiens DNA, DAB, HLA-21, PIP2, LIMP2, TAP1, LIMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
12570	25291	31840	2.74	6.0E-18	U87929.1	NT	Human acornate hydratase (AC02) gene, exon 4 q96591.11 Scara, plicon, Scovosella, 200HP820W Homo sapiens cDNA clone IMAGE1863068 3' similar to contains Alu repetitive element
1176	14218	27154	15.33	6.0E-18	AI002414.1	EST_HUMAN	Human endogenous retrovirus HERV-P-T71D
5435	18536	31378	1.08	5.0E-18	AF037913.1	NT	MRG-H10161-221099-003-006 H10161 Homo sapiens cDNA
9279	22207	35554	6.21	5.0E-18	BE143312.1	EST_HUMAN	Homo sapiens lymphocyte activation-associated protein (LOC57018) mRNA
11418	24332	37790	3.88	6.0E-18	102-2378	NT	Homo sapiens lymphocyte activation-associated protein (LOC57018) mRNA
11418	24332	37791	3.88	6.0E-18	102-2378	NT	Homo sapiens lymphocyte activation-associated protein (LOC57018) mRNA
12701	29356		11.83	5.0E-18	AW169782.1	EST_HUMAN	MRI-SN0038-060-000-001-g11 SN0038 Homo sapiens cDNA
13005	29559		30.99	6.0E-18	AV050647.1	EST_HUMAN	AY650047-010 Homo sapiens cDNA clone GLC03A02 3' contains MER29.63 repetitive element
120	13233	29149	1.4	4.0E-18	BE044076.1	EST_HUMAN	h039904.1 NOL_CGAP_UH Homo sapiens cDNA clone IMAGE-3039511 3' similar to contains MER29.63 repetitive element
129	13233	29150	1.4	4.0E-18	BE044076.1	EST_HUMAN	h039904.1 NOL_CGAP_UH Homo sapiens cDNA clone IMAGE-3039511 3' similar to contains MER29.63 repetitive element
1745	14772	27742	9.96	4.0E-18	AI021814.1	EST_HUMAN	h024111.1 NOL_CGAP_UH Homo sapiens cDNA clone IMAGE-1144845 3' similar to gb:U29526 Keratin, type I, cytochrome-like, 18 (HUMAN)
2216	15227	28231	1.08	4.0E-18	Q06430	SWISSPROT	N-ACETYLACTOSAMINIDE BETA1-6ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (BRANCHING ENZYME) (EC 2.4.1.10)
2216	15227	28232	1.09	4.0E-18	Q06430	SWISSPROT	N-ACETYLACTOSAMINIDE BETA1-6ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (BRANCHING ENZYME) (EC 2.4.1.10)
5648	18659	31601	2.33	4.0E-18	AI071565.1	EST_HUMAN	ac24646.1 Scara_NH_1_CBC_511 Homo sapiens cDNA clone IMAGE1827138 3'
5548	18659	31602	2.33	4.0E-18	AI071565.1	EST_HUMAN	ac24646.1 Scara_NH_1_CBC_511 Homo sapiens cDNA clone IMAGE1827138 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	QRT-SEQ ID NO.	Expression Signal	Mean Similar (Top Hit BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8426	21300		0.79	4.0E-18	AA74881.1	EST_HUMAN	cd44/98.41 NC1 CGAP_H1 Homo sapiens cDNA clone IMAGE:125698 similar to contains L12.L1
11443	24389	37809	6.22	4.0E-18	AA371807.1	EST_HUMAN	EST162833 Pituitary gland, subcapsular (proliferating growth hormone) II Homo sapiens cDNA 5' end similar to
874	19227	26975	6.61	3.0E-18	AA451198.1	EST_HUMAN	EST containing O form/repeat
958	14038	26975	3.14	3.0E-18	BE269834.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C047
4030	17057	22946	1.2	3.0E-18	AB5247.2	NT	PA6782.465 RIBOSOMAL PROTEIN S5.
7142	20290	33502	4.81	3.0E-18	BE501673.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C047
11304	24292	37726	1.52	3.0E-18	BE210680.1	EST_HUMAN	PA6782.465 RIBOSOMAL PROTEIN S5.
12822	25441	37726	7.17	3.0E-18	AA1022015.1	EST_HUMAN	cd44/98.41 NC1 CGAP_H1 Homo sapiens cDNA clone IMAGE:4103652 3'
270	133055	20281	2.52	2.0E-18	AA1022015.1	EST_HUMAN	cd44/98.41 NC1 CGAP_H1 Homo sapiens cDNA clone IMAGE:4103652 3'
1180	14220		63.41	2.0E-18	BE258007.1	EST_HUMAN	OV-14102036-190200-070-407 LT0038 Homo sapiens cDNA
3168	16218	28108	1.39	2.0E-18	Q96575	SWISSPROT	OV-14102036-190200-070-407 LT0038 Homo sapiens cDNA
6506	18872		4.98	2.0E-18	AA488610.1	EST_HUMAN	OV-14102036-190200-070-407 LT0038 Homo sapiens cDNA
6006	18709	31004	3.12	2.0E-18	D14547.1	NT	DYNEIN GAMMA CHAIN FLAGELLAR OUTER ARM
6506	18709	31004	3.12	2.0E-18	D14547.1	NT	4433007.41 Soares, Iselis, NHT Homo sapiens cDNA clone IMAGE:1408952 3' similar to TR014577
8003	19164	31595	1.94	2.0E-18	D14547.1	NT	O-14577 BAC CLONE RG114498 FROM T031, COMPLETE SEQUENCE. ;
6406	19454	32026	1.02	2.0E-18	BF347293.1	EST_HUMAN	Human DNA, SINE repetitive element
6406	19454	32027	1.02	2.0E-18	X00459.1	NT	6022311647 NC1 CGAP_Bim97 Homo sapiens cDNA clone IMAGE:4159670 5'
6530	19574	32756	0.88	2.0E-18	BF352840.1	EST_HUMAN	Human IFNAR gene for interferon alpha/beta receptor
6573	19914	33800	3.19	2.0E-18	AA1665863.1	EST_HUMAN	Human IFNAR gene for interferon alpha/beta receptor
7940	20768	34071	0.61	2.0E-18	AA457619.1	EST_HUMAN	HL-60/1.21 Soares, INH, T, GBC, S1 Homo sapiens cDNA clone IMAGE:2071644 3' similar to contains
8726	21605	35002	0.54	2.0E-18	BE439524.1	EST_HUMAN	MER19.12 MER19 repetitive element ;
10560	22495	36856	1.34	2.0E-18	AA151673.1	EST_HUMAN	aa89011.11 Strubeberg, Iselis, NHT Homo sapiens cDNA clone IMAGE:89485 5' similar to
10560	22496	36857	1.34	2.0E-18	AA151673.1	EST_HUMAN	aa89011.11 Strubeberg, Iselis, NHT Homo sapiens cDNA clone IMAGE:89485 5' similar to
11412	24328	37777	2.3	2.0E-18	AA107091.1	EST_HUMAN	HTM-1087 HTM Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mean Similar (Top Hit BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12154	24263	38402	3.65	2.0E-16	AF151299.1	EST_HUMAN	767/330.31 NCL CGAP_L11 Homo sapiens cDNA clone IMAGE:2639728.3 similar to contains MER19.2
12217	14220		8.71	2.0E-16	BEZ06927.1	EST_HUMAN	101114352.F11H1.M5G_16 Homo sapiens cDNA clone IMAGE:3355044.5
4523	17332		0.98	1.0E-16	T95126.1	EST_HUMAN	101114352.F11H1.M5G_16 Homo sapiens cDNA clone IMAGE:120568.0 similar to contains L1 repeat element
5540	18616	31470	2.61	1.0E-16	AV59345.1	EST_HUMAN	AV59345.1 Homo sapiens cDNA clone IMAGE:120568.0 similar to contains L1 repeat element
5762	18835	31938	2.16	1.0E-16	CD00055.1	EST_HUMAN	AV59345.1 Homo sapiens cDNA clone IMAGE:120568.0 similar to contains L1 repeat element
5762	18845	31939	2.16	1.0E-16	CD00066.1	NT	Homo sapiens mRNA for NAK ATPase alpha-subunit, complete cds
6725	19761	32008	1.24	1.0E-16	AL163260.2	NT	Homo sapiens mRNA for NAK ATPase alpha-subunit, complete cds
8010	21939	35235	1.20	1.0E-16	AL142388.1	EST_HUMAN	Homo sapiens chromosome 21 segment H52TC000
10411	23300	36718	3.07	1.0E-16	U61328.1	NT	cd59420.21 Homo sapiens cDNA clone IMAGE:1805560.3 similar to contains L1 H1 repeat element
12475	29520	31850	6.46	1.0E-16	AF035239.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT) gene, complete cds
567	13636	28547	3.3	9.0E-16	AA281961.1	EST_HUMAN	Homo sapiens phylican 3 (GPC3) gene, partial cds and flanking repeat regions
598	13636	28547	3.01	9.0E-16	AA281961.1	EST_HUMAN	z111005.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811.6 similar to contains MER19.2
6431	21393		4.16	9.0E-16	F08093.1	EST_HUMAN	MER19 repeat element
6246	22174	35528	2.80	9.0E-16	AL163303.2	NT	MER19 repeat element
6246	22174	35529	2.80	9.0E-16	AL163303.2	NT	MER19 repeat element
11537	24176	37643	4.46	9.0E-16	AB030399.1	NT	Homo sapiens chromosome 21 segment H52TC003
12256	13696	28547	17.41	9.0E-16	AA281961.1	EST_HUMAN	Homo sapiens mRNA for NAK ATPase alpha-subunit, complete cds
1074	14118		1.17	8.0E-16	AA097490.1	EST_HUMAN	z111005.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811.6 similar to contains MER19.2
8727	21567	35003	1.17	8.0E-16	BE158956.1	EST_HUMAN	MER19 repeat element
2260	15270	28276	1.46	7.0E-16	47581369	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT) gene, complete cds
6721	18163	32870	0.68	7.0E-16	AF032200.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT) gene, complete cds
7931	28915	33874	0.68	7.0E-16	F08093.1	EST_HUMAN	z111005.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811.6 similar to contains MER19.2
1238	28915	33874	0.68	7.0E-16	F08093.1	EST_HUMAN	z111005.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811.6 similar to contains MER19.2
1380	18862		1.12	6.0E-16	AF165320.1	EST_HUMAN	z111005.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811.6 similar to contains MER19.2
4574	17362	30444	1.41	6.0E-16	P26436	SWISSPROT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT) gene, complete cds

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Maxi Similar (Top)HR BLAST E Value	Top HR Accession No.	Top HR Database Source	Top Hit Descriptor
2177	15169	28195	1.8	1.0E-19	H00795.1	EST_HUMAN	Y92607.1 Scores adult brain N24415557 Homo sapiens cDNA clone IMAGE:54183 5' similar to contains
2795	15738		3.37	1.0E-19	D26041.1	NT	MEK1 (protein kinase element);
2802	15946		7.1	1.0E-19	4733677	NT	Human gene for receptor-like G-protein coupled receptor, class 7, 9
3401	16601	29403	1.2	1.0E-19	A43824957.1	EST_HUMAN	Human cytochrome P450 2C19 cDNA, non-sequenced type substrate 1 (PYPNS1) mRNA
5520	16559	31448	0.63	1.0E-19	A1600866.1	EST_HUMAN	H06812.4 Scores, beta, NBT Homo sapiens cDNA clone IMAGE:138031 3' similar to contains MER37.2
5511	16241	32531	5.05	1.0E-19	U12196.1	NT	NERF7 negative element
9452	28677		0.87	1.0E-19	A1568527.1	EST_HUMAN	W061083.1 NCI_CGAP_L102 Homo sapiens cDNA clone IMAGE:2443287 3' similar to RQ11630 Q1650
8078	20559	34306	0.85	1.0E-19	U06813.1	NT	PMS3 mRNA;
8078	20560	34307	0.85	1.0E-19	U06813.1	NT	Oxytocin nucleus sodium/calcium cotransporter mRNA, partial cds
8284	25688		0.57	1.0E-19	A1200719.1	NT	H22403.3 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:555093 similar to contains L1.1 L1
9018	21947	35303	1.84	1.0E-19	M24657.1	NT	replicative element;
9300	22228		2.82	1.0E-19	T66620.1	EST_HUMAN	Oxytocin nucleus Nerve/glucose cotransporter-related protein mRNA, complete cds
10290	23169		0.87	1.0E-19	U06022.1	NT	Oxytocin nucleus Nerve/glucose cotransporter-related protein mRNA, complete cds
10694	23570	37000	44.82	1.0E-19	A1671259.1	EST_HUMAN	Human sagittary tumor transforming gene protein (PTTG) gene, complete cds
10693	23570	37009	1.87	1.0E-19	M44031.1	EST_HUMAN	Rabbit phosphotyrosine kinase beta subunit mRNA, complete cds
12173	25069		3.8519	1.42	1.0E-19	U06103.1	Y972602.1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:123249 5' similar to contains
6938	19607	33189	2.31	8.0E-20	T667286	NT	OFK negative element;
6938	19607	33189	2.31	8.0E-20	T667286	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
7641	20653	34172	1.43	8.0E-20	A121371.1	EST_HUMAN	RO3-57074-191099-051-505 STD74 Homo sapiens cDNA
7641	20653	34172	1.43	8.0E-20	A121371.1	EST_HUMAN	Y91169.1 Scores melanocyte 2B2H1 Homo sapiens cDNA clone IMAGE:272972 5'
7941	20653	34173	1.43	8.0E-20	A121371.1	EST_HUMAN	Homo sapiens IMAGE-52 (IMAGE-52), IMAGE-53 (IMAGE-53), IMAGE-54 (IMAGE-54), and IMAGE-51
8320	16598	26208	0.7	7.0E-20	9529456.1	EST_HUMAN	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
7936	18404	31279	5.91	7.0E-20	A1138120.1	EST_HUMAN	q95900.4 Scores, NFL_T_O5C_S11 Homo sapiens cDNA clone IMAGE:162098 3'
8514	21219	34555	0.42	7.0E-20	A1181897.1	NT	q95900.4 Scores, NFL_T_O5C_S11 Homo sapiens cDNA clone IMAGE:162098 3'
8603	21692		9.3	7.0E-20	A455767.1	EST_HUMAN	P41 AN0699 050600-005-401 AN0699 Homo sapiens cDNA
6603	21692	35346	9.3	7.0E-20	A455767.1	EST_HUMAN	DK7265702.02.1 547 (unknown, flat) Homo sapiens cDNA clone DK726570202 5'
12136	24870		4.8	7.0E-20	5812633	NT	Human sapiens WRN (WRN) gene, complete cds
							H16601.4 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1043716 similar to contains MER25.2
							H16601.4 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1043716 similar to contains MER25.2
							H16601.4 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1043716 similar to contains MER25.2
							NER290 negative element
							Homo sapiens fibronectin protein L13a (FN-13a), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit ELAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descr ptor
3316	16652	25553	4.09	6.0E-20 P307189	SWISSPROT	ALU SUBFAMILY 1 SEQUENCE CONTAMINATION WARNING ENTRY	
4371	17385	30249	4.76	6.0E-20 BE022434.1	EST_HUMAN	G014412313 NH_130072 Homo sapiens cDNA clone IMAGE:3916251 5'	
4705	17171	30249	4.76	5.0E-20 A172573.1	EST_HUMAN	AV754932 HTO1 Homo sapiens cDNA clone IMAGE:3916251 5'	
7474	20414	33982	1.65	5.0E-20 AF075301.1	EST_HUMAN	AF075301 Homo sapiens fetal liver cDNA library Homo sapiens cDNA clone HA0250	
8524	21455	34797	5.82	5.0E-20 W90525.1	EST_HUMAN	271608.61 Soares, fetal liver, spleen_NHLS.S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to coronin MER30.H1 MER30 repetitive element ;	
8524	21455	34798	5.82	5.0E-20 W90525.1	EST_HUMAN	271608.61 Soares, fetal liver, spleen_NHLS.S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to coronin MER30.H1 MER30 repetitive element ;	
8602	21613	34945	1	5.0E-20 BE165660.1	EST_HUMAN	MR3-HT0487-180200-115-p01 HT0487 Homo sapiens cDNA	
9393	23231	35664	1.72	5.0E-20 A0203174.1	NT	Mus musculus UMAN-g mRNA, complete cds	
9393	23231	35665	1.72	5.0E-20 A0203174.1	NT	Mus musculus UMAN-g mRNA, complete cds	
9578	21336	36609	1.13	5.0E-20 Q63609	SWISSPROT	HYPOPHYSICAL PROTEIN D345024.1	
1643	14674	27639	1.95	4.0E-20 AL163247.2	NT	Homo sapiens chromosome 21 segment H82TQ47	
5845	18516		0.85	4.0E-20 Q63609	SWISSPROT	HISTONE H2B C (H2B/C)	
8504	21435		4.77	4.0E-20 A1674552.1	EST_HUMAN	U94903.1 NCI CGAP Q605 Homo sapiens cDNA clone IMAGE:2293396 3'	
10977	23901	37269	1.49	4.0E-20 AV167469.1	EST_HUMAN	Q13-DT0043-040200-080-c04 DT0043 Homo sapiens cDNA	
2193	15195	28167	0.99	3.0E-20 U03988.1	NT	Human BXNP21 gene	
4395	17318	30186	1.18	3.0E-20 P2273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN14	
4738	17743	30004	0.92	3.0E-20 A4037610.1	EST_HUMAN	263612.11 Somes, pregnant, uterus_NIHPU Homo sapiens cDNA clone IMAGE:484993 3' similar to consists L1, B1 L1 repetitive element ;	
9400	22418		2.55	3.0E-20 D14547.1	NT	Human DNA, SINE, repetitive element	
10810	22666	37122	1	3.0E-20 BF185264.1	EST_HUMAN	AF018350101 NH_130072 Homo sapiens cDNA clone IMAGE:4004349 9'	
11107	24038		1.89	3.0E-20 P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASEB	
12401	25173	31975	5.89	3.0E-20 BE88422.1	EST_HUMAN	207418101 NCI CGAP U4 Homo sapiens cDNA clone IMAGE:3916251 5'	
865	13909		10.52	2.0E-20 AV130388.1	EST_HUMAN	Per461 US RIBOSOMAL PROTEIN S5 ;	
1138	14190	27117	2.23	2.0E-20 A4516335.1	EST_HUMAN	U94908.1 NCI CGAP U4 Homo sapiens cDNA clone IMAGE:4004349 9'	
1138	14190	27118	2.23	2.0E-20 A4516335.1	EST_HUMAN	U94908.1 NCI CGAP U4 Homo sapiens cDNA clone IMAGE:4004349 9'	
2884	13509		4.88	2.0E-20 AV130388.1	EST_HUMAN	G-128408 ORF2: FUNCTION UNKNOWN ;	
3020	18027	30909	5.5	2.0E-20 Q2395	SWISSPROT	ZONADHESIN PRECURSOR	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5000	18037	30510	5.5	2.0E-20	G26383	SWISSPROT	ZONOHESIN PRECURSOR
8695	21630	31670	0.27	2.0E-20	A430457.1	EST_HUMAN	EST16028 Liver 11 Homo sapiens cDNA 5' end
8732	22537	33040	1.52	2.0E-20	D30383.1	NT	Homo sapiens NGH1 gene, antisense-like element
8732	22537	33041	1.52	2.0E-20	D30383.1	NT	Homo sapiens NGH1 gene, antisense-like element
12199	21701	31653	2.25	2.0E-25	U95571.1	EST_HUMAN	CHR2203.0 Chromosome 22 (2000) Homo sapiens cDNA clone C22_361.9
2025	19855	28038	4.76	1.0E-20	AA28166.1	EST_HUMAN	1141093.1 NOL CGAP CG81 Homo sapiens cDNA clone IMAGE:773211.6 similar to contains MER19.2
4549	17597	33417	1.75	1.0E-20	BF11519.1	EST_HUMAN	1154200.41 NOL CGAP CG81 Homo sapiens cDNA clone IMAGE:315165.3 similar to contains L1.12.1
7222	22321	33456	0.77	1.0E-20	AF049567.1	EST_HUMAN	AF049567 Human activated dendritic cell mRNA Homo sapiens cDNA clone GAG8
9705	20231	30010	2.35	1.0E-20	11418491	NT	Homo sapiens A136001 High5/Conserved Protein AHGP5, mRNA
11955	24828	33325	2.7	1.0E-20	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
12513	25245		5.37	1.0E-20	AA423433.1	EST_HUMAN	nc00909.1 NOL CGAP_P41 Homo sapiens cDNA clone IMAGE:746994 similar to contains L1.12.1
2945	25075		1.32	9.0E-21	AJ003514.1	EST_HUMAN	AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone NIP12-3.121
12251	25075		3.84	9.0E-21	AV1698186.1	EST_HUMAN	RC3-NN00086-090500-021-H203 NN00086 Homo sapiens cDNA
8370	22298		1.32	8.0E-21	AV1674991.1	EST_HUMAN	085109 NADHUBIQUINONE OXIDOREDUCTASE ASH1 SUBUNIT PRECURSOR ;
11291	24812	39307	5.11	8.0E-21	AA4809411.1	EST_HUMAN	cd7106.41 NOL CGAP CG81 Homo sapiens cDNA clone IMAGE:136033.9
12414	25183		0.13	8.0E-21	Q21330	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 6)
2082	16096	29054	1.39	7.0E-21	P16500	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (SLAMININ) (LAMININ CHAIN B3)
2082	16096	29055	1.39	7.0E-21	P16500	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (SLAMININ) (LAMININ CHAIN B3)
3789	19796	29595	0.86	7.0E-21	JA1163300.2	NT	Homo sapiens chromosome 21 segment H52CTC00
4353	17367		0.86	7.0E-21	AA049502.1	EST_HUMAN	2667406.1 Scores, fragment, Uterus_2_NHPU Homo sapiens cDNA clone IMAGE:407695.6
6702	19738	32540	1.03	7.0E-21	JA16326.2	NT	Homo sapiens chromosome 21 segment H52CTC018
8699	21849	35247	1.07	7.0E-21	AJ277691.1	NT	Homo sapiens INT-2 gene for mitochondrial 87S-deoxythionucleoside (INT-2) gene, exons 1-5
6234	22162	35516	8.52	7.0E-21	D14718.1	NT	Human chromosomal protein HMG31 related gene
10014	23500	35533	1.04	7.0E-21	AV1865522.1	EST_HUMAN	RC3-CT0007-2271169-031-H203 CT0007 Homo sapiens cDNA
							2673003.81 Scores, Uterus_1_H203 CT0007 Homo sapiens cDNA clone IMAGE:305851.3 similar to
							64M14308 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); contains 1HK3 OPR
11138	24497	37512	1.61	7.0E-21	AA72404.1	EST_HUMAN	1141093.1 NOL CGAP CG81 Homo sapiens cDNA clone IMAGE:773211.6 similar to contains MER19.2
11713	24615	39361	1.51	7.0E-21	77055269	NT	Homo sapiens PTD019 protein (PTD019), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4106	17716	30081	0.76	6.0E-21	BE43591.1	EST_HUMAN	301304126T1 NH_140622 Homo sapiens cDNA clone IMAGE:303510.6
4279	20703	29547	0.94	6.0E-21	BE16279.1	EST_HUMAN	PAH_H10454Q007004002-N09 HT0454 Homo sapiens cDNA
692	14002	29547	1	5.0E-21	5020031	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21) mRNA
2299	15307	28313	0.98	5.0E-21	AA92194.1	EST_HUMAN	nc24031.1 Swine_NIL_T_01C 51 Homo sapiens cDNA clone IMAGE:303580.5
4470	14081	30340	3.71	5.0E-21	BE29683.1	EST_HUMAN	002711 PRCP-POLY(ADP-RIbose) POLYPROTEIN
4799	14021	29547	0.75	5.0E-21	5020031	NT	00716497.F1 NH_140622 Homo sapiens cDNA clone IMAGE:303580.5
4617	17016	30762	6.03	5.0E-21	4886474	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21) mRNA
7658	20274		0.88	5.0E-21	AY140864.1	EST_HUMAN	Homo sapiens melanoma antigen (family C, 1) (MAGEC1) mRNA
7652	20357	33626	0.97	5.0E-21	BE35606.1	EST_HUMAN	h05610.x1 NCI CGAP P238 Homo sapiens cDNA clone IMAGE:30357814.3
12338	22133		1.74	5.0E-21	AA30357.1	EST_HUMAN	763471.x1 NCI CGAP P238 Homo sapiens cDNA clone IMAGE:303573 (5' similar to contains ORF 11
1763	14789	27759	2.09	4.0E-21	AA670713.1	EST_HUMAN	OPR repetitive element
7167	20167	33443	2.34	4.0E-21	AB119576.1	NT	0085633.1 NCI CGAP K448 Homo sapiens cDNA clone IMAGE:1673064.3 similar to TRCQ16530 Q16530
							PM33 mRNA, contains ORF 11; ORF repetitive element
							Fallun norvegicus mRNA for T1M, complete cds
10299	22189	39000	0.85	4.0E-21	U91328.1	NT	Human hereditary hemochromatosis region, histone 2A-like protein gene, hereditary hemochromatosis
1601	14883	27863	1.11	3.0E-21	AA216891.1	EST_HUMAN	(HLA-H) gene, Rb161 gene, and sodium phosphate transporter (NPT3) gene, complete cds
2293	19301	29307	1.38	3.0E-21	AL162007.2	NT	Z116006.1 Streptococcus faecalis 931202 Homo sapiens cDNA clone IMAGE:020771.3
3128	18179	29073	4.01	3.0E-21	AA007973.1	NT	Homo sapiens chromosome 21 segment H527D091
							Homo sapiens LGMD28 gene
5635	18762	31656	0.85	3.0E-21	AA277507.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3'-deoxythionucleosidase (dNT-2 gene), exons 1-5
6599	19762	31697	0.85	3.0E-21	AA277507.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3'-deoxythionucleosidase (dNT-2 gene), exons 1-5
5941	19008		0.89	3.0E-21	AA197044.1	EST_HUMAN	AV001044 C1C Homo sapiens cDNA clone G1C00A10.3
6420	19467		28.39	3.0E-21	BF184738.1	EST_HUMAN	301844059T NH_140622 Homo sapiens cDNA clone G1C00A10.3
1423	20122	33359	0.94	3.0E-21	BF301033.1	EST_HUMAN	301844059T NH_140622 Homo sapiens cDNA clone G1C00A10.3
12115	23103	35905	1.28	3.0E-21	AA1897163.1	EST_HUMAN	301844059T NH_140622 Homo sapiens cDNA clone G1C00A10.3
12639	23952	31475	3.03	3.0E-21	AA1897163.1	EST_HUMAN	301844059T NH_140622 Homo sapiens cDNA clone G1C00A10.3
12115	23103	35905	1.28	3.0E-21	AA1897163.1	EST_HUMAN	301844059T NH_140622 Homo sapiens cDNA clone G1C00A10.3
1242	14270		1.55	2.0E-21	BE284410.1	EST_HUMAN	301844059T NH_140622 Homo sapiens cDNA clone G1C00A10.3
2085	16570	28675	2.85	2.0E-21	CB2863	SWISSPROT	RC4-H10315-141199.01 N06 BT0311 Homo sapiens cDNA
2085	16570	28675	2.85	2.0E-21	CB2863	SWISSPROT	ZONADHESIN PRECURSOR
2085	16570	28675	2.85	2.0E-21	CB2863	SWISSPROT	ZONADHESIN PRECURSOR

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4391	17195	39295	3.42	7.0E-22	U61858	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
5248	23176		1.36	7.0E-22	A515103.1	NT	Homo sapiens HSC220 mRNA, complete cds
5249	23176		1.36	7.0E-22	A515103.1	NT	EST107588 (rat liver, Stratiopora (catfish)2308) Homo sapiens cDNA clone HSC207
5250	23176		2.24	7.0E-22	AF76520.1	EST_HUMAN	Homo sapiens cDNA clone TORBY753A2 to TORBY752 region
10120	23020	35615	2.60	7.0E-22	AF76600.1	NT	Homo sapiens cDNA clone TORBY753A2 to TORBY752 region
4140	21707	39041	1.02	5.0E-22	AF02040.1	EST_HUMAN	205510.11 Scores, 1e-114 NHT Homo sapiens cDNA clone IMAGE:72897.5
8818	17147		2.16	5.0E-22	AF02040.1	EST_HUMAN	W01527.1 NCL_GCAP_Genes Homo sapiens cDNA clone IMAGE:254812.3
6765	19026	33038	4	5.0E-22	AF16303.2	EST_HUMAN	Homo sapiens chromosome 21 segment 1627C103
10089	23694	37121	6.02	5.0E-22	U0822.1	NT	Human fibroblast (MD) gene, exons 7, 8 and 9 and partial cds
12824	25143		2.77	5.0E-22	BF47951.1	EST_HUMAN	ncs27003.X1 NCL_GCAP_P288 Homo sapiens cDNA clone IMAGE:325586.9 similar to contains A4u repetitive element
3704	19730		1.17	4.0E-22	A27778.1	NT	Homo sapiens Xq pseudoclonal region, segment 1/2
8984	23969		2.42	4.0E-22	AF16320.2	NT	Homo sapiens chromosome 21 segment H827C002
11155	24093	37541	2.56	4.0E-22	BF218200.1	EST_HUMAN	601182313F1 NHT_M5C_57 Homo sapiens cDNA clone IMAGE:405434.8
12370	23539		3.07	4.0E-22	AF16320.2	NT	Homo sapiens chromosome 21 segment H827C009
985	14095		1.2	3.0E-22	AF05078.1	EST_HUMAN	fm14n10.X1 NCL_GCAP_C014 Homo sapiens cDNA clone IMAGE:2750511.3 similar to gpl119503 HIGH AFFINITY INTERLEUKIN-6 RECEPTOR B (HUMAN) contains L11 L1 repetitive element
2055	15603	28597	1.11	3.0E-22	AF05038.1	EST_HUMAN	W68804.X1 NCL_GCAP_3m25 Homo sapiens cDNA clone IMAGE:242893.3 similar to SWIRL21_HUMAN
3742	16772		1.6	3.0E-22	D14718.1	NT	P45778.905 RIBOSOMAL PROTEIN L21
							Human ribosomal protein HMG1 related gene
4910	17915	30791	3.05	3.0E-22	A090125.1	EST_HUMAN	qb28207.X1 Scores, 1e-114 NHT_PU Homo sapiens cDNA clone IMAGE:1657590.3 similar to contains MER12.12 MER12 repetitive element
6508	21738		1.04	3.0E-22	BE153613.1	EST_HUMAN	OVCH10399-000300-099212 H10368 Homo sapiens cDNA
8813	21743	35091	2.20	3.0E-22	BE153613.1	EST_HUMAN	OVCH10399-000300-099212 H10368 Homo sapiens cDNA
8932	21862	35277	1.17	3.0E-22	X00600.1	NT	Rratfus RY2G8 mRNA for a potential ligand-binding protein
8932	21862	35278	1.17	3.0E-22	X00600.1	NT	Rratfus RY2G8 mRNA for a potential ligand-binding protein
1667	14985		3.78	2.0E-22	N21942.1	EST_HUMAN	Y07505.41 Scores, 1e-114 NHT_PU Homo sapiens cDNA clone IMAGE:267399.3
2655	15555	28546	1.78	2.0E-22	P24919	SWISSPROT	IMMEDIATE EARLY GENE 138 PROTEIN PRECURSOR
3481	16521	29420	5.79	2.0E-22		NT	Homo sapiens protein kinase, AMP-activated, gamma 3 non-saltatory subunit (PRKAG3), mRNA
4325	17339	30204	1.40	2.0E-22	AW817194.1	EST_HUMAN	P41573.02521159.001-472 H12762 Homo sapiens cDNA
							205011.11 Scores, 1e-114 NHT_PU Homo sapiens cDNA clone IMAGE:322673.3 similar to
6085	25695	52257	1.42	2.0E-22	W8466.1	EST_HUMAN	RC2073208 MONOCYTE CHEMOKINE PROTEIN 3 PRECURSOR (HUMAN)
8415	14405	32039	3.68	2.0E-22	BF02216.1	EST_HUMAN	RC2073208 MONOCYTE CHEMOKINE PROTEIN 3 PRECURSOR (HUMAN)
							205011.11 Scores, 1e-114 NHT_PU Homo sapiens cDNA clone IMAGE:1876269.3 similar to contains
10225	23116	38517	1.14	2.0E-22	AF16262.1	EST_HUMAN	MEB23.18 MER23 repetitive element

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Probe SEQ ID No.	Exon SEQ ID No.	ORF SEQ ID No.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10313	23222	56611	0.68	2.0E-22	U171315.1	EST_HUMAN	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
10313	23222	56611	0.68	2.0E-22	U171315.1	EST_HUMAN	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
12174	28010	38514	2	2.0E-22	AF168663.1	EST_HUMAN	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
12282	16622	31740	2.15	2.0E-22	AF152363.2	EST_HUMAN	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
16022	16622	31740	2.15	2.0E-22	AF152363.2	EST_HUMAN	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
2621	16616	26612	2.97	1.0E-22	U190571.1	EST_HUMAN	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
3471	16511	26412	1.65	1.0E-22	D14447.1	NT	Human similar ribonuclease H1 (RNH1) gene, complete cds
3209	21112	34443	1.65	1.0E-22	BE994667.1	EST_HUMAN	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
11030	23974	37306	1.09	1.0E-22	A195435.1	EST_HUMAN	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
11030	23974	37306	1.09	1.0E-22	A195435.1	EST_HUMAN	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
13016	25662	37357	1.09	1.0E-22	A195435.1	EST_HUMAN	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
3351	16607	29364	0.87	8.0E-23	AF168346.1	NT	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
3351	16607	29364	0.87	8.0E-23	AF168346.1	NT	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
11478	24389	37839	4.20	7.0E-23	5031932	NT	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
3485	16534	3485	1.88	6.0E-23	AF16333.1	NT	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
4567	17381	30245	0.91	8.0E-23	AF163246.2	NT	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
12335	26296	31832	4.89	6.0E-23	A1209130.1	EST_HUMAN	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
5620	18705	31804	3.35	5.0E-23	U62071.2	NT	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
7841	26648	32710	4.17	5.0E-23	AF178818.1	NT	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
6708	18744	32946	0.86	3.0E-23	AF18227.2	NT	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
6708	18744	32947	0.86	3.0E-23	AF18227.2	NT	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
8421	21383	54691	3.67	3.0E-23	A119168.1	EST_HUMAN	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
9791	22765	36136	3.95	3.0E-23	Z70064.1	NT	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
10005	23502	36139	3.95	3.0E-23	Z70064.1	NT	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
6581	13700	26665	2.97	3.0E-23	AF167027.1	EST_HUMAN	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'
1170	16546		3.26	2.0E-23	M63270.1	NT	WASHU11.41 NC1 CGAP P22 Homo sapiens cDNA clone IMAGE:1210289 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2843	16532	28528	1.46	2.0E-23	P22106	SWISSPROT	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
2843	16532	28529	1.46	2.0E-23	P22106	SWISSPROT	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
4326	16470		1.19	2.0E-23	A100488.1	EST_HUMAN	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
3769	16511		4.02	2.0E-23	HE10396.1	EST_HUMAN	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
4351	17037	26971	3.86	2.0E-23	HE52031.1	EST_HUMAN	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
4351	17037	26972	3.88	2.0E-23	HE52031.1	EST_HUMAN	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
8403	21395		7.43	2.0E-23	A7285107.1	NT	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
8402	22330	35992	1.35	2.0E-23	A153303.2	NT	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
12445	25133		5.2	2.0E-23	M32659.1	NT	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
12445	25449		2.72	2.0E-23	A700660.1	NT	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
12445	25895		1.83	2.0E-23	A1133931.1	EST_HUMAN	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
4870	17878		6.40	1.0E-23	A115270.2	NT	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
7021	20047		3.5	1.0E-23	HE37471.1	EST_HUMAN	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
6029	21899	36214	4.79	1.0E-23	A4446097.1	EST_HUMAN	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
11116	24046	37462	1.85	1.0E-23	HE40943.1	EST_HUMAN	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
11116	24046	37463	1.85	1.0E-23	HE40943.1	EST_HUMAN	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
674	13042		1.94	9.0E-24	A4663213.1	EST_HUMAN	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
4798	17763	30626	1.43	8.0E-24	P523269	SWISSPROT	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
4798	17763	30626	1.43	8.0E-24	P523269	SWISSPROT	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
6719	16765	32961	1.1	8.0E-24		NT	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
8383	21266	34627	0.47	8.0E-24	A11420027	NT	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
3941	19569		1.03	7.0E-24	A1637954.1	EST_HUMAN	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
5377	18501		2.8	7.0E-24	A038498.1	EST_HUMAN	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
7258	13787		1.88	6.0E-24	A001421.1	NT	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
953	13617	26861	9.62	6.0E-24	A1162492.2	NT	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
4452	17403	30312	0.73	6.0E-24	P71440	SWISSPROT	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
4054	17031	28667	11.38	5.0E-24	A122643.1	NT	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)
8225	21130	34461	0.88	5.0E-24	A1223891.1	NT	TRANSGLUTININ RECEPTOR (TLN) (H5XRAACHONLUS)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Surfer (Top) Ht BLAST E Value	Top Ht Accession No.	Top Ht Database Source	Top Hit Descriptor
2878	16572	28568	3.22	2.0E-26	F17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4286	17300	30167	1.93	2.0E-25	F17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4286	17300	30168	1.93	2.0E-25	F17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
10785	25175	35367	1.59	2.0E-25	AL449673.1	EST_HUMAN	AL449673 Homo sapiens Testis (Sawyer, GS) Homo sapiens cDNA
3385	13469	25387	0.93	1.0E-25	AL449673.1	EST_HUMAN	AL449673 Homo sapiens Testis (Sawyer, GS) Homo sapiens cDNA
1278	14310	30367	2.3	1.0E-26	U06649	EST_HUMAN	U06649 Homo sapiens cDNA
4659	17627	30626	2.95	1.0E-25	BE16277.1	EST_HUMAN	BE16277 Homo sapiens cDNA
5848	16580		0.99	1.0E-25	AA182080.1	EST_HUMAN	AA182080 Homo sapiens cDNA
2706	26927	33574	2.81	1.0E-26	AA252090.1	EST_HUMAN	AA252090 Homo sapiens cDNA
8144	21053	34386	0.49	1.0E-26	Q03L28	SWISSPROT	Q03L28 Homo sapiens cDNA
8493	21424	34754	6	1.0E-26	AA70079.1	EST_HUMAN	AA70079 Homo sapiens cDNA
10075	22590	30385	6.59	1.0E-25	X00590.1	EST_HUMAN	X00590 Homo sapiens cDNA
10075	22590	30386	6.59	1.0E-25	X00590.1	NT	X00590 Homo sapiens cDNA
11408	24324	37774	3.18	1.0E-26	U03163.1	NT	U03163 Homo sapiens cDNA
12348	25147	38170	1.95	1.0E-26	D14547.1	NT	D14547 Homo sapiens cDNA
12348	25147	38171	1.95	1.0E-26	D14547.1	NT	D14547 Homo sapiens cDNA
2505	15506	25606	1.27	9.0E-26	AL153218.2	NT	AL153218 Homo sapiens cDNA
12233	25726		1.52	9.0E-26	AL153218.2	NT	AL153218 Homo sapiens cDNA
6802	18041		2.09	8.0E-26	D14547.1	NT	D14547 Homo sapiens cDNA
1599	14630	27589	3.97	7.0E-26	AF005528.1	NT	AF005528 Homo sapiens cDNA
4095	17001	29766	1.29	7.0E-26	X89211.1	EST_HUMAN	X89211 Homo sapiens cDNA
4296	17772	30139	1.96	7.0E-26	AF0340193.1	EST_HUMAN	AF0340193 Homo sapiens cDNA
9534	18005	33020	1.05	7.0E-26	AL153202.2	NT	AL153202 Homo sapiens cDNA
12004	24639		8.16	7.0E-26	AA115896.1	EST_HUMAN	AA115896 Homo sapiens cDNA
12874	25774		10.79	7.0E-26	AF094599.1	EST_HUMAN	AF094599 Homo sapiens cDNA
2298	15248	28256	3.72	6.0E-26	AF093028.1	NT	AF093028 Homo sapiens cDNA
3395	16437	25041	1.1	6.0E-26	AF030513.1	EST_HUMAN	AF030513 Homo sapiens cDNA
12108	24646	35482	2.01	6.0E-26	AL153210.2	NT	AL153210 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12201	26326	38537	1.39	6.0E-27	U09163.1	NT	Homo sapiens IMAGE-82 (IMAGE-82), IMAGE-83 (IMAGE-83), IMAGE-84 (IMAGE-84), and IMAGE-81 (IMAGE-81) gene, complete 3' segment HSZC103
8249	21154		18.58	8.0E-27	AF135303.2	NT	Homo sapiens alpha 2(I) spectrin HSZC103
10731	27167	37044	3.59	8.0E-27	AF135303.2	EST_HUMAN	002134601F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE-421852 5'
10731	27167	37045	3.59	8.0E-27	BF96991.1	EST_HUMAN	002134601F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE-421852 5'
2105	18410	25413	1.44	4.0E-27	U02903.1	NT	Human mRNA for heparin alpha subunit, complete cds
7048	20724	33307	1.55	4.0E-27	56105568	NT	Mus musculus sperm tail associated protein (Spat), mRNA
8553	21449		1.26	4.0E-27	AF132063.2	NT	Homo sapiens chromosome 21 segment HSZC009
10294	23154	36564	0.85	4.0E-27	AF170778.1	NT	Rattus norvegicus putative four repeat for chromatin mRNA, complete cds
12633	24675	33380	1.99	4.0E-27	AF170778.1	EST_HUMAN	Q100-0710033-073500-182510 0710033 Homo sapiens cDNA
2055	15072	25073	4.43	3.0E-27	X62688.1	NT	R. rattus RYAS mRNA for a potential ligand-binding protein
4370	17384	30248	1.48	3.0E-27	BC071024.1	EST_HUMAN	FN0-8718527-090700-001-871 BT0527 Homo sapiens cDNA
5520	18609	31458	8.41	3.0E-27	AA077065.1	EST_HUMAN	7B4408 Chromosomes 7 Field Brain cDNA Library/Homo sapiens cDNA clone 7B4408
8294	21198	34334	0.91	3.0E-27	BE570351.1	EST_HUMAN	763362X1 NCI_CGAP_Lu241 Homo sapiens cDNA clone IMAGE-3264293 3'
6945	22853	35342	4.43	3.0E-27	BF033327.1	EST_HUMAN	001438531F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE-3852083 5'
44	13160	20051	10.48	2.0E-27	AF254187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1913	14834		18.23	2.0E-27	AA069346.1	EST_HUMAN	h014010.51 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE-1000559 similar to gblM17886 50S
3195	16295		17.02	2.0E-27	AF1693172.1	EST_HUMAN	ACD1C RIBOSOMAL PROTEIN P1 (HUMAN);
3271	16319	29222	1.28	2.0E-27	AF11167.2	NT	NF1112.21 Soares, NF1_T_GBC_S1 Homo sapiens cDNA clone IMAGE-2976879 3' similar to TR076040 07040 ORF2 FUNCTION UNKNOWN.
3271	16319	29223	1.28	2.0E-27	AF11167.2	NT	Homo sapiens Iba denervation protein gene, partial cds; cdc gene, complete cds; and unknown gene
6972	19956	33239	0.94	2.0E-27	H02855.1	EST_HUMAN	Y5607.1 Soares plectin N23-P Homo sapiens cDNA clone IMAGE-198040 5' similar to
8959	21600	34540	0.94	2.0E-27	AF169347.1	EST_HUMAN	SP-HMGC_MOUSE CG29H1 HOMOFOROX PROTEIN;
9600	22716		2.92	2.0E-27	AA051627.1	EST_HUMAN	h02605.51 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE-345373 similar to contains L13 L1
10310	25199	36069	0.81	2.0E-27	X00538.1	NT	Capitain RYAS mRNA for a potential ligand-binding protein
10338	24424	36840	1.00	2.0E-27	W73930.1	EST_HUMAN	EST_HOMO sapiens cDNA clone H56C67
10338	24424	36840	1.00	2.0E-27	W73930.1	EST_HUMAN	EST_HOMO sapiens cDNA clone H56C67
11353	23059	37755	3.07	2.0E-27	AF121638.1	EST_HUMAN	EST10739 5333 Homo sapiens cDNA clone IMAGE-345373 similar to contains L13 L1

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Maxi Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11619	14634		8.23	2.0E-27	AA58534.1	EST_HUMAN	H01H10.1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:100860 similar to gb:U7868.6S
489	13531		1.19	1.0E-27	AL162442.2	NT	ACDC18B350NAL PROTEIN P1 (HUMAN); Homo sapiens chromosome 21 segment 15210345
1026	14078	27014	1.05	1.0E-27	AB228968.1	NT	Homo sapiens DNA, DLEC1 to ORC1L1 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, Homo sapiens xylidulase [H. influenzae] homolog [XylB] mRNA
1724	14762	27720	1.37	1.0E-27	4627059	NT	Homo sapiens xylidulase [H. influenzae] homolog [XylB] mRNA MER29 replicase element
4198	17199		1.22	1.0E-27	BC359127.1	EST_HUMAN	Homo sapiens Rathe-derived POL-donahis factor-1 (RPE-1), mRNA
8623	15999	33068	6.79	1.0E-27	606525	NT	Homo sapiens RPE-1
7106	20196	33441	1.81	1.0E-27	F00188.1	EST_HUMAN	HSP20461 T1H8 Homo sapiens cDNA clone #4000066510
7106	20196	33442	1.81	1.0E-27	F00188.1	EST_HUMAN	HSP20461 T1H8 Homo sapiens cDNA clone #4000066510
9171	22099	35480	1.14	1.0E-27	AB007623.1	NT	Homo sapiens mRNA for KIA04054 protein, partial cds
8627	22464		1.76	1.0E-27	BE07769.1	EST_HUMAN	RC8-B10627-10200-011-E06 B10627 Homo sapiens cDNA
10243	22134	36538	3.02	1.0E-27	D87410.1	EST_HUMAN	Human mRNA for KIA0260 gene, partial cds
12126	24929	35473	3.74	1.0E-27	AF111053.1	NT	Bos taurus Mitochondrion 3' splice variant brain mRNA, complete cds
147	13246		1.85	9.0E-26	BC348398.1	EST_HUMAN	hml1711.11 NCL CGAP_L424 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR_Q0314 Q07314
831	13421	20337	2.36	9.0E-26	AU122903.1	EST_HUMAN	SECRETED NEUREXIN IIIA-ALPHA-C PRECURSOR, [B] TR_Q07280 TR_Q07313 ;
12307	28114		7.03	9.0E-26	BF37866	EST_HUMAN	CM2-TN140-070000372-g01 TN140 Homo sapiens cDNA
12005	28060		4.27	8.0E-26	AY157671.1	EST_HUMAN	aJ8108.11 Schneider field brain 000141 Homo sapiens cDNA clone IMAGE:276291 3' similar to
12008	14248	27189	8.25	7.0E-26	AU142780.1	EST_HUMAN	TR-003032 060002 KIA00095 PROTEIN, contains element MER22 repetitive element ;
11652	24638	36009	2.12	7.0E-26	AU142780.1	EST_HUMAN	AU142750 778A11 Homo sapiens cDNA clone Y78A11008E24 5'
12298	25065		4.39	7.0E-26	AV73846.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase-like activity 1008E24 5'
9475	22403		1.46	6.0E-26	AF010652	NT	AV738348 OS Homo sapiens cDNA clone CBFNA12 5'
126-6	25-000		6.74	8.0E-26	AA504692.1	EST_HUMAN	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
338	15428		2.24	5.0E-26	AB27003.1	EST_HUMAN	repetitive element contains element PTR13 repetitive element ; w01507.X1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:245592 3' similar to contains THR.b1 THR repetitive element ;
4004	17119	28666	1.51	5.0E-26	R0702.1	EST_HUMAN	AB27007.1 Sclerost placenta N2ZP1 Homo sapiens cDNA, clone IMAGE:16643 5'
2071	15507	28037	2.17	4.0E-26	AY166068.1	EST_HUMAN	AB28003.1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:239554 3' similar to SW_G065, HUMAN 1008E24 5' similar to CBFNA12 5'
7714	20546	33943	2.02	4.0E-26	AI168941.1	EST_HUMAN	1008E24 5' similar to CBFNA12 5' ; REVERSE TRANSCRIPTASE HOMOLOGY (HUMAN);

Table 4
Single Exon Probes Expressed in Adult Liver

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Probe SEQ ID	Exon SEQ ID	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E- Value	Top Hit Accession ID No.	Top Hit Database Source	Top Hit Description
11300	24216		3.29	4.0E-28 AF02308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families	
11444	27490		29.1	4.0E-28 AF03924.1	NT	Falls class GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds	
11445	26c46	33943	4.95	4.0E-28 AH89941.1	EST_HUMAN	gloV01.Xt Soares, testis, INT: Homo sapiens cDNA, clone IMAGE:75507.9 similar to gb-X19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG cDNA;	
12654	28327		1.71	4.0E-28 AV185424.1	EST_HUMAN	RQ3-C07261-29H400-210142 C10294 Homo sapiens cDNA	
1309	14342		2.17	3.0E-28 AF16592.1	NT	Homo sapiens mitochondrial ribo, distal-type-like, cytoskeleton protein 2 polypeptide (ADAM2) mRNA, complete cds	
6287	12833		1.32	3.0E-28 AF16592.1	NT	Homo sapiens T cell receptor beta locus, TORB1YSSA2 to TORB1Y252 region	
6596	22314	35678	2.31	3.0E-28 AF00560.1	EST_HUMAN	Homo sapiens T cell receptor beta locus, TORB1YSSA2 to TORB1Y252 region	
11374	24290	37734	1.65	3.0E-28 UJ35063.1	NT	Homo sapiens MHC class I region	
12680	25840		3.12	3.0E-28 AB511091.1	EST_HUMAN	W68907.X1 NCI, GOMP_Lym12 Homo sapiens cDNA, clone IMAGE:341086.9 similar to contains Aiu repetitive element-containing element HGR repeat element;	
12797	25840	28117	6.08	2.0E-28 BC025057.1	EST_HUMAN	RC2-BT1042-120300-075-803 B710624 Homo sapiens cDNA	
81	13204		9.58	2.0E-28 UJ35063.1	EST_HUMAN	RC-H10264-229330-019-208 B70624 Homo sapiens cDNA	
1182	14291	27170	9.58	2.0E-28 Y1107.3	NT	Homo sapiens TCBG, gene for integrin beta 4 subunit, exon 3-4-1	
1499	15501	28302	2.08	2.0E-28 AB46563.1	EST_HUMAN	q68360.X1 NCI, GOMP_Ly6 Homo sapiens cDNA, clone IMAGE:1910493.9 similar to contains L1.B2.L1 repetitive element;	
3471	14496	28356	2.08	2.0E-28 L10326X.2	NT	Homo sapiens chromosome 21 segment H21.C093	
8523	19333	37919	1.38	2.0E-28 BF524062.1	EST_HUMAN	L09111.NCBI, GOMP_Lym12 Homo sapiens cDNA, clone IMAGE:3751404.9 similar to contains LORI.141	
8697	19333	37919	4.18	2.0E-28 BF524062.1	EST_HUMAN	G013113.F057 NIH, MG6_54 Homo sapiens cDNA, clone IMAGE:5048751.5	
8698	21168	34896	0.76	2.0E-28 Y1107.3	EST_HUMAN	Sara codon, transmembrane 4 domain only, putative human mRNA, complete cds	
10113	22168		4.68	2.0E-28 AY027205.1	EST_HUMAN	ST5843634 NCBI, MAGL Homo sapiens cDNA, clone IMAGE:390748.5	
10113	22168		4.68	2.0E-28 AY027205.1	EST_HUMAN	W68907.X1 Soares infant brain; NIB Homo sapiens cDNA clone IMAGE:44300.5	
14927	26333		2.43	1.0E-28 Q380144.1	NT	Human gene for Ah-receptor, exon 7A	
14927	26333	27491	2.43	1.0E-28 Q380144.1	EST_HUMAN	OVI-LB10821-139900-300-403 B170821 Homo sapiens cDNA	
2234	19244	26262	2.64	1.0E-28 PF133263.1	EST_HUMAN	Homo sapiens protein to fibronectin protein L12 (H. sapientis) LOC333091 mRNA	
8442	13174		3.56	1.0E-28 6522793 NT	EST_HUMAN	Homo sapiens hypodermal protein FLJ109268 (FLJ109268) mRNA	
8597	21628		3.56	1.0E-28 6522793 NT	EST_HUMAN	EST1170615 HOC cell line (male-tetris to liver in mouse) II Homo sapiens cDNA 5' and similar to similar to retinol LTR	
9818	22724	36107	4.34	1.0E-28 AK05714.1	EST_HUMAN	Homo sapiens gamma-glutamyltransaminase-like activity 1 (GGTLA1), mRNA	
10338	23277	36659	5.69	1.0E-28 475943.7	NT	Homo sapiens gamma-glutamyltransaminase-like activity 1 (GGTLA1), mRNA	
10338	23277	36659	5.69	1.0E-28 475943.7	EST_HUMAN	Homo sapiens gamma-glutamyltransaminase-like activity 1 (GGTLA1), mRNA	
10338	23277	36659	5.69	1.0E-28 AK054182.1	NT	25fct01.JT Soares refines K24HR Homo sapiens cDNA clone IMAGE:390748.5	
10338	23277	36659	5.69	1.0E-28 AK054182.1	EST_HUMAN	25fct01.JT Soares refines K24HR Homo sapiens cDNA clone IMAGE:390748.5	

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Probe Seq ID NC:	Exon Seq ID NC:	ORF/SEQ ID NO:	Expression Signal	Most Similar (Top) Hit ELAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12972	25710		1.89	1.0E-26	AL162942.2	NT	Homo sapiens chromosome 21 segment HS21047
13037	23894	31381	3.13	0.0E-29	AF063697.1	EST_HUMAN	W55905.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:29752956 3
12977	23394		3.07	0.0E-29	X01030	SWISSPROT	W55905.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:29752956 3
1623	23936	27819	0.18	7.0E-29	AF063697.1	EST_HUMAN	W55905.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:29752956 3
13032	19655		0.18	7.0E-29	BE254703.1	EST_HUMAN	W55905.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:29752956 3
13035	25511		0.49	7.0E-29	AI132352.1	NT	Human testis cDNA for 45 kDa secretory protein, partial
616	13651		7.66	6.0E-29	A092748.1	EST_HUMAN	W55905.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:29752956 3 similar to TR-O15475
12549	25244	26554	8.63	6.0E-29	BE540436.1	EST_HUMAN	W55905.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:29752956 3 similar to TR-O15475
619	18110		1.25	5.0E-29	AL163203.2	NT	Human testis cDNA for 45 kDa secretory protein, partial
8260	22218		8.41	5.0E-29	AF063697.1	EST_HUMAN	W55905.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:29752956 3 similar to TR-O15475
3270	16327		3.10	4.0E-29	A175267.1	EST_HUMAN	W55905.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:29752956 3 similar to TR-O15475
6242	15208		7.81	4.0E-29	BE164930.1	EST_HUMAN	W55905.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:29752956 3 similar to TR-O15475
8659	21550	34927	0.65	4.0E-29	A1678101.1	EST_HUMAN	W55905.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:29752956 3 similar to TR-O15475
6059	21550	34928	0.65	4.0E-29	A1678101.1	EST_HUMAN	W55905.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:29752956 3 similar to TR-O15475
9304	22232	33552	3.49	4.0E-29	J04498.1	NT	Human SF 3D test shock protein gene, complete cds
2394	16359	29403	2.03	3.0E-29	U07947.1	NT	Human beta-tubulin alpha2 (beta-2-tubulin) mRNA, exon U
4522	17531	30384	1.85	3.0E-29	A042427.1	NT	Homo sapiens FIS gene for 6-pyruvate hydroxylase synthase, complete cds
8145	17846	30714	1.07	3.0E-29	BF33326.1	EST_HUMAN	W55905.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:29752956 3 similar to TR-O15475
8155	18213	32353	0.88	3.0E-29	BE314018.1	EST_HUMAN	W55905.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:29752956 3 similar to TR-O15475
9252	22220	33577	2.21	3.0E-29	D05044.1	NT	Human gene for A1-receptor, exon 7.9
8940	22745	35127	1.38	3.0E-29	A1630317.1	EST_HUMAN	W55905.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:29752956 3 similar to TR-O15475
10061	22977		1.82	3.0E-29	AF063697.2	NT	Human testis cDNA for 45 kDa secretory protein, partial
10485	23553		0.62	3.0E-29	BE360127.1	EST_HUMAN	W55905.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:29752956 3 similar to TR-O15475
11338	24257	37696	3.97	3.0E-29	P23295	SWISSPROT	W55905.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:29752956 3 similar to TR-O15475
13077	29607		1.75	3.0E-29	D03602.1	NT	Human HELM10 mRNA for HELM10, complete cds
5115	13355	26467	1.13	2.0E-29	AF034869.1	NT	Homo sapiens anaplastic protein RCO-5 (ent) gene, complete cds
5115	13355	26465	1.13	2.0E-29	AF034869.1	NT	Homo sapiens anaplastic protein RCO-5 (ent) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1556	14587	27545	6.77	2.0E-20	A093504.1	EST_HUMAN	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
1556	14587	27546	6.77	2.0E-20	A093504.1	EST_HUMAN	MERVE ENVELOPE GLYCOPORIN 1
4378	17392	30286	2.71	2.0E-20	AL16248.2	NT	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
6037	19036	32227	0.89	2.0E-20	A182459.1	EST_HUMAN	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
6121	19468	32641	1.55	2.0E-20	A180418.1	EST_HUMAN	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
7591	15498	32641	1.32	2.0E-20	A180418.1	EST_HUMAN	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
8696	21486	34827	1.05	2.0E-20	BE667157.1	EST_HUMAN	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
8141	22059	35430	0.56	2.0E-20	10677821	NT	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
8141	22059	35431	0.56	2.0E-20	10677821	NT	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
10359	22639	36327	3.67	2.0E-20	AL163248.2	NT	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
10359	22639	36328	3.67	2.0E-20	AL163248.2	NT	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
10733	23619	37047	4.45	2.0E-20	AL163248.2	NT	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
10733	23619	37048	4.45	2.0E-20	AL163248.2	NT	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
8398	21292	34624	0.48	1.0E-20	AV700745.1	EST_HUMAN	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
6350	22278	36940	10.42	1.0E-20	AV700745.1	EST_HUMAN	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
6894	18606	33111	3.5	9.0E-30	AA761215.1	EST_HUMAN	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
12346	26739		1.88	9.0E-30	11122745	NT	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
6574	18012		10.01	8.0E-30	G06888.1	EST_HUMAN	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
8846	21776	35123	1.37	8.0E-30	AA383973.1	EST_HUMAN	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
9241	21709	35521	3.59	8.0E-30	AI550752.1	EST_HUMAN	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
1536	14490		1	7.0E-30	BC091158.1	EST_HUMAN	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
1798	14824	27152	1.88	6.0E-30	D25303.1	NT	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
3235	16281	25181	2.69	6.0E-30	BE006028.1	EST_HUMAN	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
4871	10251	25181	0.97	0.0E-30	BE006028.1	EST_HUMAN	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
4069	17124	30001	48.86	5.0E-30	AI384602.1	EST_HUMAN	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
6169	25744		4.71	5.0E-30	317931.1	NT	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546
11324	24293		1.71	5.0E-30	AL163278.2	NT	W55410.v1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR016546 O16546

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Probe SEQ ID NO.	Exon SEQ ID NO.	QRF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10564	26/70	36966	9.11	2.0E-30	AI470791.1	EST_HUMAN	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
306	13389	26317	6.93	1.0E-30	U18638.1	EST_HUMAN	C18639 Human placenta cDNA (Tf-gamma) Homo sapiens cDNA clone cDNA:10031 5'
591	13630	26339	3.28	1.0E-30	AW458997.1	EST_HUMAN	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
386	13737	26721	9.65	1.0E-30	AI132202.2	NT	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
222	14238	26721	9.65	1.0E-30	AA56372.1	EST_HUMAN	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
1153	14338	26406	2.97	1.0E-30	BP467284.1	EST_HUMAN	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
1153	14338	26406	2.97	1.0E-30	AA315046.1	EST_HUMAN	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
8193	15163	26406	1.38	1.0E-30	BP183203.1	EST_HUMAN	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
8193	15163	34424	22.54	1.0E-30	BP183203.1	EST_HUMAN	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
12037	24836	34424	6.4	1.0E-30	H45523.1	EST_HUMAN	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
3630	16960	26743	0.73	0.0E-31	U13025.1	EST_HUMAN	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
3630	16960	26743	0.73	0.0E-31	U13025.1	EST_HUMAN	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
8869	21820	35181	0.91	0.0E-31	R18214.1	EST_HUMAN	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
8869	21820	35182	0.91	0.0E-31	R18214.1	EST_HUMAN	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
9184	22112	35472	1.57	0.0E-31	U23823.1	EST_HUMAN	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
13091	25008	31735	0.83	0.0E-31	AF078178.1	NT	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
1104	14147	27066	2.21	8.0E-31	6705441	NT	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
2438	15442	30882	11.81	8.0E-31	AI162008.2	NT	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
5027	18034	30882	1	8.0E-31	P23275	SWISSPROT	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
5027	18034	30883	1	8.0E-31	P23275	SWISSPROT	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
794	13782	28707	1.21	7.0E-31	AA372897.1	EST_HUMAN	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
2717	15710	28708	1.82	7.0E-31	BC328571.1	EST_HUMAN	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
2717	15710	28708	1.82	7.0E-31	BC328571.1	EST_HUMAN	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
8971	21691	35245	0.67	7.0E-31	AA1208541.1	NT	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
8971	21691	35245	0.67	7.0E-31	AA1208541.1	NT	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
1795	22712	31808	1.18	7.0E-31	BE409911.1	EST_HUMAN	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
1795	22712	31808	1.18	7.0E-31	BE409911.1	EST_HUMAN	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
3746	16778	31808	3.29	0.0E-31	AA1223391.1	NT	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3
8752	21602		3.32	0.0E-31	AA1050061.1	NT	hsc3466.x1 NCI CGAP_Kdr12 Homo sapiens cDNA clone IMAGE:2675490 3' similar to contains THRB3

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Probe SEQ ID NO.	Exon SEQ ID NO.	QTF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6696	21699	35192	0.79	6.0E-31	BC359127.1	EST_HUMAN	IMAGE01 at NCBI CGAP. K4618 Homo sapiens cDNA, clone IMAGE-3146256.3 similar to contains MER29.53
11179	24105	37552	1.74	6.0E-31	AF170103.1	EST_HUMAN	IMAGE01 at NCBI CGAP. K4618 Homo sapiens cDNA, clone IMAGE-3146256.3 similar to contains MER29.53
12837	29170	31974	3.26	6.0E-31	AF172888.1	EST_HUMAN	IMAGE01 at NCBI CGAP. K4618 Homo sapiens cDNA, clone IMAGE-3146256.3 similar to contains MER29.53
12812	21911	31974	1.97	6.0E-31	AF172888.1	EST_HUMAN	IMAGE01 at NCBI CGAP. K4618 Homo sapiens cDNA, clone IMAGE-3146256.3 similar to contains MER29.53
205	33534	26230	1.88	6.0E-31	AF172888.1	EST_HUMAN	IMAGE01 at NCBI CGAP. K4618 Homo sapiens cDNA, clone IMAGE-3146256.3 similar to contains MER29.53
205	13304	26221	1.95	5.0E-31	M6084.1	NT	Homo sapiens beta DNA topoisomerase gene, exon 8
9193	21942		0.67	5.0E-31	BF054540.1	EST_HUMAN	IMAGE01 at NCBI CGAP. K4618 Homo sapiens cDNA, clone IMAGE-3146256.3 similar to contains MER29.53
617	13682		4.99	4.0E-31	AF271738.1	NT	Similar to PGO ELEMENT, contains L1 L1.1, negative element.
1834	14054	27026	1.18	4.0E-31	Q10473	SWISSPROT	POLYPEPTIDE NACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-LDP)
1840	14603		2.67	4.0E-31	AF16280.2	NT	ACETYL GALACTOSAMINYL TRANSFERASE (UDP-GALNAc-POLYPEPTIDE, N-)
2837	18508		2.03	4.0E-31	5730038	NT	Homo sapiens chromosome 21, segment H8ZIG80
12651	25077		1.55	4.0E-31	A1230125.1	NT	Homo sapiens SET domain and nuclear transposase fusion gene (SETMAR) mRNA
12898	25446		1.49	4.0E-31	AB006811.1	NT	Homo sapiens GGT1 gene, exon 1
2637	16634	28631	2.8	3.0E-31	6008971	NT	Homo sapiens gene for activin receptor type IIB, complete cds
7725	20657	33954	12.5	3.0E-31	4626833	NT	Homo sapiens SEC03, endoplasmic reticulum transloc component (S. cerevisiae) like (SEC03L), mRNA
7916	20659	34142	1.42	3.0E-31	11420326	NT	Homo sapiens MADH dehydrogenase (ubiquinone) 1 beta subcomplex 8 (10H, ASH1, NDUF8) mRNA
8271	21176	34511	0.47	3.0E-31	AF168062.1	EST_HUMAN	Homo sapiens hypothetical protein FL10942 (FL10942), mRNA
8271	21176	34512	0.47	3.0E-31	AF168062.1	EST_HUMAN	CH3-NN0006-300590-132-e37 NN0006 Homo sapiens cDNA
8739	21699		1.97	3.0E-31	AF16206.2	NT	CH3-NN0006-300590-132-e37 NN0006 Homo sapiens cDNA
10109	20000	30896	9.8	3.0E-31	D14523.1	NT	Homo sapiens chromosome 21, segment H8ZIC003
11077	20009	37451	3.20	3.0E-31	PI1174	SWISSPROT	Homo mRNA for fertilin L-chain, complete cds
11683	24602		3.99	3.0E-31	BF038327.1	EST_HUMAN	40S RIBOSOMAL PROTEIN S15 (RIB PROTEIN)
11083	14654	27031	1.39	2.0E-31	AF168171.1	EST_HUMAN	60T48B551PT NH, MG2, 60 Homo sapiens cDNA, clone IMAGE-350266.5
2229	15239	28246	2	2.0E-31	A06398.1	EST_HUMAN	QY21.T0051-260302-111-401 T0051 Homo sapiens cDNA
2383	15069	28573	2.94	2.0E-31	AF111245.1	EST_HUMAN	194405.41 Soares, NE, T, GSC, 51 Homo sapiens cDNA, clone IMAGE-3111972.3
2404	15407	28166	5.87	2.0E-31	AA458824.1	EST_HUMAN	CH472761G1513.11 T001 (epitome, hamy) Homo sapiens cDNA, clone DK-22971G1513.5
5457	19538	31390		2.0E-31	AF144465.1	EST_HUMAN	es8811 at Stralagene and mRNA 517222 Homo sapiens cDNA, clone IMAGE-358413.3 similar to contains TIR121.11K, repetitive element.
							U14HBS-ab-H3-01-01-81 NCBI CGAP. Sub5 Homo sapiens cDNA, clone IMAGE-2753583.3

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12407	25213		3.51	7.0E-32	X17263.1	NT	Human chromosome 22 intron angiotensin V(X) gene, part, with 5' breakpoint between exon and intron
2781	15772	28757	0.94	6.0E-32	A178104.1	EST_HUMAN	Human cDNA clone IMAGE:215994.3 similar to contains MER29.13
7758	20698		1.16	6.0E-32	U628016.1	EST_HUMAN	Human cDNA clone IMAGE:391007.9
1353	26690		2.14	6.0E-32	A486453.1	EST_HUMAN	Human cDNA clone IMAGE:145992.3 similar to contains L1.13 L1
1350	14104	27042	2.79	5.0E-32	A171882.1	NT	Human cDNA clone IMAGE:313970.1
959	14039		2.03	4.0E-32	A145248.2	NT	Human cDNA clone IMAGE:313970.1
8047	20690	34274	3.28	4.0E-32	U1432574	NT	Human cDNA clone IMAGE:313970.1
8047	20690	34275	3.28	4.0E-32	U1432574	NT	Human cDNA clone IMAGE:313970.1
1478	13149	29468	2.86	3.0E-32	A175160.1	EST_HUMAN	Human cDNA clone IMAGE:313970.1
1473	14104	27468	11.44	3.0E-32	A175160.1	EST_HUMAN	Human cDNA clone IMAGE:313970.1
6800	22835	36224	8.8	3.0E-32	A1756834.1	EST_HUMAN	Human cDNA clone IMAGE:313970.1
6800	22835	36225	9.8	3.0E-32	A1756834.1	EST_HUMAN	Human cDNA clone IMAGE:313970.1
11393	24281	37724	3.39	3.0E-32	A477621.1	EST_HUMAN	Human cDNA clone IMAGE:313970.1
12499	25231		5.74	3.0E-32	BE270065.1	EST_HUMAN	Human cDNA clone IMAGE:313970.1
12831	18428	31346	4.39	3.0E-32	5174674	NT	Human cDNA clone IMAGE:313970.1
12831	18428	31347	4.39	3.0E-32	5174674	NT	Human cDNA clone IMAGE:313970.1
12878	25538		4.9	3.0E-32	BE270065.1	EST_HUMAN	Human cDNA clone IMAGE:313970.1
4891	17890	30847	0.79	2.0E-32	B206613.1	EST_HUMAN	Human cDNA clone IMAGE:313970.1
6941	18646	32724	0.78	2.0E-32	M65418.1	NT	Human cDNA clone IMAGE:313970.1
6743	19787	33039	5.02	2.0E-32	238133.1	NT	Human cDNA clone IMAGE:313970.1
6743	19787	33039	5.02	2.0E-32	238133.1	NT	Human cDNA clone IMAGE:313970.1
8854	21784	35132	4.49	2.0E-32	A4114294.1	EST_HUMAN	Human cDNA clone IMAGE:313970.1
8854	21784	35132	4.49	2.0E-32	A4114294.1	EST_HUMAN	Human cDNA clone IMAGE:313970.1
7409	20177	33442	6.17	1.0E-32	11430780	NT	Human cDNA clone IMAGE:313970.1
9198	22095	35445	0.85	1.0E-32	A4720374.1	EST_HUMAN	Human cDNA clone IMAGE:313970.1
3540	16578		5.3	9.0E-33	BE327112.1	EST_HUMAN	Human cDNA clone IMAGE:313970.1

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Probe SEQ ID NO.	Exon SEQ ID NO.	QTF SEQ ID NO.	Expression Signal	Meq Starler (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2444	15448		2.75	4.0E-33	AA026921.1	EST_HUMAN	455111.11 Staphylococcus aureus 837218 Homo sapiens cDNA clone IMAGE:384317 5' similar to
2676	13575	25571	7.3	4.0E-33	AL163210.2	NT	containing A11 sapiens and containing 115270910
4397	17605	30462	1.76	4.0E-33	AT123356.1	EST_HUMAN	UHLER-24300-01-011 NCJ CGAP S104 Homo sapiens cDNA clone IMAGE:2727463
8598	16695	31541	20.44	4.0E-33	AA05095.1	EST_HUMAN	371429.1 Staphylococcus aureus 837218 Homo sapiens cDNA clone IMAGE:103818 5' similar to
8599	16695	32690	0.73	4.0E-33	BA33264.1	NT	371429.1 Staphylococcus aureus 837218 Homo sapiens cDNA clone IMAGE:103818 5' similar to
8599	16695	32691	0.73	4.0E-33	BA33264.1	NT	371429.1 Staphylococcus aureus 837218 Homo sapiens cDNA clone IMAGE:103818 5' similar to
8599	16695	32691	0.73	4.0E-33	BA33264.1	NT	371429.1 Staphylococcus aureus 837218 Homo sapiens cDNA clone IMAGE:103818 5' similar to
1116	14158		4.65	3.0E-33	BE350127.1	EST_HUMAN	Homo sapiens polyomavirus (DNA directed), alpha POLA1 mRNA
1117	14158		2.57	3.0E-33	BE350127.1	EST_HUMAN	Homo sapiens polyomavirus (DNA directed), alpha POLA1 mRNA
2474	15624		3.3	3.0E-33	AA047851.1	EST_HUMAN	NER20 repetitive element
10920	23905	37232	0.97	3.0E-33	AA091510.1	EST_HUMAN	NER20 repetitive element
108	13133		3.44	2.0E-33	AI160186.1	EST_HUMAN	NER20 repetitive element
1399	14430	27354	1.82	2.0E-33	AA101024.1	EST_HUMAN	NER20 repetitive element
1399	14430	27355	1.82	2.0E-33	AA101024.1	EST_HUMAN	NER20 repetitive element
4526	17635		3.76	2.0E-33	BE158039.1	EST_HUMAN	NER20 repetitive element
8107	18104	30651	2.21	2.0E-33	AA026983.1	EST_HUMAN	NER20 repetitive element
8228	18217	31055	1.77	2.0E-33	11421332	NT	NER20 repetitive element
8228	18217	31054	1.77	2.0E-33	11421332	NT	NER20 repetitive element
6951	19727	32927	1.07	2.0E-33	AA27492.1	EST_HUMAN	NER20 repetitive element
6945	22571		1.77	2.0E-33	AA06255.1	EST_HUMAN	NER20 repetitive element
9	13124		1.06	1.0E-33	AA026928.1	NT	NER20 repetitive element
5782	18654	31850	0.99	1.0E-33	AA159430.1	NT	NER20 repetitive element
7695	20735	34338	1.03	1.0E-33	AA159430.1	NT	NER20 repetitive element
13024	24995		1.04	1.0E-33	U03822.1	NT	NER20 repetitive element
11785	24995	35152	1.91	1.0E-33	AA166516.1	EST_HUMAN	NER20 repetitive element
12089	24930	35435	2.78	1.0E-33	U03822.1	NT	NER20 repetitive element

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
12739	25579		1.45	1.0E-33	AB27191.1	EST_HUMAN	w88305.01 NCL CGAP_KRT11 Homo sapiens cDNA clone IMAGE:2462140 3'
12869	13124		3.50	1.0E-38	AF030328.1	NT	Homo sapiens X-linked ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
12927	25501		0.97	1.0E-33	AF127396.1	EST_HUMAN	AV127809.H1C Homo sapiens cDNA clone HTOCONC17 9'
4724	117720		2.44	9.0E-34	BE16753.1	EST_HUMAN	PM44-T0592-BT190-H01-L02-T10532 Homo sapiens cDNA
13078	14778		0.66	9.0E-34	AJ271735.1	NT	Homo sapiens Xq pseudobisomical region, segment 12'
2184	15195	28200	0.96	9.0E-34	8922761	NT	Homo sapiens hypothetical protein FL10900 (FL-17000), mRNA
8276	14191	34619	0.65	9.0E-34	BC089882.1	EST_HUMAN	NR44-T0356-200100-001-503 BT0389 Homo sapiens cDNA
1463	14484	27485	3.65	7.0E-34	U70948.5	EST_HUMAN	Y14505.11 Soares f4c1 liver spleen N1FLS3 Homo sapiens cDNA clone IMAGE:1088320 5'
105056	14404	27455	0.66	7.0E-34	U70948.5	EST_HUMAN	Y14505.11 Soares f4c1 liver spleen N1FLS3 Homo sapiens cDNA clone IMAGE:1088320 5'
12924	18287		2.38	7.0E-34	U128968.1	EST_HUMAN	J14C10T1 Soares f4c1c1c1 N02P-1P Homo sapiens cDNA clone IMAGE:148722 5'
403	13563	25481	1.43	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
483	13063	26482	1.4	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
6288	18774	31152	0.97	6.0E-34	U496461.1	EST_HUMAN	PM6-BN005-10300-001-008 BN0085 Homo sapiens cDNA
12366	18724	31152	1.3	6.0E-34	U308989.1	NT	Non-muscle DAB22 half-specific (non-1) gene
1902	14923		1.91	5.0E-34	7705900.1	NT	Homo sapiens Nucleosome-binding protein NucleoB1 (NCLB1) mRNA
5196	18181	31029	5.67	5.0E-34	U30893.1	NT	Human splicing factor SF6085.1 (SF6P-50) mRNA, complete cds
8424	22852	35718	1.58	5.0E-34	U167876.1	NT	Human no-virgatus (HUMAN) protein (HUMAN) mRNA, complete cds
11098	24209	34743	2.34	5.0E-34	U535785.1	NT	Human no-virgatus (HUMAN) protein (HUMAN) mRNA, complete cds
11701	24633		1.72	5.0E-34	U163399.2	NT	Human no-virgatus (HUMAN) protein (HUMAN) mRNA, complete cds
2014	16833	28038	2.02	5.0E-34	U304047	EST_HUMAN	h04092.1 NCL CGAP_P22a Homo sapiens cDNA clone IMAGE:22449 34 3'
3215	16233	39102	0.68	4.0E-34	U304047	EST_HUMAN	h04092.1 NCL CGAP_P22a Homo sapiens cDNA clone IMAGE:22449 34 3'
9279	23338	39102	0.68	4.0E-34	U304047	EST_HUMAN	h04092.1 NCL CGAP_P22a Homo sapiens cDNA clone IMAGE:22449 34 3'
10718	23338	39102	1.26	4.0E-34	BP20078.1	EST_HUMAN	435670.11 Soares, testis, N4T1 Homo sapiens cDNA clone IMAGE:1407690 5'
6439	16524	32702	0.8	3.0E-34	U33277.1	NT	Human 16S ribosomal protein L16, partial cds
11892	24981		3.26	3.0E-34	FR038321.1	EST_HUMAN	Human 16S ribosomal protein L16, partial cds
9505	22483	35796	0.85	2.0E-34	U67891.1	EST_HUMAN	w875400.11 Soares, N1FL-1, GBC, S31 Homo sapiens cDNA clone IMAGE:2330170 5' similar to cofilin
9506	22483	35797	0.85	2.0E-34	U67891.1	EST_HUMAN	w875400.11 Soares, N1FL-1, GBC, S31 Homo sapiens cDNA clone IMAGE:2330170 5' similar to cofilin
11601	24010	37678	1.57	2.0E-34	251905	EST_HUMAN	MEF29.2 MEF29 repetitive element
11601	24010	37677	1.57	2.0E-34	251905	EST_HUMAN	MEF29.2 MEF29 repetitive element
11601	24010	37677	1.57	2.0E-34	251905	EST_HUMAN	MEF29.2 MEF29 repetitive element
1524	14855	27616	5.3	1.0E-34	P12295	SWISSPROT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar RefSeq BLAST E Value	Top HA Accession No.	Top Hit Database Source	Top Hit Descriptor
3741	16773	29559	1.87	1.0E-34	AF005926.1	NT	Homo sapiens V-hind anti-oncogene subdermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4188	17179	30051	1	1.0E-34	AF005937.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4188	17179	30052	1	1.0E-34	AF005937.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4093	17601	30052	7.12	1.0E-34	BE071414.1	EST HUMAN	RC231106B11 (H1) NC_001610.1 Homo sapiens cDNA clone IMAGE338892.9
8378	16427	32593	2.35	1.0E-34	BE374032.1	EST HUMAN	801414102F1 NH_145627.1 Homo sapiens cDNA clone IMAGE338892.9
8378	16427	32594	2.35	1.0E-34	BE374032.1	EST HUMAN	801414102F1 NH_145627.1 Homo sapiens cDNA clone IMAGE338892.9
8609	22781	35710	0.69	1.0E-34	F23295	SWISSPROT	CLF4CTORY RECEPTOR-LIKE PROTEIN F5
10219	28110	35511	10.3	1.0E-34	LA086353.1	EST HUMAN	04752644.1559.1 (54) for protein: H1021 Homo sapiens cDNA clone DMP059441553.5'
11628	24834	35033	1.58	1.0E-34	BE717960.1	EST HUMAN	04752644.1559.1 (54) for protein: H1021 Homo sapiens cDNA clone IMAGE337478.5'
11628	24834	35034	1.56	1.0E-34	BE717960.1	EST HUMAN	04752644.1559.1 (54) for protein: H1021 Homo sapiens cDNA clone IMAGE337478.5'
12708	25602		2.69	1.0E-34	AA807092.1	EST HUMAN	cc3141.11 NCL CGAP CG61 Homo sapiens cDNA clone IMAGE1351813.3' similar to gb:368209
12708	25602		2.69	1.0E-34	AA807092.1	EST HUMAN	cc3141.11 NCL CGAP CG61 Homo sapiens cDNA clone IMAGE1351813.3' similar to gb:368209
12708	25602		2.69	1.0E-34	AA807092.1	EST HUMAN	cc3141.11 NCL CGAP CG61 Homo sapiens cDNA clone IMAGE1351813.3' similar to gb:368209
3714	16748	29534	2.2	9.0E-35	AF065302.1	EST HUMAN	TYROSINE-PROTEIN KINASE RECEPTOR FL14 P1ECU/RBOR (HUMAN);
242	13339		10.64	8.0E-35	6051160	NT	Homo sapiens diuretic 21 segment HB27C010
1796	14792	27762	4.72	8.0E-35	BF58937.1	EST HUMAN	Homo sapiens prohibitin (PHB) mRNA
1796	14792	27763	4.72	8.0E-35	BF58937.1	EST HUMAN	new33403.1 NCL CGAP Kd41 Homo sapiens cDNA clone IMAGE3259134.3' similar to TR:075612
4075	17978	30334	3.13	8.0E-35	BF183195.1	EST HUMAN	new33403.1 NCL CGAP Kd41 Homo sapiens cDNA clone IMAGE3259134.3' similar to TR:075612
11132	24031	37529	2.21	8.0E-35	BE378490.1	EST HUMAN	075912 DIACYLGLYCEROL KINASE IOTA ;
12405	28212		5.01	8.0E-35	BF569282.1	EST HUMAN	075912 DIACYLGLYCEROL KINASE IOTA ;
6759	19763	33007	1.69	7.0E-35	11425417	NT	601259426F1 NH_145627.1 Homo sapiens cDNA clone IMAGE33695513.5'
1983	15001	27866	1.35	6.0E-35	6005976	NT	602134024F1 NH_145627.1 Homo sapiens cDNA clone IMAGE3300860.3'
4137	17188	30034	0.73	6.0E-35	AW787191.1	EST HUMAN	Homo sapiens phosphatidylinositol 4-kinase, class L (PI4K), mRNA
3310	18294	31147	0.79	6.0E-35	AW787191.1	EST HUMAN	Homo sapiens phosphatidylinositol 4-kinase, class L (PI4K), mRNA
8477	21408	34746	4.62	6.0E-35	X64292.1	NT	UHH-BW0-4d-460-0 ULG1 NCL CGAP S3.06 Homo sapiens cDNA clone IMAGE2751433.3'
6287	22195	33552	0.59	6.0E-35	X64292.1	NT	PMH CT0257-0617289-004-H08 CT0257 Homo sapiens cDNA
6287	22195	33553	0.59	6.0E-35	X64292.1	NT	Homo sapiens triple functional domain (PTPRF) interacting (TRIC), mRNA
10191	23092	39463	0.79	6.0E-35	AB002384.1	NT	Homo sapiens mRNA for novel T-cell activation protein
10414	23093	39720	2.76	6.0E-35	AB003786.1	NT	Homo sapiens mRNA for KIAA1065 protein, partial cds
13088	25594	31726	7.98	6.0E-35		NT	Homo sapiens beta-undopropione (LOC31733), mRNA
13088	25594	31727	7.98	6.0E-35	11417871	NT	Homo sapiens beta-undopropione (LOC31733), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similar (Tco) HR BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
151	15241	26169	38.71	5.0E-35	AF154830.1	NT	Homo sapiens calyculin phosphatase 1 mRNA, complete cds
1738	14753	27735	5.09	5.0E-35	U03302.1	NT	H sapiens immunoglobulin kappa light chain variable region 1-4
3052	16155	28209	1.45	5.0E-35	6912639	NT	Homo sapiens Bag1 and YY1 binding protein (RYBP), mRNA
4516	17625	30391	1.68	5.0E-35	AF223268.1	NT	Homo sapiens d3c kinase (CLU30, proprii, cdc1, glucocorticoid-induced (GSA), and reovirus genes, complete cds
9732	21692		5.28	5.0E-35	BE589992.1	EST_HUMAN	Homo sapiens phosphatase and glucocorticoid-induced phosphatase, and transcription factors (THBS3) gene, partial cds
8798	21718	35006	2.81	5.0E-35	AI208795.1	EST_HUMAN	U014198AF1 NH_120622 Homo sapiens cDNA clone IMAGE:381728 3'
8798	21718	35007	2.81	5.0E-35	AI208795.1	EST_HUMAN	U038065x1 Sources: testis, NHF Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW12496 HUMAN Q92350 -HYPOTHETICAL PROTEIN KIAA0249.1
11620	24527		3.16	5.0E-35	AA001766.1	EST_HUMAN	U038065x1 Sources: testis, NHF Homo sapiens cDNA clone IMAGE:1837448 3' similar to ZH9412.1 Sources: testis, liver, spleen, INFLS_31 Homo sapiens cDNA clone IMAGE:426018 5'
1454	14486	27447	6.73	4.0E-35	BE257007.1	EST_HUMAN	U01189710F1 NH_120622 Homo sapiens cDNA clone IMAGE:3359408 5'
1841	14854	27845	11.9	4.0E-35	HY1193.1	EST_HUMAN	U08407.1 Sources: fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTRG repetitive element;
4820	17919		0.72	4.0E-35	AF003528.1	NT	Homo sapiens X-linked arylsulfatase ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5245	18232		1.01	4.0E-35	BE402102.1	EST_HUMAN	U01300709F1 NH_120622 Homo sapiens cDNA clone IMAGE:3834401 3'
7975	20611		1.75	4.0E-35	BE350127.1	EST_HUMAN	U09501.1 NC1 CGAP J4413 Homo sapiens cDNA clone IMAGE:3146266 3' similar to contains MER26.53 MER29 repetitive element;
9093	22012	33839	9.85	4.0E-35	AI048561.1	EST_HUMAN	DKFZ544148.1 J1 434 (synonym: Thes3) Homo sapiens cDNA clone DKFZ544148.1
1091	14632	27932	17.44	3.0E-35	BE268182.1	EST_HUMAN	U01125200F1 NH_120622 Homo sapiens cDNA clone IMAGE:3343993 5'
2353	15391		4.16	3.0E-35	AI224462.1	NT	Homo sapiens phosphatidylethanolamine 1 gene, complete cds
5524	18603	31451	23.83	3.0E-35	BF493100.1	EST_HUMAN	U025940x1 NC1 CGAP L104 Homo sapiens cDNA clone IMAGE:3665951 3' similar to TR G0G2H7 Q04247 F404 PROTEIN F02.1;
9524	18603	31452	23.83	3.0E-35	BF493100.1	EST_HUMAN	U025940x1 NC1 CGAP L104 Homo sapiens cDNA clone IMAGE:3665951 3' similar to TR G0G2H7 Q04247 F404 PROTEIN F02.1;
10291	22971		1.52	3.0E-35	AF223391.1	NT	Homo sapiens calcium channel alpha1C subunit (CACNA1C) gene, conts 7-49, and partial cds, alternatively spliced
16711	23557	36989	0.97	3.0E-35	AI000303.1	EST_HUMAN	U08405x1 NC1 CGAP C03 Homo sapiens cDNA clone IMAGE:2480482 3' similar to SW12496 HUMAN P40286 RETROVIRUS RELATED POLYPROTEIN (CONTAINS REVERSE TRANSCRIPTASE);
112	16608	25135	0.91	2.0E-35	NB8835.1	EST_HUMAN	U03023F Human fetal heart L umbilic 229 Express Homo sapiens cDNA clone K0552 2' similar to REPTITIVE ELEMENT

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Best Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1216	14254	27168	1.36	2.0E-35	U1309.1	EST_HUMAN	4971F Head Homo sapiens cDNA clone A971
2282	15242	28226	3.34	2.0E-35	AB018418.1	NT	Homo sapiens mRNA for GAB2, candidate cdc
2732	16726	28721	1.13	2.0E-35	AY166305.1	EST_HUMAN	NS842.74 Splice 1, C8C, S1 Homo sapiens cDNA clone IMAGE:2079148 3' similar to
3327	16401	28701	1.07	2.0E-35	6012458	EST_HUMAN	SV4TR12 HUMAN Q1469 T1470D RECEPTOR INTERACTING PROTEIN 12,
3337	16401	28701	0.70	2.0E-35	6012458	NT	Homo sapiens GAB2-associated linker 2 (GAB2GLT1) mRNA
3616	16662	29002	0.54	2.0E-35	AB022702.1	NT	Homo sapiens GAB2-associated linker 2 (GAB2GLT1) mRNA
3644	17012	29000	0.88	2.0E-35	BE247575.1	EST_HUMAN	TCBAP-2E-628 Pediatric pro-B cell acute lymphoblastic leukemia Bayler-HGSC project=TCBA Homo sapiens
3944	17012	29001	0.88	2.0E-35	BE247575.1	EST_HUMAN	TCBAP-2E-628 Pediatric pro-B cell acute lymphoblastic leukemia Bayler-HGSC project=TCBA Homo sapiens
4781	17766	31201	3.68	2.0E-35	BA0226.1	EST_HUMAN	cDNA clone TC9AP-428
8412	18393	31200	1.08	2.0E-35	AY129108.1	EST_HUMAN	MT9a12.11 Sources (full liver spleen INHLS Homo sapiens cDNA clone IMAGE:27479 6'
8412	18393	31201	1.08	2.0E-35	AY129108.1	EST_HUMAN	LI-H-82-agg-B-10-CUL11 NCI CGAP Subd Homo sapiens cDNA clone IMAGE:272982 3'
8774	18847	31960	1.77	2.0E-35	BF332417.1	EST_HUMAN	Q10-B10701-210-400-169-404 B10701 Homo sapiens cDNA
7463	20403	33679	0.73	2.0E-35	BE632664.1	EST_HUMAN	CM2MT0125-200-600-297-502 MT0125 Homo sapiens cDNA
7463	20403	33679	0.73	2.0E-35	BE632664.1	EST_HUMAN	CM2MT0125-200-600-297-502 MT0125 Homo sapiens cDNA
11237	24169	37010	2.88	2.0E-35	EX94171.1	NT	H-sapiens PROS-27 mRNA
12001	25469	31950	1.51	2.0E-35	BF332417.1	EST_HUMAN	Q10-B10701-210-400-169-404 B10701 Homo sapiens cDNA
49	13195	20050	6.38	2.0E-35	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21010
40	13196	20051	4.55	1.0E-35	AA031946.1	EST_HUMAN	hinc10 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
778	13633	20795	82.36	1.0E-35	AY138473.1	EST_HUMAN	hinc10 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
778	13633	20796	82.36	1.0E-35	AY138473.1	EST_HUMAN	hinc10 Regional genomic DNA specific cDNA library Homo sapiens cDNA
944	13696	20795	1.78	1.0E-35	BT87947.1	EST_HUMAN	YR6301.1 Sources (full liver spleen INHLS Homo sapiens cDNA clone IMAGE:118755 5' similar to
2573	15571	28586	2.29	1.0E-35	7702594	NT	SP-A44282.44082 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
2916	15607	28805	2.11	1.0E-35	BE394127.1	EST_HUMAN	Homo sapiens hypothetical protein (LOC517233), mRNA
2818	15907	28909	2.11	1.0E-35	BE394127.1	EST_HUMAN	hinc901.1 NCI CGAP J04F15 Homo sapiens cDNA clone IMAGE:3142256 3' similar to contains MER29.03
3208	16294	29150	1.73	1.0E-35	AY554421.1	EST_HUMAN	hinc901.1 NCI CGAP J04F15 Homo sapiens cDNA clone IMAGE:3142256 3' similar to contains MER29.03
4629	17538	30639	6.72	1.0E-35	7026506	NT	hinc901.1 NCI CGAP J04F15 Homo sapiens cDNA clone IMAGE:3142256 3' similar to contains MER29.03

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4629	17638	30400	5.72	1.0E-36	7656905	NT	Matr. muscle actin receptor interacting protein 1 (Aip1-binding), mRNA
5700	18773	31702	1.44	1.0E-35	11520236	NT	Homo sapiens chromatin assembly factor 1, subunit 8 (CAF8), mRNA
7337	18505	31780	0.97	1.0E-35	AY180865.1	EST_HUMAN	hAT-31011-111185-011-487 310111 Homo sapiens cDNA
7593	20028	34131	0.82	1.0E-35	AD021051	NT	Homo sapiens mRNA for KIAA1219 (KIAA1219), mRNA
8000	27002	34325	1.02	1.0E-35	11418002	NT	Homo sapiens KIAA1219 gene product (KIAA1219), mRNA
10071	25622	36380	1.83	1.0E-35	AJ158595.1	EST_HUMAN	U158595 PLACED Homo sapiens cDNA clone IMAGE300382 3'
10071	25622	36381	1.85	1.0E-35	AJ158595.1	EST_HUMAN	U158595 PLACED Homo sapiens cDNA clone IMAGE300382 3'
11000	28304	37373	0.83	1.0E-35	BF56564.1	EST_HUMAN	hsp4005-1 NCI CGAP Proa Homo sapiens cDNA clone IMAGE3254051 3' similar to TR-031341
11080	26524	37374	0.83	1.0E-35	BF56564.1	EST_HUMAN	hsp4005-1 NCI CGAP Proa Homo sapiens cDNA clone IMAGE3254051 3' similar to TR-031341
12172	29008	38511	1.87	1.0E-35	AB028980.1	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
12172	29008	38512	1.87	1.0E-35	AB028980.1	NT	homo-7.D01.7 butanol Homo sapiens cDNA 5'
12180	28016	38512	1.86	1.0E-35	AJ251181	EST_HUMAN	Homo sapiens Itubulin 1 (ITUB1), mRNA
12176	28607	38512	1.95	1.0E-35	11418274	NT	hsp4005-1 NCI CGAP Proa Homo sapiens cDNA clone IMAGE300382 3'
12600	28426	38512	2.23	1.0E-35	BE76232.1	EST_HUMAN	hsp4005-1 NCI CGAP Proa Homo sapiens cDNA clone IMAGE300382 3'
6240	18284	32453	0.87	8.0E-36	X78476.1	NT	8. beta BBS2 mRNA for scd-16
6771	22695	36081	0.91	8.0E-36	AA348490.1	EST_HUMAN	EST154938 Hippocampus II Homo sapiens cDNA 5' and similar to endogenous retrovirus 9, 5' LTR
2075	19035	28025	2.11	7.0E-36	AV157192.1	EST_HUMAN	GMT-CT103-0510259-003-007 CT10311 Homo sapiens cDNA
3163	18213	34341	6.32	7.0E-36	4557498	NT	Homo sapiens Chemokine binding protein 2 (CTBP2) mRNA
8103	21015	34341	6.04	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CEM12) gene, exons 1 and 2
8103	21015	34342	6.04	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CEM12) gene, exons 1 and 2
12610	28303	31814	1.95	7.0E-36	AF050351.1	NT	Homo sapiens glutathione transferase M4 gene, exon 1
2020	19038	28032	1.45	6.0E-36	7706022	NT	Homo sapiens mitogen 2 (M2), mRNA
2443	18447	34341	10.07	6.0E-36	AB030346.1	NT	Homo sapiens TCE6 gene, exon 12
3707	16739	28028	0.84	6.0E-36	BF15101.1	EST_HUMAN	U118471 avic-12.01.1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE3003942 3'
8077	18074	30923	0.90	6.0E-36	AB030501.1	NT	Human peroxisome biogenesis factor 1 (PBI1), complete cds
5514	18893	31441	8.6	6.0E-36	AA49180.1	EST_HUMAN	hsp4005-1 NCI CGAP Proa Homo sapiens cDNA clone IMAGE3003942 3'
7468	20408	33695	3.1	6.0E-36	AV1709143.1	EST_HUMAN	hsp4005-1 NCI CGAP Proa Homo sapiens cDNA clone IMAGE3003942 3'
8211	22130	35496	2.81	6.0E-36	AF209191.1	NT	hsp4005-1 NCI CGAP Proa Homo sapiens cDNA clone IMAGE3003942 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11980	24623	38318	2.78	6.0E-36	AI004469.1	EST_HUMAN	NR6500.1 NCL COMP_CLL1 Homo sapiens cDNA clone IMAGE:210724.3 similar to contains MERG.32
142	13244	26762	9.93	5.0E-36	AI277135.1	NT	MEMO repetitive element;
2600	18180	26768	7.93	5.0E-36	BE33336.1	EST_HUMAN	Human sapiens HLA-DQB1 pseudogenes region, segment 1/2
3676	19709	26588	2.471	5.0E-36	AL15200.2	NT	12252773 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:360728.5'
4600	17689	30795	1.16	5.0E-36	773972	NT	Human sapiens chromosome 2; unspliced H82/CO30
4600	17689	30795	0.16	5.0E-36	773972	NT	Human sapiens AP15.1 (AP15.1) mRNA
5000	21309	31709	0.16	5.0E-36	1029728	NT	Human sapiens AP15.1 (AP15.1) mRNA
13246	13244	34163	7.07	5.0E-36	AI277135.1	NT	Human sapiens HLA-DQB1 pseudogenes region, segment 1/2
13511	25248	31895	2.83	5.0E-36	AI277135.1	NT	Human sapiens Xq pseudocentromere region, segment 1/2
1672	14298	27231	2.41	4.0E-36	BE010038.1	EST_HUMAN	Human sapiens caldesmon binding protein 1 (KRA03330) mRNA
1672	14702	27963	1.83	4.0E-36	BE332574.1	EST_HUMAN	PM8-2N017C-100-001-g04 B20173 Homo sapiens cDNA
2290	13246	28632	1.85	4.0E-36	AI277135.1	EST_HUMAN	12252773 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:360728.5'
3403	16445	28632	0.87	4.0E-36	BE330299.1	EST_HUMAN	2620020 Spvrne NIH_MGC_7 Homo sapiens cDNA clone IMAGE:262020.5'
3403	16445	28632	0.87	4.0E-36	BE330299.1	EST_HUMAN	8071282296T NIH_MGC_44 Homo sapiens cDNA clone IMAGE:360418.5'
4687	17687	30731	0.92	4.0E-36	AL15200.2	NT	Human sapiens chromosome 2; segment H82/CO34
5281	16287	31115	0.84	4.0E-36	AA006391.1	EST_HUMAN	340581.51 Soares, NEF, T_OGC_S1 Homo sapiens cDNA clone IMAGE:190609.3 similar to
5971	18655		0.86	4.0E-36	RF4028.1	EST_HUMAN	SV-D3H1 FAT P29683-5-HYDROXYBUTYRATE DEHYDROGENASE PRECURSOR ;
6200	16341	32509	2.46	4.0E-36	M33320.1	NT	y1906.11 Soares placenta N23P8 Homo sapiens cDNA clone IMAGE:139713.5'
8102	21014	34340	1.89	4.0E-36	M33320.1	NT	Human sapiens a disintegrin and metalloproteinase domain 22 (ADAM22) transcript variant 3, mRNA
9118	22046	35403	1.4	4.0E-36	D07675.1	NT	Human skeletal Glycoprotein Iib (GPIIb) gene, exon 2-29
8118	22046	35404	1.4	4.0E-36	D07675.1	NT	Human sapiens RNA for amyloid precursor protein, complete cds
11426	24342	37787	1.6	4.0E-36	AA400370.1	EST_HUMAN	Human sapiens DNA for amyloid precursor protein, complete cds
12598	28202	37787	2.02	4.0E-36	11420516	NT	Human sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
12598	28202	37787	3.64	4.0E-36	AV769329.1	EST_HUMAN	AV769329 TP Homo sapiens cDNA clone TPC016H1.5'
720	13178	29700	8.9	3.0E-36	AF008810.1	NT	Human sapiens neuron alpha gene, partial cds
4223	17930	30454	8.32	3.0E-36	10181136	EST_HUMAN	Mus musculus parvalbumin 1 (p1-pending), mRNA
3211	16289	29159	1.03	2.0E-36	BE29267.1	EST_HUMAN	Q071050.8P1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:342706.5'
5073	18070	30919	2.48	2.0E-36	AV860376.1	NT	Q10-01030-240300-171-N04 OT0050 Homo sapiens cDNA
9574	18748	31650	2.71	2.0E-36	AF267447.1	NT	Mus musculus p17-phox gene, complete cds
6002	18734	32352	4.78	2.0E-36	T06786.1	EST_HUMAN	EST106688 Human Brain, Brain, Homo sapiens cDNA clone HBB129.5' and
8988	19800	33104	11.42	2.0E-36	T06629.1	EST_HUMAN	Y14407.11 Shapagene test (850/225) Homo sapiens cDNA clone IMAGE:3560.5'
9925	22830	36216	0.97	2.0E-36	BF512734.1	EST_HUMAN	U144BW-ranno-5-110-UE1 NCL COMP_S308 Homo sapiens cDNA clone IMAGE:5091132.3'

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10078	22871	36200	0.73	2.0E-36	4507848	NT	Homo sapiens desiglin specific peptidase 9 (desiglin-9) (SPT9) mRNA
10078	22871	36201	0.73	2.0E-36	4507848	NT	Homo sapiens desiglin specific peptidase 9 (desiglin-9) (SPT9) mRNA
910	15952	28699	2.47	1.0E-36	BE4083.0.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
2217	18278	28293	1.94	1.0E-36	BF93761.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
3353	19368		1.38	1.0E-36	AF183562.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
6031	16669	32518	0.82	1.0E-36	AD44463.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
6118	19177	32672	1.07	1.0E-36	4687064	NT	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
6424	19471		4.02	1.0E-36	AB87714.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
6963	19902	32886	1.46	1.0E-36	R25012.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
6953	19902	32886	1.46	1.0E-36	R25012.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
6978	20005	33297	0.7	1.0E-36	AL120542.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
8538	21469	34003	3.87	1.0E-36	AA14903.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
8538	21469	34003	3.87	1.0E-36	AA14903.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
8531	21802	34699	1.3	1.0E-36	AA429467.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
8531	21802	34699	1.3	1.0E-36	AA429467.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
9500	22307	35871	2.38	1.0E-36	AF100588.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
10515	22301	36034	4.83	1.0E-36	BF354169.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
10817	22703	37130	1.29	1.0E-36	AF185998.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
10817	22703	37130	1.29	1.0E-36	AF185998.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
11387	24303	37750	2.92	1.0E-36	AF187638.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
11820	24741	38232	3.95	1.0E-36	AF154143.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
12410	25179		3.85	1.0E-36	1141871	NT	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
12836	25644		6.38	1.0E-30	AF103212.2	NT	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
13003	26664		2.46	1.0E-30	AF120723.1	NT	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
7774	20704	34004	2.82	9.0E-37	AF1006277.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
7774	20704	34006	2.82	9.0E-37	AF1006277.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
12851	26526		1.85	9.0E-37	W12818.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
3405	16047	20366	1.21	8.0E-37	4757979	NT	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
5429	18511		1.54	8.0E-37	BE68907.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA
9040	19102	32229	3.98	8.1E-37	BC589197.1	EST_HUMAN	Homo sapiens carbonic anhydrase 13 (CA13) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6940	19102	32290	3.98	8.0E-37	BE36127.1	EST_HUMAN	hUGT1A1 NCI, CGAP, KUD81 Homo sapiens cDNA, clone IMAGE:3140259.3 similar to contains MFC03.03
6982	19153	32289	3.98	8.0E-37	AV749646.1	EST_HUMAN	hUGT1A1 NCI, CGAP, KUD81 Homo sapiens cDNA, clone IMAGE:3140259.3 similar to contains MFC03.03
8464	21395	34736	7.32	8.0E-37	X87944.1	NT	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
1311	14344		2.02	7.0E-37	AL025800.1	EST_HUMAN	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
11197	24126	37556	3.64	7.0E-37	A817700.1	EST_HUMAN	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
11333	24252	37895	2.04	7.0E-37	AI93702.1	EST_HUMAN	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
5275	16281		4.44	6.0E-37	R10039.1	EST_HUMAN	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
5007	21636	35522	0.66	6.0E-37	AF169660.1	NT	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
12847	26459		1.5	6.0E-37	U75308.1	NT	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
12847	26512		4.27	6.0E-37	AF202729.1	NT	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
6330	16380	32547	5.54	5.0E-37	AA307123.1	EST_HUMAN	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
6330	16380	32548	5.54	5.0E-37	AA307123.1	EST_HUMAN	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
9319	22424	35905	1.33	6.0E-37	AV750211.1	EST_HUMAN	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
11357	24275		4.86	6.0E-37	7657117	NT	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
12405	25176		5.01	6.0E-37	AF149773.1	NT	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
2447	15451	25447	4.71	4.0E-37	AA702794.1	EST_HUMAN	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
6540	19553	32767	0.61	4.0E-37	AV7794502.1	EST_HUMAN	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
8964	22069	35189	0.62	4.0E-37	AA849503.1	EST_HUMAN	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
2030	19047	26143	2.37	3.0E-37	AL048955.1	EST_HUMAN	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
2030	19047	26144	2.37	3.0E-37	AL048955.1	EST_HUMAN	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
2538	15538		1.99	3.0E-37	AV1601150.1	EST_HUMAN	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
9106	16058		4.1	3.0E-37	AV1601150.1	EST_HUMAN	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
0078	19140	32276	0.85	3.0E-37	AL138274.1	EST_HUMAN	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
7664	20791	34094	0.83	3.0E-37	T03060.1	EST_HUMAN	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
7687	20906	34222	0.9	3.0E-37	AF149652.1	EST_HUMAN	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
4022	13515	26336	0.67	2.0E-37	DB0750.1	NT	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
4022	13515	26437	0.97	2.0E-37	DB0750.1	NT	h. sapiens DNA, DMB, HUK21, P2.2, LUP2, TAP1, LUP1, TAP2, DOB, DOB2 and RING8, 9, 13 and 14

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1108	14190	27090	1.88	2.0E-37	AF131202.1	EST_HUMAN	AF131202.1:NT2RP3 Homo sapiens cDNA, clone NT2RP3:3052188 5'
1108	14190	27091	1.88	2.0E-37	AF131202.1	EST_HUMAN	AF131202.1:NT2RP3 Homo sapiens cDNA, clone NT2RP3:3052188 5'
1975	14557	27562	1.21	2.0E-37	AL16342.2	NT	Homo sapiens chromosome 21 segment HS21C317
2695	16931	28075	7.1	2.0E-37	4893210	NT	Homo sapiens cytochrome P450, subfamily XA (cyp27A1) cDNA, clone IMAGE:346308 5'
5573	19631	32070	0.87	2.0E-37	BF035327.1	EST_HUMAN	BF035327.1:NT Homo sapiens cDNA, clone IMAGE:346308 5'
8635	19638	32070	0.84	2.0E-37	BF035327.1	EST_HUMAN	BF035327.1:NT Homo sapiens cDNA, clone IMAGE:346308 5'
8253	21652	34803	0.97	2.0E-37	AA34672.1	EST_HUMAN	Homo sapiens protease binding, prolyserine protease binding (PRP1), mRNA
8253	21652	34803	0.97	2.0E-37	AA34672.1	EST_HUMAN	EST15331.1:NT Homo sapiens cDNA, 5' end
8675	21658	34897	0.87	2.0E-37	BE337704.1	EST_HUMAN	BE337704.1:NT Homo sapiens cDNA, clone IMAGE:346867 5'
8675	21658	34897	0.87	2.0E-37	BE337704.1	EST_HUMAN	BE337704.1:NT Homo sapiens cDNA, clone IMAGE:346867 5'
8675	21658	34897	2.9	2.0E-37	BF204932.1	EST_HUMAN	BF204932.1:NT Homo sapiens cDNA, clone IMAGE:346867 5'
11092	24634	35332	10.6	2.0E-37	AF179013.1	NT	Homo sapiens 1 domain containing protein 1 isoform 5 (LJDF1) mRNA, complete cds
13043	26034	35332	5.22	2.0E-37	AF179013.1	NT	Homo sapiens 1 domain containing protein 1 isoform 5 (LJDF1) mRNA, complete cds
2100	15114	28118	6.86	1.0E-37	AL153281.2	NT	Homo sapiens chromosome 21 segment HS21C381
3241	16299	30148	1.23	1.0E-37	AF739743.1	EST_HUMAN	AF739743.1:NT Homo sapiens cDNA
4280	17278	30148	1.98	1.0E-37	BE2678.1	EST_HUMAN	BE2678.1:NT Homo sapiens cDNA, clone IMAGE:346266 5'
5053	18090	30903	2.8	1.0E-37	BF37178.1	EST_HUMAN	BF37178.1:NT Homo sapiens cDNA, clone IMAGE:346266 5'
6238	16290		0.87	1.0E-37	7203530	NT	Mito nucleolus strogilin (Orog), mRNA
8733	21723	33070	0.89	1.0E-37	BE54032.1	EST_HUMAN	BE54032.1:NT Homo sapiens cDNA, clone IMAGE:346308 5'
9294	22292	35860	3.16	1.0E-37	AA71406.1	EST_HUMAN	AA71406.1:NT Homo sapiens cDNA, clone IMAGE:346308 5'
11071	23945	37391	0.81	1.0E-37	AF739743.1	EST_HUMAN	AF739743.1:NT Homo sapiens cDNA, clone IMAGE:346308 5'
11141	24070	37519	2.19	1.0E-37	ME2678.1	NT	Homo sapiens cDNA, clone IMAGE:346266 5'
12696	29352		3.76	1.0E-37	BE71781.1	EST_HUMAN	BE71781.1:NT Homo sapiens cDNA, clone IMAGE:346308 5'
15996	19041	32176	2.07	6.0E-38	100482	NT	Homo sapiens cDNA, clone IMAGE:346308 5'
1260	14285	27229	1.88	6.0E-38	11436656	NT	Homo sapiens cDNA, clone IMAGE:346308 5'
2621	16522	28026	1.41	6.0E-38	BF343221.1	EST_HUMAN	BF343221.1:NT Homo sapiens cDNA, clone IMAGE:346308 5'
2197	16208	28212	1.36	7.0E-38	AF172625.1	EST_HUMAN	AF172625.1:NT Homo sapiens cDNA, clone IMAGE:346308 5'
3098	16140	29038	1.89	6.0E-38	BF030338.1	EST_HUMAN	BF030338.1:NT Homo sapiens cDNA, clone IMAGE:346308 5'
5783	18845	31591	1.38	6.0E-38	11425114	NT	Homo sapiens cDNA, clone IMAGE:346308 5'
5783	18845	31591	1.38	6.0E-38	11425114	NT	Homo sapiens cDNA, clone IMAGE:346308 5'
7713	20645	33542	0.58	6.0E-38	AF10568.1	EST_HUMAN	AF10568.1:NT Homo sapiens cDNA, clone IMAGE:346308 5'
7780	20769	34011	0.54	6.0E-38	AJ01068.1	NT	Homo sapiens cDNA, clone IMAGE:346308 5'
7780	20769	34012	0.54	6.0E-38	AJ01068.1	NT	Homo sapiens cDNA, clone IMAGE:346308 5'

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5270	13296	31107	0.76	2.0E-38	BE360224.1	EST_HUMAN	501773857.1 NH1_MGC_17 Homo sapiens cDNA clone IMAGE359250.5'
5280	16235	31095	0.76	2.0E-38	AA437151.1	EST_HUMAN	50166101.1 Scores: 16451 HIT Homo sapiens cDNA clone IMAGE75872.6 similar to TRG817857
5920	19387	32105	0.04	2.0E-38	Z23534.2	NT	5017387.1 CLTONE RECEPTOR SUBUNIT ALPHA 4,
5920	19387	32105	0.04	2.0E-38	Z23534.2	NT	Homo sapiens mRNA for anion channel ACP1, LOC
6160	21037	34421	1.3	2.0E-38	Z271103.1	EST_HUMAN	1V27103.1 HT8 Homo sapiens cDNA clone HT8AH11.5
6033	21982	35742	4.63	2.0E-38	BE360224.1	EST_HUMAN	NS3-H10497.1 10225-113-201 HT0487 Homo sapiens cDNA
6432	22330	35742	0.33	2.0E-38	BE360224.1	EST_HUMAN	USC1105031 normalized infant brain cDNA Homo sapiens cDNA clone c-1863
9517	22444	33507	1.72	2.0E-38	AF060755.1	NT	Homo sapiens orphan G protein-coupled receptor HQ20 (HQ20) mRNA, complete cds
9752	22686		1.03	2.0E-38	BE222565.1	NT	ht10992.1 NCI CGAP P224 Homo sapiens cDNA clone IMAGE3160130.5' similar to TR02710 002710
10929	23814	37243	1.81	2.0E-38	D55179.2	NT	GAG POLYPROTEIN.
11633	24537	38064	4.61	2.0E-38	AA595490.1	EST_HUMAN	Homo sapiens mRNA for KIAA0145 protein, partial cds
11633	24537	38064	4.61	2.0E-38	AA595490.1	EST_HUMAN	nc54993.1 NCI CGAP P224 Homo sapiens cDNA clone IMAGE1102612.3 similar to TR-E12318
11633	24537	38064	4.61	2.0E-38	AA595490.1	EST_HUMAN	E242816.1 NADP DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE.1
11633	24537	38064	4.61	2.0E-38	AA595490.1	EST_HUMAN	nc54993.1 NCI CGAP P224 Homo sapiens cDNA clone IMAGE1102612.3 similar to TR-E12319
11633	24537	38064	4.61	2.0E-38	AA595490.1	EST_HUMAN	E242816.1 NADP DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE.1
11922	24767	38264	4.98	2.0E-38	BE112760.1	EST_HUMAN	QV22-H10595-356000-355-403 HT0039 Homo sapiens cDNA
12095	24906	39407	3.95	2.0E-38	AF160501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 9 (LGR9) mRNA, partial cds
12095	24906	39407	3.95	2.0E-38	AF160501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 9 (LGR9) mRNA, partial cds
12327	25126		8.26	2.0E-38	AV720568.1	EST_HUMAN	AV720568.1 HTC Homo sapiens cDNA clone HTCCDH07.5
12329	25126		8.26	2.0E-38	AB012723.1	NT	Homo sapiens gene for kinase-like protein, complete cds
12940	25297		2.05	2.0E-38	M59530.1	NT	Human taurinomycinase 1 pseudogene 2
12941	25297	31248	3.76	2.0E-38	1155641.1	EST_HUMAN	CH2205040 Chromosome 22 exon Homo sapiens cDNA clone C22_798.5
12963	25334		2.34	2.0E-38	1749063.1	NT	ET1 beta-tyrosine dehydrogenase beta (promoter) [human, placenta, Genomic, 1280 nt]
1120	14192		2.81	1.0E-38	AA401570.1	EST_HUMAN	ET1 beta-tyrosine dehydrogenase beta (promoter) [human, placenta, Genomic, 1280 nt]
12015	15033	23027	1.5	1.0E-38	4983298	NT	MER19 repetitive element
2033	15090	25077	1.07	1.0E-38	7601969	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1) mRNA
2517	16518	25622	2.35	1.0E-38	AF170831.1	NT	Homo sapiens KIAA0173 gene product (KIAA0173) mRNA
2568	16534	25854	17.34	1.0E-38	4758371	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
4330	17441	30301	3.04	1.0E-38	AL160203.2	NT	Homo sapiens (Hs)genin-like 1 (FGL1) mRNA
4330	17441	30301	3.04	1.0E-38	AL160203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4330	17441	30301	3.04	1.0E-38	AL160203.2	NT	Homo sapiens chromosome 21 segment HS21C003

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50	13167	20093	10.7	3.0E-39	AA031940.1	EST_HUMAN	linc1618 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR124
50	13167	20094	10.7	3.0E-39	AA031940.1	EST_HUMAN	linc1618 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR124
12319	29120	39157	5.05	3.0E-39	A094657.1	EST_HUMAN	cds3010.11 SmaII, NheI, PstI Homo sapiens cDNA clone IMAGE:1600890 3' similar to SW:GTR8_RAT
12319	29120	39158	5.05	3.0E-39	A094657.1	EST_HUMAN	cds3010.11 SmaII, NheI, PstI Homo sapiens cDNA clone IMAGE:1600890 3' similar to SW:GTR8_RAT
12360	29149		8.33	3.0E-39	A094657.1	EST_HUMAN	P-43427 GLUCOSE TRANSPORTER TYPE 6, SMALL INTESTINE
822	13374		8.72	2.0E-39	BE40205.1	EST_HUMAN	P-43427 GLUCOSE TRANSPORTER TYPE 6, SMALL INTESTINE
937	13360		41.15	2.0E-39	A1326116.1	EST_HUMAN	9013016071 NIH MGCC 211 homo sapiens cDNA clone IMAGE:100543 3'
1057	14101		3.78	2.0E-39	A1000575.1	NT	procrna7.2D91L bcl2 tumor Homo sapiens cDNA clone IMAGE:3930280 5'
1553	14584		17.9	2.0E-39	AW127318.1	EST_HUMAN	Homo sapiens homogenizate 1,2-dioxygenase gene, complete cds
1589	15007	27596	3.94	2.0E-39	AA720574.1	EST_HUMAN	PVQ-310340-21299-303-402 BT0340 Homo sapiens cDNA
2075	15071	28970	2.37	2.0E-39	AA163248.2	NT	THR1202.51 NCL CGAP SC30 Homo sapiens cDNA clone IMAGE:1241133 3' similar to contains THR13
4500	17519	30385	1.77	2.0E-39	BF370227.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS27C048
5070	19793	31974	4.28	2.0E-39	AA008960.1	EST_HUMAN	RC4-RN0037-280700-011-s10 RN0037 Homo sapiens cDNA
7761	20091	33950	2.1	2.0E-39	AA080957.1	EST_HUMAN	pro0002.1 Stralagene NR1 neuron (6637235) Homo sapiens cDNA clone IMAGE:540851 5'
7558	20850	34191	0.75	2.0E-39	AL163202.2	NT	Homo sapiens chromosome 21 segment HS27C0502
7558	20850	34192	0.75	2.0E-39	AL163202.2	NT	Homo sapiens chromosome 21 segment HS27C0502
8377	21281	34412	1.41	2.0E-39	A138173.1	EST_HUMAN	17600.41 NCL CGAP K611 Homo sapiens cDNA clone IMAGE:2137868 3' similar to TR-Q3357 Q1357
8895	21916	35100	0.85	2.0E-39	A1376776.1	NT	ME137 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE ;
10027	22427		0.85	2.0E-39	AA194331.1	EST_HUMAN	Refus nonrepetitive putative four repeat on chemical mRNA, complete cds
10152	23043		0.89	2.0E-39	A085660.1	EST_HUMAN	emb651.11 Stralagene sch60 brain ST1 Homo sapiens cDNA clone IMAGE:1630195 3'
11864	24794	35449	3.05	2.0E-39	D0564.1	NT	US5603.1 NCL CGAP P728 Homo sapiens cDNA clone IMAGE:228092 3'
12228	26052	35950	1.57	2.0E-39	A1152976	NT	Human mRNA for UGA4226 gene, partial cds
1534	14594	27524	3.13	1.0E-39	AJ06345.1	NT	Homo sapiens GLO1.2 for gonadotropin follicle transcription represson-2 (GLO1-2), mRNA
1534	14594	27525	3.13	1.0E-39	AJ06345.1	NT	Homo sapiens KLU10.11 gene
1534	14594	27526	3.13	1.0E-39	AJ06345.1	NT	Homo sapiens DVE2201.11 gene
1534	14594	27527	3.13	1.0E-39	AJ06345.1	NT	CHP2201.81 Chromosome 21 human cDNA clone C22_236 5'
1534	14594	27528	3.13	1.0E-39	AJ06345.1	NT	Homo sapiens mRNA for KLU10877 protein, partial cds
4033	17020	20349	1.15	1.0E-39	A052684.1	EST_HUMAN	Homo sapiens calinin (calinin-associated protein), alpha 2 (CTNNA2), mRNA
4312	17226	30095	1.15	1.0E-39	A1143203	NT	Homo sapiens calinin (calinin-associated protein), alpha 2 (CTNNA2), mRNA
4312	17226	30097	1.13	1.0E-39	A1143203	NT	Homo sapiens calinin (calinin-associated protein), alpha 2 (CTNNA2), mRNA
4725	17750	30580	0.99	1.0E-39	AW29073.1	EST_HUMAN	U1-H1E10-alk-b05-0-0.11 NCL CGAP_S401 Homo sapiens cDNA clone IMAGE:2738860 3'

Single Exon Probes Expressed in Adult Liver

[illegible]

Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	Orig SEQ ID NO.	Expression Signal	Most Similar (Top) HE BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7265	20174	33415	3.95	6.0E-40	11439763	NT	Homo sapiens fatty acid desaturase 1 (FADS1) mRNA
7265	20174	33416	3.95	6.0E-40	11439763	NT	Homo sapiens fatty acid desaturase 1 (FADS1) mRNA
10493	23371	36764	9.8	8.0E-40	AV955028.1	EST_HUMAN	AV955028 GCLC Homo sapiens cDNA clone GCLCOP04.3
10493	23371	36765	9.8	8.0E-40	AV955028.1	EST_HUMAN	AV955028 GCLC Homo sapiens cDNA clone GCLCOP04.3
2047	19493	28422	3.38	5.0E-40	AL032852.1	NT	Homo sapiens microsome 21 segment H220035
1899	14920	27920	4.08	4.0E-40	AB860955.1	EST_HUMAN	h14920.1 NCL COAP_F26 Homo sapiens cDNA clone IMAGE:2248973.3 similar to TR-073555 O73555 POL-PROTEIN-1
2120	16733	33161	5.68	4.0E-40	AF90928.1	NT	Homo sapiens X-linked and/oric endosomal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4165	17195	33972	12.55	4.0E-40	AF90928.1	NT	Homo sapiens KIA04439 protein (KIA04439) mRNA
8489	21802	34765	0.9	4.0E-40	U127831.1	EST_HUMAN	U127831.1 NT7827 Homo sapiens cDNA clone NT28P2002172.9
8874	21802	34766	4.58	4.0E-40	U127831.1	EST_HUMAN	U127831.1 NT7827 Homo sapiens cDNA clone IMAGE:122122
8907	22333	35922	8.07	4.0E-40	BE019418.1	EST_HUMAN	P40-EN0167-070500-002-H2 BN0187 Homo sapiens cDNA
8907	22333	35923	5.07	4.0E-40	BE019418.1	EST_HUMAN	P40-EN0167-070500-002-H2 BN0187 Homo sapiens cDNA
9007	22333	35923	5.07	4.0E-40	BE019418.1	EST_HUMAN	P40-EN0167-070500-002-H2 BN0187 Homo sapiens cDNA
4280	17246	30116	1.94	3.0E-40	AI22549.1	EST_HUMAN	wt1267.1 NCL CGAP_K411 Homo sapiens cDNA clone IMAGE:2380549.3
9739	19770	32950	0.91	3.0E-40	4506736	NT	Homo sapiens ribosomal protein S6, intrase, 70kD, polypeptide 1 (RPS6K1) mRNA
9831	18950	33161	7.22	3.0E-40	11417342	NT	Homo sapiens sensa domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
8952	21882	35241	3.77	3.0E-40	9454167	NT	Homo sapiens HBV associated factor (XAP4) mRNA
8952	22448	35811	1.3	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
6752	22676	35950	1.75	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
11105	24035	37481	1.57	3.0E-40	D58634.1	NT	Human mRNA for KIA0209 gene, partial cds
11711	24613	38089	1C.95	3.0E-40	6005913	NT	Human sapiens serine threonine protein kinase (NDR), mRNA
345	13434		7.41	2.0E-40	AL22036.1	EST_HUMAN	np2008.01 Soares, Jellis, NHT Homo sapiens cDNA clone IMAGE:193267.7.3
821	13876		8.11	2.0E-40	AW30958.1	EST_HUMAN	np24010.41 NCL CGAP_UH1 Homo sapiens cDNA clone IMAGE:193267.7.3
1846	14870		9.06	2.0E-40	AV731007.1	EST_HUMAN	P97461 40S RIBOSOMAL PROTEIN S6.1
1849	14938	27949	1.3	2.0E-40	4506198	NT	Homo sapiens proteasome (prosome, mannosin) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
1849	14939	27950	1.3	2.0E-40	4506198	NT	Homo sapiens proteasome (prosome, mannosin) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2095	15099	26095	1.02	2.0E-40	AB08562.1	EST_HUMAN	wd0011.1 NCL CGAP_G06 Homo sapiens cDNA clone IMAGE:254748.3 similar to TR-091629 Q91629 ZINC FINGER PROTI-N.1
2182	15193	26108	1.48	2.0E-40	5453902	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA

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Table 4
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Probe SEQ ID NO.	Exon ID NO.	CRS SEQ ID NO.	Expression Signal	Max Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13081	29820	26312	6.62	7.0E-41	11417972	NT	Homo sapiens pascallin (pascallin) homolog, containing BNC1 domain (PES1), mRNA
300	13363	26312	1.02	6.0E-41	AB307463.1	NT	Homo sapiens DSG130 mRNA, complete cds
8129	15138	29142	1.98	6.0E-41	767042	NT	Homo sapiens Down syndrome critical region 1 (DSCR1), mRNA
2549	21460	34821	1.38	8.0E-41	BF15763.1	EST_HUMAN	U-H8Y1 ramp-3-03-03-11-01 NC1 CGAP, 3487 Homo sapiens cDNA clone IMAGE:3070421.3
1824	14947	27623	1.11	5.0E-41	162623.1	EST_HUMAN	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
4202	17720	27623	1.23	5.0E-41	405650	NT	Homo sapiens cDNA clone IMAGE:76038.3
6627	10660	27623	2.48	5.0E-41	BE567462.1	EST_HUMAN	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
412	13455	27623	2.25	4.0E-41	BE156318.1	EST_HUMAN	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
1123	14197	27104	1.33	4.0E-41	AF116344.1	EST_HUMAN	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
1430	14464	27416	15.71	4.0E-41	AK27117.1	EST_HUMAN	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
1430	14464	27419	18.71	4.0E-41	AK27117.1	EST_HUMAN	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
1448	14476	27438	6.91	4.0E-41	AB036861.1	NT	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
1821	14391	27651	6.8	4.0E-41	AB030408.1	EST_HUMAN	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
2530	15533	29881	5.42	4.0E-41	AJ220041.1	NT	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
2530	15533	29882	5.42	4.0E-41	AJ220041.1	NT	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
4242	17268	30124	2.16	4.0E-41	X02895.1	NT	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
6727	19820	30507	1.5	4.0E-41	AF759293.1	EST_HUMAN	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
10216	23107	36507	7.78	4.0E-41	BF304683.1	EST_HUMAN	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
12697	24658	36507	6.35	4.0E-41	AF710480.1	EST_HUMAN	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
12873	25734	36507	1.85	4.0E-41	AF710480.1	EST_HUMAN	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
675	14136	26069	1.79	3.0E-41	AB320176.1	NT	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
4444	17455	30314	2.6	3.0E-41	AB028986.1	NT	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
6980	18754	31070	8.05	3.0E-41	X87699.1	NT	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
7642	19691	32872	1.23	3.0E-41	AB037806.1	NT	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
6952	20067	33862	0.84	3.0E-41	AJ055168.1	EST_HUMAN	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
6298	21171	34505	0.46	3.0E-41	RZ4785.1	EST_HUMAN	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
12190	24689	38489	1.49	3.0E-41	AJ220041.1	NT	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3
12282	25095	38489	2.71	3.0E-41	AJ600798.1	EST_HUMAN	Y03510.11 Stragelans (tag) (T03510.11) Homo sapiens cDNA clone IMAGE:76038.3

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Probe SEQ ID NO.	Expr SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12441	285935		61.24	8.0E-42	AA468395.1	EST_HUMAN	h107602.11 NCL CGAP_T197 Homo sapiens cDNA clone IMAGE:594566 similar to FR.G434304 G434304 387BP EXPRESSED SEQUENCE TAG mRNA;
						EST_HUMAN	h274797.1 NCL CGAP_Gm535 Homo sapiens cDNA clone IMAGE:2902174 3' similar to contains ORF.12
						EST_HUMAN	ORF repetitive element;
12458	287126		2.18	7.0E-42	AW058902.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C088
6900	1410		2.25	7.0E-42	AI162385.2	EST_HUMAN	h595712.1 Soares testis NHT Homo sapiens cDNA clone IMAGE:128174 9'
9040	219460		0.65	7.0E-42	AI10663.1	EST_HUMAN	h595712.1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1754278 3'
9786	219460		1.63	7.0E-42	AI204398.1	EST_HUMAN	h595712.1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:514662
11616	24524		3.7943	7.0E-42	AA599992.1	EST_HUMAN	h595712.1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:514662
11616	24524		3.7694	7.0E-42	AA599992.1	EST_HUMAN	h595712.1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:514662
11933	24771		1.45	7.0E-42	AA404950.1	EST_HUMAN	h595712.1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:514662
1890	14901		2.7893	2.07E-42	AF184718.1	EST_HUMAN	Homo sapiens phospholipid transfer protein 230 (p42c230) mRNA, complete cds
1890	14901		2.7894	2.07E-42	AF184718.1	EST_HUMAN	Homo sapiens phospholipid transfer protein 230 (p42c230) mRNA, complete cds
2308	18316		2.48	6.0E-42	AW238593.1	EST_HUMAN	h595712.1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:2741760 3' similar to contains L1.L1 L1 repetitive element;
6654	18728		3.1633	1.43E-42	AF228990.1	EST_HUMAN	Homo sapiens mRNA for KIAA1037 protein, partial cds
5918	18728		3.1633	1.23E-42	AF228990.1	EST_HUMAN	Homo sapiens mRNA for KIAA1037 protein, partial cds
140	13242		6.66	6.0E-42	AF228990.1	NT	Homo sapiens mRNA for KIAA1037 protein, partial cds
481	13383		20.483	6.0E-42	AF217915.1	EST_HUMAN	h274797.1 NCL CGAP_L202 Homo sapiens cDNA clone IMAGE:3175952 3'
509	13381		2.77	6.0E-42	AF228990.1	EST_HUMAN	Homo sapiens SET domain and nuclear transposase fusion gene (SET/NTAR) mRNA
510	13381		2.08	6.0E-42	AF228990.1	EST_HUMAN	Homo sapiens SET domain and nuclear transposase fusion gene (SET/NTAR) mRNA
6683	20010	33241	1.00	5.0E-42	U1439069	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Argentinian syndrome) (UBES3A) mRNA
6939	20010	33242	1.09	5.0E-42	U1439063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Argentinian syndrome) (UBES3A) mRNA
7112	20316	33556	3.11	6.0E-42	U1417957	NT	Homo sapiens multifunctional calyculin/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds
7599	20504	33702	2.33	6.0E-42	AF0711506.1	NT	Homo sapiens methyl (REL)N mRNA
8325	21941	34660	0.281	6.0E-42	AB037718.1	NT	Homo sapiens mRNA for KIAA1724 protein, partial cds
93381	22255	35929	2.5	5.0E-42	AF037718.1	NT	Homo sapiens mRNA for KIAA1724 protein, partial cds
11070	23983	37369	0.64	5.0E-42	U1431169	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAC) mRNA
11070	23984	37369	0.94	5.0E-42	U1431169	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAC) mRNA
11435	24352	37600	2.75	6.0E-42	8029162	NT	Homo sapiens hypothetical protein FLJ20163 (FLJ20163) mRNA
12265	25040	38543	2.03	5.0E-42	U58411.1	NT	H sapiens mRNA for myosin-IE
12265	25040	38544	2.03	5.0E-42	U58411.1	NT	H sapiens mRNA for myosin-IE

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Max Similar (Top) HR BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
777	13834	26767	6.96	4.0E-42	AF055006.1	NT	Homo sapiens MHC class I region
777	13834	26768	6.96	4.0E-42	AF055006.1	NT	Homo sapiens MHC class I region
1063	14136	27073	1.14	4.0E-42	AF189011.1	NT	Homo sapiens ribonuclease II (RNS) mRNA, complete cds
4290	17304	30773	1.25	4.0E-42	X65417.1	NT	Human spleen ribonuclease II (RNS) mRNA, complete cds
4327	17341	30237	1.11	4.0E-42	AF246210.1	NT	Homo sapiens SV40 T antigen (SV40 T) mRNA, complete cds
4347	17351	30228	5.79	4.0E-42	AF246210.1	NT	Homo sapiens SV40 T antigen (SV40 T) mRNA, complete cds
4697	17702	30595	13.24	4.0E-42	4695463	NT	Homo sapiens SV40 T antigen (SV40 T) mRNA, complete cds
11382	23846	37272	0.76	4.0E-42	AF137120.1	EST_HUMAN	Human SV40 T antigen (SV40 T) mRNA, complete cds
11383	24234	37456	2.34	4.0E-42	AF181836.1	EST_HUMAN	Human SV40 T antigen (SV40 T) mRNA, complete cds
10355	24234	37457	2.34	4.0E-42	AF181836.1	EST_HUMAN	Human SV40 T antigen (SV40 T) mRNA, complete cds
1301	18332	27497	4.37	2.0E-42	AF189344.1	EST_HUMAN	Human SV40 T antigen (SV40 T) mRNA, complete cds
2437	18341	28449	4.39	2.0E-42	AF189344.1	EST_HUMAN	Human SV40 T antigen (SV40 T) mRNA, complete cds
5263	19330	32150	16.37	2.0E-42	AF194539.1	EST_HUMAN	Human SV40 T antigen (SV40 T) mRNA, complete cds
5263	19330	32150	16.37	2.0E-42	AF194539.1	EST_HUMAN	Human SV40 T antigen (SV40 T) mRNA, complete cds
7674	19998	33010	0.95	2.0E-42	M29145.1	NT	Human SV40 T antigen (SV40 T) mRNA, complete cds
7674	19998	33015	0.91	2.0E-42	A032366.1	EST_HUMAN	Human SV40 T antigen (SV40 T) mRNA, complete cds
10355	23145	36964	1.37	2.0E-42	BE338216.1	EST_HUMAN	Human SV40 T antigen (SV40 T) mRNA, complete cds
10357	23443	36964	0.95	2.0E-42	P81649	SWISSPROT	Human SV40 T antigen (SV40 T) mRNA, complete cds
10557	23443	36965	0.98	2.0E-42	P81649	SWISSPROT	Human SV40 T antigen (SV40 T) mRNA, complete cds
757	13013	26742	1.38	1.0E-42	X57147.1	NT	Human SV40 T antigen (SV40 T) mRNA, complete cds
1028	14112	27052	1.1	1.0E-42	AF126809.1	EST_HUMAN	Human SV40 T antigen (SV40 T) mRNA, complete cds
1128	14170	27107	12.36	1.0E-42	AJ251818.1	NT	Human SV40 T antigen (SV40 T) mRNA, complete cds
1128	14170	27108	12.36	1.0E-42	AJ251818.1	NT	Human SV40 T antigen (SV40 T) mRNA, complete cds
1270	13896	27254	13.15	1.0E-42	AF007106.1	NT	Human SV40 T antigen (SV40 T) mRNA, complete cds
1270	13896	27255	13.15	1.0E-42	AF007106.1	NT	Human SV40 T antigen (SV40 T) mRNA, complete cds
1727	14754	27724	0.95	1.0E-42	11432319	NT	Human SV40 T antigen (SV40 T) mRNA, complete cds
2044	15091	28952	1.28	1.0E-42	AF110268.1	NT	Human SV40 T antigen (SV40 T) mRNA, complete cds
2575	15574	28570	1.77	1.0E-42	5174158	NT	Human SV40 T antigen (SV40 T) mRNA, complete cds
3005	10057	28991	8.99	1.0E-42	4695524	NT	Human SV40 T antigen (SV40 T) mRNA, complete cds
3771	16803	26900	2.39	1.0E-42	7632027	NT	Human SV40 T antigen (SV40 T) mRNA, complete cds

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Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3896	16898	26773	0.99	1.0E-42	5651610	NT	Homo sapiens Cg1 vesicular function trafficking protein p 15 (BET1) mRNA
4000	17277	25916	1.64	1.0E-42	AL163267.2	NT	Homo sapiens chromosome 21 segment 1 (HSD17C08)
4244	17359	30223	2.11	1.0E-42	AL163268.2	NT	Homo sapiens chromosome 21 segment 1 (HSD17C08)
4896	17851	30726	1.92	1.0E-42	863122	NT	Homo sapiens phosphatase 1A (P1A) mRNA
4899	17851	30727	1.82	1.0E-42	863122	NT	Homo sapiens phosphatase 1A (P1A) mRNA
4899	17850	30756	0.88	1.0E-42	453758	NT	Homo sapiens proteinase 3 (RYR3) mRNA
5074	18071	30920	0.97	1.0E-42	Z46126	EST_HUMAN	HSQDEF07 normalised fetal brain cDNA Homo sapiens cDNA clone c-0107
10398	23474	29871	3.13	8.0E-43	U37998	EST_HUMAN	Homo sapiens chromodomain protein, Y chromosome-linked (CDYL) mRNA
678	17377	26860	1.99	8.0E-43	AV73834	EST_HUMAN	AV73834 GB Homo sapiens cDNA clone CBLA4H08.5
719	17377	26860	1.99	8.0E-43	AV73834	EST_HUMAN	AV73834 GB Homo sapiens cDNA clone CBLA4H08.5
724	17373	26704	14.26	8.0E-43	AV73834.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20297 (FLJ20297) mRNA
724	17373	26705	3.77	8.0E-43	8623276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297) mRNA
724	17373	26706	3.77	8.0E-43	8623276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297) mRNA
5887	18099	32034	0.95	8.0E-43	H13952.1	EST_HUMAN	AB011171 Sperm NIH MG0.7 Homo sapiens cDNA clone IMAGE:2822251.5
3706	16741	25380	10.66	7.0E-43	AV126642.1	EST_HUMAN	AB011171 Sperm NIH MG0.7 Homo sapiens cDNA clone IMAGE:2822251.5
6328	22266		3.22	7.0E-43	AV39748.1	EST_HUMAN	W63001.x1 NCL CGAP Brn05 Homo sapiens cDNA clone IMAGE:2466586.3 similar to TR-O 1475
1372	14404		5.64	6.0E-43	AA61800.1	EST_HUMAN	W63001.x1 NCL CGAP Brn05 Homo sapiens cDNA clone IMAGE:2466586.3 similar to TR-O 1475
2633	19531		3.13	6.0E-43	AV708301.1	EST_HUMAN	O15475 UNMATED HERV-H PROTEIN contains LTR/2.81 LTR repetitive element;
6586	19807	32762	2.69	6.0E-43	9455973	NT	RIBOSOMAL PROTEIN L30 (r-L30);
7296	20145	33046	2.3	6.0E-43	AV468897.1	EST_HUMAN	AV708301 ADO Homo sapiens cDNA clone ADAC010.5
10395	23264	30874	2.34	6.0E-43	AA166154.1	EST_HUMAN	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA
11545	24444		1.91	6.0E-43	AI119158.1	EST_HUMAN	MD03001.x1 Sorensen, N.F., T., GBO, 31 Homo sapiens cDNA clone IMAGE:2910951.5 similar to contains MER1.18 MER1 repetitive element;
148	13248		1.86	5.0E-43	AL163213.2	NT	Z356063.1 Sorensen, N.H.M.P., 51 Homo sapiens cDNA clone IMAGE:96410.5 similar to TR-G02841
525	13595	25506	3.69	5.0E-43	AA382780.1	EST_HUMAN	G5094H DB1, COMPLETE CDS, contains element PRY3 repetitive element;
2891	16945	28840	1.9	5.0E-43	AV732578.1	EST_HUMAN	DNF2791L1712.71 161 (cysteine); hamy/31 Homo sapiens cDNA clone D1729761L1712.5
6650	20740	33379	0.98	5.0E-43	AA181933.1	EST_HUMAN	ES1160333 tests: Homo sapiens cDNA 5' end
7251	20140	33379	0.94	5.0E-43	AA181933.1	EST_HUMAN	W22847.x1 NCL CGAP Brn02 Homo sapiens cDNA clone IMAGE:2380453.3
7251	20140	33379	0.94	5.0E-43	AA181933.1	EST_HUMAN	W22847.x1 NCL CGAP Brn02 Homo sapiens cDNA clone IMAGE:2380453.3
8768	21695	33377	0.97	5.0E-43	AA442271.1	EST_HUMAN	Z249633.1 Sorensen, N.H., T., GBO, 31 Homo sapiens cDNA clone IMAGE:787420.5
8768	21695	33377	0.97	5.0E-43	AA442271.1	EST_HUMAN	Z249633.1 Sorensen, N.H., T., GBO, 31 Homo sapiens cDNA clone IMAGE:787420.5

Table 4

[illegible]

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9436	22264		0.8	5.0E-43	R7427.1	EST_HUMAN	9456121r1 Scores field liver INFL3 Homo sapiens cDNA clone IMAGE:226610 5'
9436	22264		4.55	5.0E-43	AA05266.1	EST_HUMAN	acc33408.1 NC1 CGAP C331 Homo sapiens cDNA clone IMAGE:451005 5'
10883	20767	37193	1.76	5.0E-43	AA32444.1	EST_HUMAN	o032c103 NC1 CGAP Lur1 Homo sapiens cDNA clone IMAGE:159810 3' similar to TRP90997 P03051 PV14 GENE ;
20116	27802	37230	2.19	5.0E-43	AL04110.1	EST_HUMAN	DFZ494040119 17 t334 (synonym: hies3) Homo sapiens cDNA clone DFZ454-05119
11202	24128	37575	5.3	5.0E-43	AA095007.1	EST_HUMAN	MF2-2349007-2349008-400-027 3'NOT7 Homo sapiens cDNA Homo sapiens x-chrom embryonic ectodermal cytoplasm protein gene (E2N), exon 2 and flanking repeat
999	18647	26982	3.43	4.0E-43	AA09538.1	NT	Homo sapiens x-chrom embryonic ectodermal cytoplasm protein gene (E2N), exon 2 and flanking repeat
6440	18647	31247	1.13	4.0E-43	AB09326.1	EST_HUMAN	9749333.1 NC1 CGAP B2433 Homo sapiens cDNA clone IMAGE:166913 3'
8620	20316	32554	0.78	4.0E-43	0685009	NT	9749333.1 NC1 CGAP B2433 Homo sapiens cDNA clone IMAGE:166913 3'
7490	20430		2.01	4.0E-43	11410793	NT	9749333.1 NC1 CGAP B2433 Homo sapiens cDNA clone IMAGE:166913 3'
8756	21889	35025	0.4	4.0E-43	N244341.1	EST_HUMAN	9749333.1 NC1 CGAP B2433 Homo sapiens cDNA clone IMAGE:166913 3'
8756	21889	35025	0.4	4.0E-43	N244341.1	EST_HUMAN	9749333.1 NC1 CGAP B2433 Homo sapiens cDNA clone IMAGE:166913 3'
8756	21889	35025	0.4	4.0E-43	N244341.1	EST_HUMAN	9749333.1 NC1 CGAP B2433 Homo sapiens cDNA clone IMAGE:166913 3'
10894	23060	37118	1.43	4.0E-43	6305957	NT	9749333.1 NC1 CGAP B2433 Homo sapiens cDNA clone IMAGE:166913 3'
12384	25162		3.79	4.0E-43	R20950.1	EST_HUMAN	9749333.1 NC1 CGAP B2433 Homo sapiens cDNA clone IMAGE:166913 3'
1241	14277		2.63	3.0E-45	AF22391.1	NT	9749333.1 NC1 CGAP B2433 Homo sapiens cDNA clone IMAGE:166913 3'
1721	14749	27717	0.96	3.0E-43	AF37868.1	NT	9749333.1 NC1 CGAP B2433 Homo sapiens cDNA clone IMAGE:166913 3'
3632	16008	28106	0.96	3.0E-43	360002.1	NT	9749333.1 NC1 CGAP B2433 Homo sapiens cDNA clone IMAGE:166913 3'
4350	17454	30272	1.58	3.0E-43	AA06154.1	EST_HUMAN	9749333.1 NC1 CGAP B2433 Homo sapiens cDNA clone IMAGE:166913 3'
5535	16614	31493	0.5	3.0E-43	AA02591.1	NT	9749333.1 NC1 CGAP B2433 Homo sapiens cDNA clone IMAGE:166913 3'
5535	16614	31493	0.5	3.0E-43	AA02591.1	NT	9749333.1 NC1 CGAP B2433 Homo sapiens cDNA clone IMAGE:166913 3'
8111	19171	32003	0.79	3.0E-43	D34615.1	NT	9749333.1 NC1 CGAP B2433 Homo sapiens cDNA clone IMAGE:166913 3'
9710	18557	32540	1.94	3.0E-43	7205359	NT	9749333.1 NC1 CGAP B2433 Homo sapiens cDNA clone IMAGE:166913 3'
6010	18557	32540	1.94	3.0E-43	7205359	NT	9749333.1 NC1 CGAP B2433 Homo sapiens cDNA clone IMAGE:166913 3'
7030	20359	32559	4.68	3.0E-43	U05487.1	EST_HUMAN	9749333.1 NC1 CGAP B2433 Homo sapiens cDNA clone IMAGE:166913 3'
8741	21671		0.87	3.0E-43	AA458824.1	EST_HUMAN	9749333.1 NC1 CGAP B2433 Homo sapiens cDNA clone IMAGE:166913 3'
9759	22027	35538	0.62	3.0E-43	2661724	NT	9749333.1 NC1 CGAP B2433 Homo sapiens cDNA clone IMAGE:166913 3'

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Table 4

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) HR BLAST E Value	Top HR Accession No.	Top HR Database Source	Top HR Description
12388	25582	31729	1.51	8.0E-44	11418006	NT	Homo sapiens putative nuclear protein (HSPH19-2122). mRNA
12915	25719	31570	1.67	8.0E-44	11418006	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCAP2). mRNA
682	13744		0.88	7.0E-44	R000351	EST_HUMAN	559001.11 Scores fall for spken. NFI5 Homo sapiens cDNA clone IMAGE:124822.5
22569	14256	32627	2.15	7.0E-44	3001898	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP). mRNA
30071	19552	33662	2.27	7.0E-44	AF0494720.1	NT	Homo sapiens antisense RNA 337 repeat region
30071	19552	33665	2.27	7.0E-44	AF0494720.1	NT	Homo sapiens antisense RNA 337 repeat region
30223	16937	33940	3.77	7.0E-44	AF163284.2	NT	Homo sapiens chromosome 21 segment HS21C984
4424	17554	30217	1.04	7.0E-44	AF163284.2	NT	Homo sapiens chromosome 21 subunit mRNA
4920	17663	30218	1.04	7.0E-44	AF163219.1	EST	Homo sapiens chromosome 21 subunit mRNA
8739	21454	30219	1.71	7.0E-44	AF163931.1	EST_HUMAN	AF163939.1 Homo sapiens cDNA clone 798A100496.5
8739	21454	30219	1.71	7.0E-44	AF163931.1	EST_HUMAN	85AAALVEUP Human fetal Brain White tissue Homo sapiens cDNA
8941	16391	32560	0.73	6.0E-44	U759510.1	EST_HUMAN	EST398120.1 MAGE csequences, MAGE Homo sapiens cDNA
12180	20076	38526	1.7	6.0E-44	AF165050.1	EST_HUMAN	Homo sapiens KIA0851 gene (partial), X13 gene and LZ1FL1 gene
323	13415		2.68	5.0E-44	AF209060.1	NT	Homo sapiens KIA0851 gene (partial), X13 gene and LZ1FL1 gene
323	13439		2.24	5.0E-44	AF209060.1	NT	Homo sapiens KIA0851 gene (partial), X13 gene and LZ1FL1 gene
8469	21950	34726	4.6	5.0E-44	AF69528.1	EST_HUMAN	H4002.11 NC. QCAP. Bm26. Homo sapiens cDNA clone IMAGE:2170083.5 similar to contains ORF.11
8921	22503		1.7	5.0E-44	AF124671.1	EST_HUMAN	H4002.11 NC. QCAP. Bm26. Homo sapiens cDNA clone IMAGE:2170083.5 similar to contains ORF.11
3476	18515	20914	2.37	4.0E-44	AF10330.2	NT	Human chromosome 21 segment HS21C103
3871	16916		0.92	4.0E-44	BE169360.1	EST_HUMAN	MR3-HITC81-150200-115-g01 HITC81 Homo sapiens cDNA
5140	18135		1.89	4.0E-44	AF10330.2	EST_HUMAN	11H02.11 NCI QCAP. Panti Homo sapiens cDNA clone IMAGE:2130417.3
7860	20177	34122	0.62	4.0E-44	BE98378.1	EST_HUMAN	01500031.01 NIH. MGC. 71 Homo sapiens cDNA clone IMAGE:3910152.5
8847	21711	35124	0.82	4.0E-44	121048.1	NT	Human fibroblast (FBM1) locus polynucleotide
9435	22593		0.6	4.0E-44	BE70918.1	EST_HUMAN	RC3-HITC85-010400-025-018 HITC85 Homo sapiens cDNA
11985	24996	35099	12.08	4.0E-44	U06781.1	NT	Human osteoblast terminal LIM domain protein (CLIM). mRNA, complete cds
2550	15555	25858	1.3	3.0E-44	BE880620.1	EST_HUMAN	01491020F NIH. MGC. 60 Homo sapiens cDNA clone IMAGE:3893859.5
3145	16195	23048	7.34	3.0E-44	AA16985.1	EST_HUMAN	01491020F NIH. MGC. 60 Homo sapiens cDNA clone IMAGE:3893859.5
3390	16098	20874	2.48	3.0E-44	AA33724.1	EST_HUMAN	EST12290.9 E-cadherin tumor Homo sapiens cDNA 5' end similar to alpha-1-antitrypsinase F
8230	21713	34828	0.6	3.0E-44	BE884820.1	EST_HUMAN	01510570F NIH. MGC. 71 Homo sapiens cDNA clone IMAGE:391210.5
00049	22585	30354	0.65	3.0E-44	AF050275.1	NT	Site specific demethylation subunit/specific polyoma virus mRNA, complete cds
1075	14719	217058	1.99	2.0E-44	4820958	NT	Human sapiens DEAD/H (Asp-Glu-Als-Asp) box polypeptides 1 (DDX1). mRNA
1075	14716	27057	1.99	2.0E-44	4820958	NT	Human sapiens DEAD/H (Asp-Glu-Als-Asp) box polypeptides 1 (DDX1). mRNA
1075	14716	27057	1.99	2.0E-44	5003270	NT	Homo sapiens transmembrane trafficking protein (TMF2). mRNA
1235	14716	27214	4.6	2.0E-44	5003270	NT	Homo sapiens transmembrane trafficking protein (TMF2). mRNA
1235	14716	27214	4.6	2.0E-44	5003270	NT	Homo sapiens transmembrane trafficking protein (TMF2). mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Eno1 SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (BLAST) Hit Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1338	14371	27323	2.45	2.0E-44	AF133588.1	NT	Homo sapiens RAB38 (RAB38) mRNA, complete cds
1395	14426	27380	1.26	2.0E-44	BE465325.1	EST_HUMAN	hwt149057.1 NCL COGAP 14c11 Homo sapiens cDNA clone IMAGE3182598 3' similar to SW OX5B_HUMAN
2166	15714	28184	1.85	2.0E-44	AF170681.1	NT	P22019 OXYOCT-BINDING PROTEIN ;
2570	15568		1.85	2.0E-44	4607552.1	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
2572	15510	289005	1.59	2.0E-44	0253003.1	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
2693	16648		1.05	2.0E-44	5901983.1	NT	Human mRNA for integrin alpha subunit, complete cds
4685	17560	30357	1.83	2.0E-44	AV1684979.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPSD4) mRNA
4601	17600	30757	1.07	2.0E-44	7709128.1	NT	PM4-3N001615-2000-003-201 SN01010 Homo sapiens cDNA
4601	17600	30757	1.07	2.0E-44	7709128.1	NT	Homo sapiens cytoskeletal 7alpha-hydroxylase (CYP3A11) mRNA
4601	17600	30758	1.07	2.0E-44	7709128.1	NT	Homo sapiens cytoskeletal 7alpha-hydroxylase (CYP3A11) mRNA
6332	19382	32850	1.53	2.0E-44	11448901.1	NT	Homo sapiens chemokine (C-C motif) receptor 9 (CCR9) mRNA
7178	18450	31319	1.12	2.0E-44	AF938988.1	NT	Homo sapiens general transcription factor 2 (GTF2B) mRNA, alternatively spliced product, complete cds
7814	20763	34047	3.51	2.0E-44	11148222.1	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
7814	20763	34048	3.51	2.0E-44	11148222.1	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
8698	21627	35281	0.82	2.0E-44	70031010.1	NT	Homo sapiens gamma-tubulin complex component 3 (G3BP3) mRNA
8698	21627	35282	0.82	2.0E-44	70031010.1	NT	Homo sapiens gamma-tubulin complex component 3 (G3BP3) mRNA
9178	22106	34494	1.81	2.0E-44	BE368958.1	EST_HUMAN	Homo sapiens vesicle transport-related protein (Vsta0917) mRNA
12248	22607		3.64	2.0E-44	BE448922.1	EST_HUMAN	601288914F1 NH M252 44 Homo sapiens cDNA clone IMAGE3313580 5'
151	19172	28671	4.62	1.0E-44	7657333.1	NT	TGAP2L127095 Pseudo-pg-8 cell acute myeloblastic leukemia Baylar-HCSG project+TGBA Homo sapiens cDNA clone TGBA/P-2765
55	19172	28671	4.62	1.0E-44	7657333.1	NT	Homo sapiens Musashi/NK-related kinase (MINK) mRNA
85	19172	28672	4.62	1.0E-44	7657333.1	NT	Homo sapiens Musashi/NK-related kinase (MINK) mRNA
602	13868	28871	2.58	1.0E-44	AW85132.1	EST_HUMAN	RG1-CT0249-010300-028-R12 CT0249 Homo sapiens cDNA
1225	14262		1.93	1.0E-44	AA440403.1	EST_HUMAN	RG1-BN0035-110300-012-501 BN0035 Homo sapiens cDNA
1565	14626		7.72	1.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment H871C1C103
2237	15247	28253	5.03	1.0E-44	AA434154.1	EST_HUMAN	zifw3402.1 Soares, total, adult, M24-IF8, 521 Homo sapiens cDNA clone IMAGE:73785 5' similar to contains THR 8 THR repetitive element ;
2237	15247	28254	5.03	1.0E-44	AA434154.1	EST_HUMAN	zifw3402.1 Soares, total, adult, M24-IF8, 521 Homo sapiens cDNA clone IMAGE:73785 5' similar to contains THR 8 THR repetitive element ;
2810	15705	28708	2.11	1.0E-44	AF106779.1	NT	Homo sapiens transcription factor GCM enhancer 3, -M11 protein, -M6 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophycin genes, complete cds ; and -L-type calcium channel alpha-
3786	18820		2.83	1.0E-44	AA458869.1	EST_HUMAN	af01c00.3 Soares, INH10F3 311 Homo sapiens cDNA clone IMAGE3311884 3'
8841	19711	35117	1.02	1.0E-44	AA190707.1	EST_HUMAN	EST379147 Soares, IMAGE379147 Homo sapiens cDNA

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8841	21771	35118	1.02	1.0E-44	AY060703.1	EST_HUMAN	EST379147 IMAGE retrosequences, IMAGE Homo sapiens cDNA
9206	22134	35451	0.93	1.0E-44	AL062062.2	NT	Homo sapiens chromosome 21 segment HS21C036
9577	22574	35698	0.89	1.0E-44	A0357.83.1	EST_HUMAN	g85937.1 X1 NCL CGAP Q43 Homo sapiens cDNA clone IMAGE:200863.3'
11452	24398		3.65	1.0E-44	AY174038.1	EST_HUMAN	AY174038 D38 Homo sapiens cDNA clone D381E3.5'
11991	24834	38393	4.28	1.0E-44	1009269	NT	Homo sapiens small ribosomal subunit containing (5S/5.8S) 2' mRNA
12020	24892	38392	2.2	1.0E-44	AY046967.1	EST_HUMAN	RC1410185-150020-011028 CT0168 Homo sapiens cDNA
12020	24892	38393	2.2	1.0E-44	AY046957.1	EST_HUMAN	RC1410185-150020-011028 CT0168 Homo sapiens cDNA
8841	19570	33193	1.28	9.0E-45	AB22247.1	NT	Homo sapiens TRF-1 mRNA for TRF-1 protein, 3' end cts
2551	15551	25649	3.7	8.0E-45	8114748	NT	Homo sapiens TRF-1 fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5217	16207	31052	10.51	8.0E-45	AY02765.1	EST_HUMAN	Homo sapiens TRF-1 fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
8184	18153	31053	0.51	8.0E-45	AY02765.1	EST_HUMAN	CHCHN0005-103300-265109 NN005 Homo sapiens cDNA
8865	21918	34955	0.92	8.0E-45	A037565.1	EST_HUMAN	EST109695 Synovial sarcoma Homo sapiens cDNA 5' end
1975	14895		1.15	6.0E-45	AB75426.1	EST_HUMAN	w19600.x1 NCL CGAP P228 Homo sapiens cDNA clone IMAGE:231302.3' similar to contains L1, L1 L1 repetitive element;
4003	17089		1.93	9.0E-45	AW16750.1	EST_HUMAN	ab8907.x1 Schwedler fetal brain 00004 Homo sapiens cDNA clone IMAGE:278209.3' similar to SW-R13A, HUMAN P49159.605 RIBOSOMAL PROTEIN L13A;
12844	25924		1.51	9.0E-45	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
817	13399		0.25	5.0E-45	AL06203.2	NT	Homo sapiens chromosome 21 segment HS21C033
2018	19030	28050	3.85	5.0E-45	BF333627.1	EST_HUMAN	CH4-CH0044-180200-515407 ON004 Homo sapiens cDNA
3239	18034	22510	2.98	5.0E-45	AL623706.1	EST_HUMAN	Y64007.X1 NCL CGAP CLL1 Homo sapiens cDNA clone IMAGE:211949.3' similar to SW-PAX1_MOUSE P00084 PAIRED BOX PROTEIN PAX-1;
5702	19776	31793	8.95	5.0E-45	AA397781.1	EST_HUMAN	272403.at Source, testis, NNT Homo sapiens cDNA clone IMAGE:727677.3' similar to contains element, TARI repetitive element;
6252	19305	32467	1.25	5.0E-45	Y18903.1	NT	Homo sapiens MCF-1 gene and enhancer region
9292	19305	32468	1.25	5.0E-45	Y18903.1	NT	Homo sapiens MCF-1 gene and enhancer region
8300	19351	32516	0.95	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
8300	19351	32520	0.95	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
8430	19477	32953	1.15	5.0E-45	11492098	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
8430	19477	32954	1.15	5.0E-45	11492098	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
8952	21792	35129	0.82	5.0E-45	11416704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
8952	22519	35882	1.81	5.0E-45	4755223	NT	Homo sapiens programmed cell death 5 (PDCD5), mRNA
12116	24900	39403	2.87	5.0E-45	8023698	NT	Homo sapiens gadin-like protein (GLP), mRNA
1171	14211	27148	7.87	5.0E-45	X995206.1	NT	Homo sapiens ART1 gene
2310	18318	28510	2.48	4.0E-45	BE26522.1	EST_HUMAN	90119440H1 NH_MGC_7 Homo sapiens cDNA clone IMAGE:359425.5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4628	17654	30498	0.69	4.0E-46	4769246	NT	Homo sapiens TRAF-family member-associated NF- κ B activator (TANK) mRNA
6611	22408		0.69	4.0E-46	A422626.1	EST HUMAN	hG3907.1 NOT CGAP P71 Homo sapiens cDNA IMAGE:100294 similar to contains element L1 replicable element
3370	19422		1.33	3.0E-48	A174465.1	EST HUMAN	X65907.1 Scores full liver placenta (H.3) Homo sapiens cDNA clone IMAGE:16246 5'
4175	18422		1.17	3.0E-48	U74465.1	EST HUMAN	X65907.1 Scores full liver placenta (H.3) Homo sapiens cDNA clone IMAGE:16246 5'
6464	19528	32707	1.24	3.0E-48	678365	NT	Mus musculus Uptake, actin, heart, skin, liver, placenta (1) (Oncop1) mRNA
6464	19528	32708	1.24	3.0E-48	678365	NT	Mus musculus Uptake, actin, heart, skin, liver, placenta (1) (Oncop1) mRNA
8018	21646		1.55	3.0E-48	AY72691.1	EST HUMAN	AY72691.1 H.3 Homo sapiens cDNA, clone H7BA4201.5
8349	22277	36586	0.43	3.0E-48	AY72691.1	EST HUMAN	Homo sapiens OGG1 nucleoside glycosylase, p907 subfamily, 2 (GOLGA2) mRNA
10797	23883	37111	0.70	3.0E-48	AA19327.2	NT	Homo sapiens chromosome 21 segment HST1027
12027	23888	37112	1.37	3.0E-48	AA19327.2	NT	Homo sapiens chromosome 21 segment HST1027
2426	18527		2.26	3.0E-48	X68241.1	NT	H. sapiens DNA for endogenous retroviral like element
3079	16130	28026	0.91	2.0E-45	A41931.2	NT	Homo sapiens chromosome 21 segment HST1019
6800	18833	33044	5.42	2.0E-45	A42431.3	NT	Homo sapiens partial 2-H14 receptor gene, exons 2 to 5
8054	20097	34282	1.36	2.0E-48	BE762184.1	EST HUMAN	Human osteophilic Chrooc-Leyden crystal (CLC) protein (lyso-phospholipase) gene, promoter and exon 1
8690	21815	35271	0.6	2.0E-48	AV634834.1	EST HUMAN	RCOL17001-19200-032-471 L70301 Homo sapiens cDNA
11242	25927	37614	6.63	2.0E-48	BE384350.1	EST HUMAN	MPD-H10923-10900-201-402 L70923 Homo sapiens cDNA
11610	24528	37095	3.41	2.0E-48	AA488770.1	EST HUMAN	sa6712.1 Striatagene field notes 671202 Homo sapiens cDNA clone IMAGE:588319 5' similar to
11937	24781	39277	1.76	2.0E-48	AW27020.1	EST HUMAN	X772403.1 NOT CGAP Ovi40 Homo sapiens cDNA clone IMAGE:2746968 3'
11937	24781	39278	1.76	2.0E-48	AW27020.1	EST HUMAN	X772403.1 NOT CGAP Ovi40 Homo sapiens cDNA clone IMAGE:2746968 3'
13022	29565	39276	4.02	2.0E-48	11418197	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1 subunit (CACNA1), mRNA
128	13503		1.76	1.0E-48	BE38685.1	EST HUMAN	501294306F1 INH.M5C-44 Homo sapiens cDNA clone IMAGE:3606183 5'
432	13503		2.04	1.0E-48	BE38685.1	EST HUMAN	501294306F1 INH.M5C-44 Homo sapiens cDNA clone IMAGE:3606183 5'
465	13565	28484	0.97	1.0E-48	4506412	NT	Homo sapiens RAH1A, member of RAS oncogene family (RAH1A), mRNA
1202	14241	27162	1.82	1.0E-48	U02169.1	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGRIN), mRNA
3150	10200	29652	10.86	1.0E-49	U02169.1	NT	Human pro- α 2 chain of collagen type XI (COL11A2) gene, complete cds
3031	18856	29466	0.51	1.0E-48	6969566	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf1), mRNA
3034	16670	29657	0.76	1.0E-48	AB040811.1	NT	Homo sapiens mRNA for KIAA1991 protein, partial cds
4690	17968	30456	7.63	1.0E-48	BE386853.1	EST HUMAN	601294306F1 INH.M5C-8 Homo sapiens cDNA clone IMAGE:3619688 5'
4636	17940		1.36	1.0E-48	H67143.1	EST HUMAN	Y06022.1 Scores full liver spleen (H.3) Homo sapiens cDNA clone IMAGE:204369 5'
8906	21540	34881	0.79	1.0E-48	11422296	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8669	21540	34882	0.76	1.0E-46	11422298	NT	Homo sapiens putative small ubiquitin ligase factor 14 (PEX14), mRNA
9168	22660	35455	0.95	1.0E-46	06167676.1	NT	Homo sapiens DNA topoisomerase protein complex subunit 1 (TOPBP1), mRNA
8665	22591	35904	4.71	1.0E-46	BE587645.1	EST_HUMAN	95161722591 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:3917553.5
10032	22433	36557	0.88	1.0E-45	AB002971.1	NT	Human HNRK (HNRK, HNRK gene), protein
12435	23163	31860	3.16	1.0E-46	11416369	NT	Homo sapiens histone H3.3 (H3.3), mRNA
12003	23259		16.13	1.0E-45	11423339	NT	Homo sapiens hypothetical protein FLJ129434 (FLJ129434), mRNA
12038	23302		4.78	1.0E-45	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12697	23550	31765	3.18	1.0E-46	11418177	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
8193	21216	35055	8.32	9.0E-46	AB193209.2	NT	Mus musculus keratin complex 2, gene Bc (K204p), mRNA
9103	21421	37268	8.32	9.0E-46	AB193209.2	NT	Homo sapiens keratin complex 2, gene Bc (K204p), mRNA
10558	22942	37268	8.32	9.0E-46	AB193209.2	NT	Homo sapiens keratin complex 2, gene Bc (K204p), mRNA
2495	15490	28495	6.18	6.0E-46	AB433261.1	EST_HUMAN	2823446 Sporne NIH_MGC_77 Homo sapiens cDNA clone IMAGE:2822449.5
2495	15490	28495	6.18	6.0E-46	AB433261.1	EST_HUMAN	3326531 NCL_GGAP_Gas1 Homo sapiens cDNA clone IMAGE:2132169.3 similar to gh-003314_m92
9332	21503	28495	3.32	6.0E-46	AB433261.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
4824	17659		1.97	7.0E-46	BE167244.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
4921	17620		1.05	7.0E-46	BE005386.1	EST_HUMAN	RC5-1170595-260290-912-G12 HT0509 Homo sapiens cDNA
6277	19328	32404	5.01	7.0E-46	6622708	NT	9512772591 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3518119.5
6770	19804	33015	2.89	7.0E-46	BF108454.1	EST_HUMAN	RC4-B10310-110330-915-410 B10310 Homo sapiens cDNA
12731	23573		1.73	7.0E-46	AL163245.2	NT	6918255951 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4942796.5
2003	15792	28791	6.23	6.0E-46	AB84381.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
2603	15792	28792	6.23	6.0E-46	AB84381.1	EST_HUMAN	6918255951 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4942796.5
5190	18162		0.78	6.0E-46	BE335440.1	EST_HUMAN	6918255951 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4942796.5
6989	18148	32594	10.05	6.0E-46	AB034481.1	EST_HUMAN	6918255951 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4942796.5
7595	20021	33603	0.86	6.0E-46	AB034481.1	EST_HUMAN	6918255951 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4942796.5
11828	22683	34008	0.41	6.0E-46	BE503740.1	EST_HUMAN	6918255951 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4942796.5
2177	13316		2.26	6.0E-46	BE784871.1	EST_HUMAN	6918255951 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4942796.5
5990	16627	29550	1.96	5.0E-46	AL163270.2	NT	6918255951 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4942796.5
5990	16627	29550	1.96	5.0E-46	BE37184.1	EST_HUMAN	6918255951 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4942796.5

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12633	23314		1.36	2.0E-46	AA007798.1	EST_HUMAN	3447/21.1 Sarcosine, fetal liver, pituitary, INR5. S1 Homo sapiens cDNA clone IMAGE:28915 5'
12634	23340	31670	4.32	2.0E-46	AI127214.1	EST_HUMAN	747/19.03.1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2767183 3'
12635	23341	31671	4.46	1.0E-46	753269.1	NT	Homo sapiens adult thymus cyclic 10 nucleotides cDNA, 5' & 3' consensus (CDC10) mRNA
12636	23342	31672	0.98	1.0E-46	7532177	NT	Homo sapiens KIA00555 gene product (KIA00555) cDNA
12637	23343	31673	0.98	1.0E-46	7532177	NT	Homo sapiens KIA00555 gene product (KIA00555) cDNA
2001	18503	26315	4.34	1.0E-46	AI197864.1	EST_HUMAN	EST1830625 IMAGE sequences, MA3P Homo sapiens cDNA
2422	18428	26427	5.47	1.0E-46	H07330.1	EST_HUMAN	EST1830625 IMAGE sequences, MA3P Homo sapiens cDNA
3284	16941		7.22	1.0E-46	AA651812.1	EST_HUMAN	no7802.v1 NCI CGAP P22 Homo sapiens cDNA clone IMAGE:132396 similar to gb:X78717 H. sapiens
4691	17079	26843	3.75	1.0E-46	AB028187.1	NT	Homo sapiens mRNA for KIA00380 protein, partial cds
5958	18607	32655	7.4	1.0E-46	BF184707.1	EST_HUMAN	7625201.v1 NCI CGAP OV18 Homo sapiens cDNA clone IMAGE:3543705 3'
6206	25643	32410	5.23	1.0E-46	8923702	NT	Homo sapiens centaurin-alpha 2 protein (HSA/27186), mRNA
6206	25643	32411	5.23	1.0E-46	8923702	NT	Homo sapiens centaurin-alpha 2 protein (HSA/27186), mRNA
6598	19026	33145	0.95	1.0E-46	BF195247.1	EST_HUMAN	7118607.v1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3567862 3' similar to contig element
71207	19067	32055	4.47	1.0E-46	BF194707.1	EST_HUMAN	7625201.v1 NCI CGAP OV18 Homo sapiens cDNA clone IMAGE:3543705 3'
752	13847		4.57	6.0E-47	A.271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 12
5043	18040	30695	2.99	9.0E-47	AI177028.1	EST_HUMAN	H18644.v1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3009534 3' similar to TRC075703 O75703
9037	19577	32835	0.94	9.0E-47	11425436	NT	HYPOHETICAL, 12.4 KD PROTEIN, ;
12637	23326	31488	3.95	9.0E-47	11471966	NT	Homo sapiens zinc finger protein ZNF295 (ZNF295) mRNA
1850	14853	27831	20.02	8.0E-47	Y181536.1	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1830	14853	27832	20.02	9.0E-47	Y181536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 18023
2785	19757	29752	1.36	8.0E-47	5453855	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PP2R2B) mRNA
3008	16121	25022	2.41	8.0E-47	AB220043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3530	16723	25616	0.88	8.0E-47	AB044036.1	NT	Homo sapiens mRNA for GSK family kinase MNK-2, complete cds
3301	16723	25617	0.88	8.0E-47	AB044036.1	NT	Homo sapiens mRNA for GSK family kinase MNK-2, complete cds
3371	15563	31169	0.02	9.0E-47	7662421	NT	Homo sapiens KIA00571 protein (KIA00571), mRNA
12629	25739	28572	1.78	7.0E-47	AY185284.1	EST_HUMAN	AV058254 GSK Homo sapiens cDNA clone GKASH11 5'
2579	19578	28572	4.46	6.0E-47	AL103480.2	NT	Homo sapiens chromosome 21 segment H521C046
5230	22178	36552	0.93	6.0E-47	U77094.1	EST_HUMAN	HSU7004.Human Homo sapiens cDNA clone H4
5816	22722	36105	7.41	6.0E-47	AB061881.1	EST_HUMAN	2580242 NCI CGAP, NCI1 Homo sapiens cDNA clone IMAGE:226656 3'
10234	23125	36256	0.94	6.0E-47	AB043824.1	NT	Homo sapiens RECU4 beta mRNA for DNA helicase RECQ3 beta, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	OPF SEQ ID NO:	Expression Signal	Most Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description *
10224	19125	36027	0.84	6.0E-47	AB049284.1	NT	Homo sapiens RECQL3 beta mRNA for DNA helicase recq3 beta, complete cds
6859	18891	33105	7.45	5.0E-47	11425972	NT	Homo sapiens CD-37 (cell adhesion cycle 37, 5' carboxin, 1000bp) CD37 mRNA
11226	24162		3.62	5.0E-47	MT9560.1	EST_HUMAN	EST107328 Fetal brain, Straglers (285009) Homo sapiens cDNA clone IMAGE176767
11226	14486	27410	2.84	4.0E-47	4657956	NT	Homo sapiens E1A binding protein p300 (EBP300) mRNA
7145	20263	32005	0.77	4.0E-47	BE593863.1	EST_HUMAN	hNC-1100585 Human cDNA clone IMAGE322467 5'
6090	21979	35353	2.12	4.0E-47	BE591963.1	EST_HUMAN	hNC-1100585 Human cDNA clone IMAGE322467 5'
6090	21979	35358	2.12	4.0E-47	BE591963.1	EST_HUMAN	hNC-1100585 Human cDNA clone IMAGE322467 5'
9177	27105	35408	0.83	4.0E-47	AW99377.1	EST_HUMAN	hNC-1100585 Human cDNA clone IMAGE322467 5'
12063	24904		2.46	4.0E-47	AW165509.1	EST_HUMAN	hNC-1100585 Human cDNA clone IMAGE322467 5'
588	13335	25543	1.77	3.0E-47	BE307044.1	EST_HUMAN	hNC-1100585 Human cDNA clone IMAGE322467 5'
588	13335	25545	1.77	3.0E-47	BE307044.1	EST_HUMAN	hNC-1100585 Human cDNA clone IMAGE322467 5'
843	13305	25535	3.47	3.0E-47	BE307044.1	EST_HUMAN	hNC-1100585 Human cDNA clone IMAGE322467 5'
873	14024	25538	8.15	3.0E-47	AL165200.2	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRK1) mRNA
3348	13334	25535	0.31	3.0E-47	U93181.1	NT	Homo sapiens nuclear dual-specific phosphatase (NSP1) mRNA, partial cds
3348	13334	25535	0.31	3.0E-47	U93181.1	NT	Homo sapiens nuclear dual-specific phosphatase (NSP1) mRNA, partial cds
9246	12229	32457	4.93	3.0E-47	AW468820.1	EST_HUMAN	hNC-1100585 Human cDNA clone IMAGE322467 5'
9246	12229	32458	4.93	3.0E-47	AW468820.1	EST_HUMAN	hNC-1100585 Human cDNA clone IMAGE322467 5'
8845	19877	34006	0.97	3.0E-47	AB19765.1	EST_HUMAN	hNC-1100585 Human cDNA clone IMAGE322467 5'
7776	20705	34007	0.73	3.0E-47	AW93799.1	EST_HUMAN	hNC-1100585 Human cDNA clone IMAGE322467 5'
9391	22319	35061	0.73	3.0E-47	AW93799.1	EST_HUMAN	hNC-1100585 Human cDNA clone IMAGE322467 5'
153	13258	26176	1.28	2.0E-47	AL165200.2	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRK1) mRNA
594	14044	26966	1.85	2.0E-47	AL165200.2	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRK1) mRNA
1887	14618	26967	1.85	2.0E-47	AL165200.2	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRK1) mRNA
1616	14646	27005	1.39	2.0E-47	7602109	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRK1) mRNA
1704	14753	27060	3.83	2.0E-47	AA274514.1	EST_HUMAN	hNC-1100585 Human cDNA clone IMAGE322467 5'
22457	15057	282634	1.12	2.0E-47	AF007068.1	NT	Homo sapiens ring finger protein (RFP) gene, complete cds
4491	17502	30365	2.02	2.0E-47	AA698992.1	EST_HUMAN	hNC-1100585 Human cDNA clone IMAGE322467 5'
4491	17502	30366	2.02	2.0E-47	AA698992.1	EST_HUMAN	hNC-1100585 Human cDNA clone IMAGE322467 5'
4627	17503	30487	3.41	2.0E-47	5174648	NT	Homo sapiens RING finger protein domain binding protein-related (RFBP) mRNA

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5994	19099	32166	0.84	2.0E-47	AF078251.1	NT	Homo sapiens regulator of G-protein signaling 5 variant form (RGS5) mRNA, complete cds
6205	19291	32408	1.39	2.0E-47	BE78476.1	EST_HUMAN	g01463325F1 NH1_MGC_97 Homo sapiens cDNA clone IMAGE:3807487 5'
6205	19291	32409	1.39	2.0E-47	BE78476.1	EST_HUMAN	g01463325F1 NH1_MGC_97 Homo sapiens cDNA clone IMAGE:3807487 5'
8183	20684		1.43	2.0E-47	U07531.1	NT	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
8404	21007	34039	0.4	2.0E-47	U116317	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTN12) mRNA
8542	21473	34814	0.89	2.0E-47	U07673.1	NT	Homo sapiens DNA topoisomerase protein, complete cds
8542	21473	34815	0.85	2.0E-47	U07673.1	NT	Homo sapiens DNA topoisomerase protein, complete cds
8777	22203	35862	1.35	2.0E-47	AF071771.1	NT	Homo sapiens BRCA1-binding factor 1 (BRCA1) cDNA
10022	22822	39910	0.98	2.0E-47	U158196	NT	Homo sapiens 5' UTR, mRNA (5'UTR) mRNA
12424	28868	31472	0.48	2.0E-47	R41429.1	EST_HUMAN	g01463325F1 NH1_MGC_97 Homo sapiens cDNA clone IMAGE:3807487 5'
1430	24467	27143	5.11	1.0E-47	AF333429.1	EST_HUMAN	g01463325F1 NH1_MGC_97 Homo sapiens cDNA clone IMAGE:3807487 5'
1430	24467	27143	5.11	1.0E-47	AF333429.1	EST_HUMAN	g01463325F1 NH1_MGC_97 Homo sapiens cDNA clone IMAGE:3807487 5'
3805	18924	29801	0.98	1.0E-47	BE26477.1	EST_HUMAN	g01156321F1 NH1_MGC_21 Homo sapiens cDNA clone IMAGE:3135893 5'
3805	18924	29801	0.98	1.0E-47	BE26477.1	EST_HUMAN	g01156321F1 NH1_MGC_21 Homo sapiens cDNA clone IMAGE:3135893 5'
8210	19200	31044	0.95	1.0E-47	AF183593.1	EST_HUMAN	RC3-3'UTR1F-19400-017-A02 5'0167 Homo sapiens cDNA
7995	20094	33328	27.78	1.0E-47	AF60696.1	EST_HUMAN	af6069.1 Barbed acute HPLR88 Homo sapiens cDNA clone IMAGE:2955588 3' similar to gp-M22695
8420	22354		2.21	1.0E-47	AF064648.1	EST_HUMAN	RAS-RELATED PROTEIN RAP-1A (HUMAN);
10842	23728	37151	2.82	1.0E-47	U30116.1	NT	h6441.1; Scores: NFI_1_GBC_S1 Homo sapiens cDNA clone IMAGE:2978972 3' similar to g03125329
1635	14695	27827	4.35	9.0E-48	AF22391.1	NT	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
3817	10009	29054	0.73	9.0E-48	BF326947.1	EST_HUMAN	Fapo hemodyne alcohol dehydrogenase class I (ADH) gene, 5' region
5877	18649	32062	0.74	9.0E-48	BE368196.1	EST_HUMAN	spliced
5877	18649	32063	0.74	9.0E-48	BE368196.1	EST_HUMAN	CM2-MT0100-310700-290-005 MT0100 Homo sapiens cDNA
6338	15388	32957	0.49	9.0E-48	AF633168.1	EST_HUMAN	g01517747F1 NH1_MGC_71 Homo sapiens cDNA clone IMAGE:381105 5'
8470	19515	32980	0.73	9.0E-48	AF123240.1	EST_HUMAN	g01517747F1 NH1_MGC_71 Homo sapiens cDNA clone IMAGE:381105 5'
11559	24405	37390	3.95	9.0E-48	BE363816.1	EST_HUMAN	af6069.1 Barbed acute HPLR88 Homo sapiens cDNA clone IMAGE:237869 3' similar to Tc-090844
1278	14312		2.99	8.0E-48	AF501900	NT	060844 HOMOLOG OF RAT ZMOGEN GRANULE MEMBRANE PROTEIN. ;
1278	14312		2.99	8.0E-48	AF501900	NT	AF123240 NT28M Homo sapiens cDNA clone NT28M100978 5'
1278	14312		2.87	8.0E-48	4501900	NT	g01123240 NT28M Homo sapiens cDNA clone NT28M100978 5'
3180	10230	29124	4.29	8.0E-49	AF789477.1	EST_HUMAN	Homo sapiens aminocysteine 1 (ACTY1) mRNA
							Homo sapiens aminocysteine 1 (ACTY1) mRNA
							h6441.1; NC1 CGMP-Lyrt12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gp36107
							PREST-AS1 CONSERVED PROTEIN 1 (HUMAN);

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3180	10250	28125	4.26	8.0E-48	AF169477.1	EST_HUMAN	hKIN30.1 NCI CGAP L1012 Homo sapiens cDNA clone IMAGE:2001133.3 similar to gp-36-707
513	13984		1.91	7.0E-48	AF533335.1	NT	PREST BASIC CONSERVED PROTEIN 1 (HUMAN)
514	13984		12.95	7.0E-48	AB332351	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
1693	14693	27653	6	7.0E-48	9750398	NT	Homo sapiens SET domain and protein phosphatase fusion gene (SETMAR) mRNA
8350	15003	33552	24.69	7.0E-48	U1745531	NT	Homo sapiens HMG4/HMG1 synthetase (HARS) mRNA
3500	15055	25991	0.94	8.0E-48	AF191111	EST_HUMAN	u69H3.1 NCI CGAP K1212 Homo sapiens cDNA clone IMAGE:208613.3
8632	17835	33973	0.34	8.0E-48	AF32682.1	EST_HUMAN	u69H3.1 NCI CGAP K1212 Homo sapiens cDNA clone IMAGE:208613.3
5253	18350	35562	0.34	8.0E-48	AB30565.1	NT	Homo sapiens mRNA for AIE-75, complete cds
3293	20550	35562	0.31	8.0E-48	11420966	NT	Homo sapiens BAX non-receptor tyrosine kinase (BAX) mRNA
7677	26678	34705	0.6	8.0E-48	AB34484.1	NT	Homo sapiens mRNA for KIAA1924 protein, partial cds
7677	26678	34705	0.6	8.0E-48	AB34484.1	NT	Homo sapiens putative oncogene protein mRNA, partial cds
9458	22964	36049	1.33	8.0E-48	AF022616.1	NT	Homo sapiens putative oncogene protein mRNA, partial cds
10370	22686	36579	1.91	8.0E-48	11427428	NT	Homo sapiens NNT neuron (6637233) Homo sapiens cDNA clone IMAGE:533527.3 similar to 2445006.1
10212	22173	38504	3.85	6.0E-48	AA185096.1	EST_HUMAN	contains Alu repetitive element;
22677	12707	28263	1.50	5.0E-48	4527059	NT	Homo sapiens xylulokinase (H. influenzae) homolog (XYLB) mRNA
2277	12528	28204	0.91	5.0E-48	4827059	NT	Homo sapiens xylulokinase (H. influenzae) homolog (XYLB) mRNA
3355	15400	29300	2.59	5.0E-48	4823891	NT	Homo sapiens phosphotriesterase 1A, catimodilin-dependent (PDE1A) mRNA
11355	14311	37757	3.3	4.0E-48	AB20430.1	EST_HUMAN	u47d02.1 NCI CGAP P122 Homo sapiens cDNA clone IMAGE:225418.3
1412	14443	27365	1.26	3.0E-48	AF75094.1	EST_HUMAN	AV050664 GKC Homo sapiens cDNA clone OKCORE12.5
1932	18070	27999	7.85	3.0E-48	4885170	NT	Homo sapiens chromocorne X open reading frame 6 (CXORF6) mRNA
1982	13070	28000	7.85	3.0E-48	4885170	NT	Homo sapiens chromocorne X open reading frame 6 (CXORF6) mRNA
3478	18519	29418	1.04	3.0E-48	AF175403.1	NT	Homo sapiens opid growth factor receptor mRNA, complete cds
3696	18730	29821	1.22	3.0E-48	AF054591.1	EST_HUMAN	H14612.1 NCI CGAP G111 Homo sapiens cDNA clone IMAGE:297228.3 similar to SW-DOR6_HUMAN
6112	19172	32904	2.29	3.0E-48	BC045671.1	EST_HUMAN	PE655 DOWN SYNDROME CRITICAL REGION PROTEIN B.1
7954	20398	33827	1.04	3.0E-48	AF37913.1	NT	Human endogenous retrovirus HERV-2-1.27D
6902	21862		3.87	3.0E-48	AF059650.1	EST_HUMAN	u69H3.1 NCI CGAP P122 Homo sapiens cDNA clone IMAGE:121913.3 similar to contains PIRs.b1
11359	24228	37674	7.95	3.0E-48	BF51470.1	EST_HUMAN	U1H3W1 Homo sapiens cDNA clone IMAGE:3042287.3
5	13121	28008	1.1	2.0E-48	AA465097.1	EST_HUMAN	28008.11 Sources: everyblast 100/100 Homo sapiens cDNA clone IMAGE:107055.5
48	13198	26559	1.54	2.0E-48	AA63194.1	EST_HUMAN	10067 Regional genome DNA specific cDNA library Homo sapiens cDNA clone CR17-28

Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4646	17654	30520	1.34	2.0E-48	BE242065.1	EST_HUMAN	TG6A14D38.2 Pediatric pre-B cell acute lymphoblastic leukemia Bxfor-HGSC project CBA Homo sapiens cDNA clone TCBP-3942
6025	15057	32712	0.99	2.0E-48	AA613717.1	EST_HUMAN	no15971.11 NC1, CGAP, Cor10 Homo sapiens cDNA clone IMAGE:119372.3
6026	15057	32713	0.99	2.0E-48	AA613717.1	EST_HUMAN	no15971.11 NC1, CGAP, Cor10 Homo sapiens cDNA clone IMAGE:119372.3
7942	20694	34174	3.76	2.0E-48	AB046384.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
7942	20694	34175	3.76	2.0E-48	AB046384.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
7659	20691	34193	4.66	2.0E-48	11406228	NT	Homo sapiens vcl cell cytochrome b5-deficient cDNA clone GBCGG10.5
8928	21538	35213	3.93	2.0E-48	AV732453.1	EST_HUMAN	A734547.0E Homo sapiens cDNA clone GBCGG10.5
12338	31721	31563	3.93	2.0E-48	AA459074.1	EST_HUMAN	z69030.11 Scaevola hairy tumor NHOT Homo sapiens cDNA clone IMAGE:310325.5
12768	35126	31563	2.22	2.0E-48	BE731544.1	EST_HUMAN	901305504F1 NH1 MGSC_39 Homo sapiens cDNA clone IMAGE:333782.5
89	13175	25076	46.76	1.0E-48	7776634	NT	Homo sapiens cisplatin resistance-associated overexpressed protein, LOC517471, mRNA
898	13021	25068	4.6	1.0E-48	4522166	NT	Homo sapiens amyloid beta (A4) precursor protein (precursor protein, Alzheimer disease) (APP), mRNA
1103	14146	27684	2.39	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1103	14146	27685	2.39	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1322	14396	27693	2.88	1.0E-48	6032032	NT	Homo sapiens RNA binding motif protein 5 (RBM5) mRNA
1634	14655	27692	25.02	1.0E-48	AL163022.2	NT	Homo sapiens chromosome 21 segment HS21C102
3547	16555	25460	0.95	1.0E-48	AL163262.2	NT	Homo sapiens chromosome 21 segment HS21C102
6541	10584	32766	0.21	1.0E-48	AI859077.1	EST_HUMAN	18T7601.1 NC1, CGAP, Cor10 Homo sapiens cDNA clone IMAGE:2075964.3 similar to TRC14396 O14589 SIMILARITY TO U79341
6541	10584	32769	0.94	1.0E-48	AI859077.1	EST_HUMAN	18T7601.1 NC1, CGAP, Cor10 Homo sapiens cDNA clone IMAGE:2075964.3 similar to TRC14396 O14589 SIMILARITY TO U79341
6718	18810	33125	0.81	1.0E-48	Y18000.1	NT	Homo sapiens NF2 gene
6880	18910	33125	0.96	1.0E-48	AB025894.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds
6880	18910	33126	0.96	1.0E-48	AB025894.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds
7630	20465	33859	2.99	1.0E-48	4759197	NT	Homo sapiens huntingtin (Huntington disease) (HD) mRNA
9754	22678	36065	1.03	1.0E-48	4002898	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
9905	22714	36987	7.14	1.0E-48	AB033071.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
10111	23002	36988	4.89	1.0E-48	BF304683.1	EST_HUMAN	10T188050P1 NH1 MGSC_37 Homo sapiens cDNA clone IMAGE:1122119.5
10838	28744	37167	4.46	1.0E-48	11428908	NT	Homo sapiens B cell linker protein (SLP-65), mRNA
10838	28744	37168	4.46	1.0E-48	11428908	NT	Homo sapiens B cell linker protein (SLP-65), mRNA
2022	15040	28034	1.26	8.0E-49	AB026497.1	NT	Mus musculus Myo-PDZ mRNA for myon containing PDZ domain, complete cds
6288	18339	32506	3.59	8.0E-49	1008841	NT	Mus musculus 14ox.20 (10x20), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORE SEQ ID NO.	Expression Signal	Most Similar (BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6283	10339	33507	3.36	8.0E-49	10088417	NT	Mus musculus T-box 28 (Tbox28) mRNA
7195	20264	33518	0.57	8.0E-49/AJ64033.1	EST_HUMAN		nt181603.1 NC1 CGAP 20201 Homo sapiens cDNA clone IMAGE:184621.5
8971	21801	35155	4.45	8.0E-49/U29390.1	NT		Human insulin 1/2,2 triproline receptor type 1 mRNA, partial cds
10495	23053	35795	1.43	8.0E-49/AB08981.1	NT		Homo sapiens proteinase (protease, macrophage) 28S subunit, A1Praw.4 (PSN04) mRNA
144	13488	25407	2.05	7.0E-49	5726950	NT	Homo sapiens proteinase (protease, macrophage) 28S subunit, A1Praw.4 (PSN04) mRNA
145	13488	25407	2.05	7.0E-49	5726950	NT	Homo sapiens proteinase (protease, macrophage) 28S subunit, A1Praw.4 (PSN04) mRNA
415	13488	25407	2.48	7.0E-49	5726950	NT	Homo sapiens proteinase (protease, macrophage) 28S subunit, A1Praw.4 (PSN04) mRNA
415	13488	25407	2.71	7.0E-49	5726950	NT	Homo sapiens proteinase (protease, macrophage) 28S subunit, A1Praw.4 (PSN04) mRNA
415	13488	25407	2.71	7.0E-49	5726950	NT	Homo sapiens proteinase (protease, macrophage) 28S subunit, A1Praw.4 (PSN04) mRNA
1249	14255	27235	1.88	7.0E-49/AL152294.2	NT		Homo sapiens chromosome 21 segment H521C10
4159	17704	36527	1.02	7.0E-49	CR53.1	SWISSPROT	H-PROTHETICAL PROTEIN:R46024.3
5645	18719	31623	1.71	7.0E-49/AB07191.1	EST_HUMAN		MF5804.x1 Soares, NFL_T_05C, 31 Homo sapiens cDNA clone IMAGE:245663.3 similar to TR.054623
5656	18730	31635	1.09	7.0E-49/AL120817.1	EST_HUMAN		Q49823 RSEC15.1 DNF77620333.31 762 (synonym: hml2) Homo sapiens cDNA clone DNF7620333.3
8616	18719	31623	1.07	7.0E-49/AB07191.1	EST_HUMAN		MF5804.x1 Soares, NFL_T_05C, 31 Homo sapiens cDNA clone IMAGE:245663.3 similar to TR.054623
210	13309	26226	29.3	6.0E-49/AV175140.1	EST_HUMAN		complete (MOUSE); R60500.x1 NIH MACG, 10 Homo sapiens cDNA clone IMAGE:220504.3 similar to gk.X17225.40S
8045	19107	32237	0.49	6.0E-49/AV151123.1	EST_HUMAN		complete (MOUSE); R60500.x1 NIH MACG, 10 Homo sapiens cDNA clone IMAGE:220504.3 similar to gk.X17225.40S
5701	19748	32849	0.69	6.0E-49/AL140742.1	EST_HUMAN		R60500.x1 NIH MACG, 10 Homo sapiens cDNA clone IMAGE:220504.3 similar to gk.X17225.40S
7615	26714	34649	0.50	6.0E-49/AV151123.1	EST_HUMAN		R60500.x1 NIH MACG, 10 Homo sapiens cDNA clone IMAGE:220504.3 similar to gk.X17225.40S
11725	24627	35107	4.38	6.0E-49/AV145218.1	EST_HUMAN		R60500.x1 NIH MACG, 10 Homo sapiens cDNA clone IMAGE:220504.3 similar to gk.X17225.40S
12088	24629	35433	3.13	6.0E-49/AA308595.1	EST_HUMAN		R60500.x1 NIH MACG, 10 Homo sapiens cDNA clone IMAGE:220504.3 similar to gk.X17225.40S
12695	25723	35434	3.13	6.0E-49/AA308595.1	EST_HUMAN		R60500.x1 NIH MACG, 10 Homo sapiens cDNA clone IMAGE:220504.3 similar to gk.X17225.40S
735	13763	28716	9.93	6.0E-49/AV077697.1	EST_HUMAN		R60500.x1 NIH MACG, 10 Homo sapiens cDNA clone IMAGE:220504.3 similar to gk.X17225.40S
735	13763	28716	9.93	6.0E-49/AV077697.1	EST_HUMAN		R60500.x1 NIH MACG, 10 Homo sapiens cDNA clone IMAGE:220504.3 similar to gk.X17225.40S
735	13763	28716	9.93	6.0E-49/AV077697.1	EST_HUMAN		R60500.x1 NIH MACG, 10 Homo sapiens cDNA clone IMAGE:220504.3 similar to gk.X17225.40S
735	13763	28716	9.93	6.0E-49/AV077697.1	EST_HUMAN		R60500.x1 NIH MACG, 10 Homo sapiens cDNA clone IMAGE:220504.3 similar to gk.X17225.40S
1817	14841	27618	6.22	6.0E-49/AA172121.1	EST_HUMAN		R60500.x1 NIH MACG, 10 Homo sapiens cDNA clone IMAGE:220504.3 similar to gk.X17225.40S

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Model Similar (Top) HI BLAST E Value	Top HI Accession No.	Top HI Database Source	Top HI Descriptor
2789	15788	28787	6.37	5.0E-49	U17744.1	NT	Homo sapiens putative tumor suppressor S119 (S119) mRNA, complete cds
3317	10394	28204	2.42	5.0E-49	11409335	NT	Homo sapiens similar to fibronectin protein 527 (nucleophosmin 1) (H. sapiens) (LOC35362). mRNA
548	13617	28524	28.86	4.0E-49	AW189693.1	EST_HUMAN	AB0801.AT NCI CGAP_UH Homo sapiens cDNA clone IMAGE:2075593 5' similar to NP-B03002.B
7618	20581	33843	0.89	4.0E-49	Z26934.2	NT	Homo sapiens cDNA clone IMAGE:2075593 5' similar to NP-B03002.B
7618	20581	33844	0.96	4.0E-49	Z26934.2	NT	Homo sapiens cDNA clone IMAGE:2075593 5' similar to NP-B03002.B
7648	20582	33979	0.84	4.0E-49	11529737	NT	Homo sapiens LDP-N-acetyl-alpha-D-galactosaminyl-polyoxylase N-acetyl-galactosaminyltransferase 8 (GALNAc-T8) (GALNT8). mRNA
7648	20582	33980	0.84	4.0E-49	11529737	NT	Homo sapiens LDP-N-acetyl-alpha-D-galactosaminyl-polyoxylase N-acetyl-galactosaminyltransferase 8 (GALNAc-T8) (GALNT8). mRNA
7658	20883	34135	0.48	4.0E-49	AB002342.2	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
8325	21200	34563	0.7	4.0E-49	7562200	NT	Homo sapiens KIAA0823 gene product (KIAA0823). mRNA
12555	25918		4.86	4.0E-49	AA210758.1	EST_HUMAN	z60063.AT NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:382977 5'
12849	25323		12.03	4.0E-49	AF240798.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
552	13820	26556	1.04	3.0E-49	X08928.1	NT	H. sapiens mRNA for acyl-CoA carboxylase
2886	19920		3.49	3.0E-49	AA016131.1	EST_HUMAN	z83106.AT Scores reflect N24HR Homo sapiens cDNA clone IMAGE:390584 5' similar to contains L1 L1 repetitive element;
8105	18102	30050	2.73	3.0E-49	U42590.1	NT	Human type IV collagen (COL4A9) gene, exon 40
7820	20749	34054	9.14	3.0E-49	H94478.1	EST_HUMAN	EST125712 VAMT1 Homo sapiens cDNA clone 25a12
11748	24649	38130	1.84	3.0E-49	AA337591.1	EST_HUMAN	EST125712 Endometrial tumor Homo sapiens cDNA 5' end
684	13746		2.4	2.0E-49	BE16990.1	EST_HUMAN	MR3-H10497-110200-113-gp1 H10497 Homo sapiens cDNA
9239	16317	29220	1.4	2.0E-49	N28446.1	EST_HUMAN	y22606.AT Scores reflect N28HR Homo sapiens cDNA clone IMAGE:382971 5'
3629	16035	29693	0.85	2.0E-49	AF102564.1	NT	Homo sapiens RNA binding protein 1 (RBM1) gene, complete cds
4024	17923	30787	0.71	2.0E-49	BF311846.1	EST_HUMAN	UHH-B4-4pc-202-DJ-1.1 NCI CGAP_Sual Homo sapiens cDNA clone IMAGE:388338 3'
7040	20068		1.16	2.0E-49	AV177898.1	EST_HUMAN	UHH-B4-4pc-202-DJ-1.1 NCI CGAP_Sual Homo sapiens cDNA clone IMAGE:388338 3'
8678	21609	33300	3.33	2.0E-49	MR003.1	EST_HUMAN	EST102598 Test brain, Sialagene (cal0932020) Homo sapiens cDNA clone IMAGE:388338 3'
12326	25501		1.83	2.0E-49	Y10766.1	NT	H. sapiens mRNA for CAP-binding protein complex interacting protein 1
7267	25911		2.85	2.0E-49	AF163864.1	NT	H. sapiens mRNA for CAP-binding protein complex interacting protein 1
504	13978		4.83	1.0E-49	BC05337.1	EST_HUMAN	UHH-B4-4pc-202-DJ-1.1 NCI CGAP_Sual Homo sapiens cDNA clone IMAGE:388338 3'
1576	14606	27665	13.36	1.0E-49	AB252116.1	NT	Homo sapiens Nucleosome assembly factor 1 (NAF1) gene, complete cds
1823	14846	27822	2.37	1.0E-49	RE252116.1	EST_HUMAN	UHH-B4-4pc-202-DJ-1.1 NCI CGAP_Sual Homo sapiens cDNA clone IMAGE:388338 3'
5544	18522	31488	5.89	1.0E-49	BF151007.1	EST_HUMAN	EST123038F1 NHI_MGC_88 Homo sapiens cDNA clone IMAGE:405055 5'

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Table 4
Probes Expressed in Adult Liver[illegible]

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expressed Signal	Most Similar (Top) HE BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
45360	17374	35237	0.71	2.0E-50	D82424.1	NT	Mus musculus mRNA for high-sulfur keratin protein, partial cds
71103	20153	35457	0.50	2.0E-50	U142005.1	EST_HUMAN	U142005 NT28M2 Homo sapiens cDNA clone NT87M201059 5'
8891	21821	35172	0.50	2.0E-50	AJ303810.2	EST	Human sapiens TFF gene cluster for Tef4 factor, complete cds
8891	21821	35173	0.50	2.0E-50	AJ303810.2	NT	Human sapiens TFF gene cluster for Tef4 factor, complete cds
9024	21821	35310	5.27	2.0E-50	Z00856.1	NT	Human HALPH444 gene for alpha-tubulin, exon 1-3
9024	21821	35311	5.27	2.0E-50	Z00856.1	NT	Human HALPH444 gene for alpha-tubulin, exon 1-3
10396	23245	36790	1.64	2.0E-50	9510293.1	NT	Mus musculus keratin complex 2, gene 6p (K02-5p), mRNA
10396	23245	36790	1.64	2.0E-50	9510293.1	NT	Mus musculus keratin complex 2, gene 6p (K02-5p), mRNA
12087	24628	36707	1.59	2.0E-50	AJ233861.1	NT	Mus musculus cyclophilin A mRNA, complete cds
484	13555	26471	1.52	1.0E-50	AJ163209.2	NT	Mus musculus chromosome 21 segment H627009
2388	15553	37351	13.03	1.0E-50	AJ277175.1	NT	Human sapiens Xq pseudautosomal region, segment 1/2
2388	15553	37351	13.03	1.0E-50	AJ277175.1	NT	Human sapiens Xq pseudautosomal region, segment 1/2
10396	23245	36708	1.07	1.0E-50	AJ277175.1	NT	Human sapiens RGH2 gene, retrovirus-like element
10396	23245	36708	1.07	1.0E-50	AJ277175.1	NT	Human sapiens RGH2 gene, retrovirus-like element
8150	21678	37008	1.34	1.0E-50	D11078.1	NT	Human sapiens cDNA clone IMAGE4841868 3' similar to
8150	21678	37008	1.34	1.0E-50	D11078.1	NT	Human sapiens cDNA clone IMAGE4841868 3' similar to
8212	12687	32418	1.16	6.0E-51	AY591225.1	EST_HUMAN	95B565 CAMP-RELATED GUANINE NUCLEOTIDE EXCHANGE FACTOR1L1 ;
6469	19574	32689	0.93	6.0E-51	AY744857.1	EST_HUMAN	95B565 CAMP-RELATED GUANINE NUCLEOTIDE EXCHANGE FACTOR1L1 ;
9230	22158	35512	0.65	6.0E-51	AY791154.1	EST_HUMAN	actg094.3 Streptococcus pyogenes cDNA clone IMAGE4841868 3' similar to
9230	22158	35512	0.65	6.0E-51	AY791154.1	EST_HUMAN	actg094.3 Streptococcus pyogenes cDNA clone IMAGE4841868 3' similar to
8894	22778	35108	1.19	6.0E-51	AJ4043758.1	EST_HUMAN	SWP58A.HUMAN Q40690 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
8894	22778	35108	1.19	6.0E-51	AJ4043758.1	EST_HUMAN	SWP58A.HUMAN Q40690 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
10032	22802	33318	0.9	6.0E-51	AY791154.1	EST_HUMAN	SWP58A.HUMAN Q40690 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
10032	22802	33318	0.9	6.0E-51	AY791154.1	EST_HUMAN	SWP58A.HUMAN Q40690 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
10032	22802	33319	0.6	6.0E-51	AY791154.1	EST_HUMAN	SWP58A.HUMAN Q40690 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
11007	23409	37418	2.0	6.0E-51	AJ003810.2	EST_HUMAN	SWP58A.HUMAN Q40690 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
11007	23409	37419	2.0	6.0E-51	AJ003810.2	EST_HUMAN	SWP58A.HUMAN Q40690 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
4545	17554	30115	2.48	9.0E-51	U13807.1	EST_HUMAN	w526967.1 Morion Fetus, Cossack Homo sapiens cDNA clone IMAGE238320 5'
4545	17554	30115	2.48	9.0E-51	U13807.1	EST_HUMAN	w526967.1 Morion Fetus, Cossack Homo sapiens cDNA clone IMAGE238320 5'
4545	17554	30418	2.48	9.0E-51	U13807.1	EST_HUMAN	Human sapiens glycine amidotransferase (L-arginine:glycine amidotransferase) (GATM) mRNA
4545	17554	30418	2.48	9.0E-51	U13807.1	EST_HUMAN	Human sapiens glycine amidotransferase (L-arginine:glycine amidotransferase) (GATM) mRNA
4894	17969	30555	1.85	8.0E-51	AJ610842.1	EST_HUMAN	nc90049.31 Human sapiens cDNA clone IMAGE4841868 3' similar to
4894	17969	30555	1.85	8.0E-51	AJ610842.1	EST_HUMAN	nc90049.31 Human sapiens cDNA clone IMAGE4841868 3' similar to
7584	20473	33701	0.49	8.0E-51	AF094294.1	NT	HEPETOGENOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUN) ;
8907	21013	34355	1.85	8.0E-51	U1343567.1	EST_HUMAN	HEPETOGENOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUN) ;
8907	21013	34355	1.85	8.0E-51	U1343567.1	EST_HUMAN	HEPETOGENOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUN) ;
8987	22814	35691	1.01	8.0E-51	AJ138500.1	EST_HUMAN	Human sapiens PDI2-7.3 protein (PDI2-73NT-CO-38), mRNA
8987	22814	35691	1.01	8.0E-51	AJ138500.1	EST_HUMAN	Human sapiens PDI2-7.3 protein (PDI2-73NT-C

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3326	16372	29273	1.53	7.0E-51	AY186219.1	EST_HUMAN	Q144110926.204900-186-405 NT0926 Homo sapiens cDNA
3416	19460	20366	0.96	7.0E-51	AY274720.1	EST_HUMAN	Q144110926.204900-186-405 NT0926 Homo sapiens cDNA
4254	17260	30146	1.96	7.0E-51	AF076826.1	EST_HUMAN	Q144110926.204900-186-405 NT0926 Homo sapiens cDNA
4336	17372	30336	2.16	7.0E-51	AF076826.1	EST_HUMAN	Q144110926.204900-186-405 NT0926 Homo sapiens cDNA
4481	17472	30526	1.22	7.0E-51	AY256603.1	EST_HUMAN	Q144110926.204900-186-405 NT0926 Homo sapiens cDNA
1550	14581	27541	0.92	6.0E-51	AF076826.1	EST_HUMAN	Q144110926.204900-186-405 NT0926 Homo sapiens cDNA
1965	15013	28003	5.46	6.0E-51	7657296	NT	Homo sapiens KIAA0926 protein Mec2 interacting nuclear target (MINT) homolog (KIAA0926), mRNA
3353	16571	26475	15.72	6.0E-51	7657296	NT	Homo sapiens KIAA0926 protein Mec2 interacting nuclear target (MINT) homolog (KIAA0926), mRNA
4413	17424	30285	1.06	6.0E-51	6970553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
4413	17424	30289	1.06	6.0E-51	6970553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
6222	10271	32431	122.6	6.0E-51	X01788.1	NT	Human haaptoglobin related (Hpr) gene exon 3
6223	10287	32445	9.71	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKKK1) gene, exon 4
6233	10287	32448	9.71	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKKK1) gene, exon 4
7036	20272	33626	1.03	6.0E-51	4506736	NT	Homo sapiens fibronectin protein 56 kDa, 70KD, polypeptide 1 (F56K61), mRNA
7219	19470	31292	1.82	6.0E-51	11416751	NT	Homo sapiens non-kinase Cdc42 effector protein BPC2 (LOC55990), mRNA
8400	22013	35676	0.73	6.0E-51	11420985	NT	Homo sapiens central cell adhesion molecule (LOC51148), mRNA
8650	22039	35678	0.73	6.0E-51	11420985	NT	Homo sapiens central cell adhesion molecule (LOC51148), mRNA
10238	20069	36168	1.85	6.0E-51	7661836	NT	Homo sapiens hypocalcemic protein FLJ11042 (FLJ11042), mRNA
10252	22172	36594	0.78	6.0E-51	UE0063.1	NT	Homo sapiens hypocalcemic protein FLJ11042 (FLJ11042), mRNA
11703	24605	38080	1.67	6.0E-51	11823269	NT	Homo sapiens ankyrin (ANK1) gene, exon 2
11980	24903	38501	1.4	6.0E-51	5463949	NT	Homo sapiens ankyrin (ANK1) gene, exon 2
11980	24903	38502	1.4	6.0E-51	5463949	NT	Homo sapiens ankyrin (ANK1) gene, exon 2
816	13673	26810	7.71	5.0E-51	AL162032.2	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (P50), alpha isoform (PPP2R5A), mRNA
828	13684	26822	1.86	5.0E-51	4507500	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (P50), alpha isoform (PPP2R5A), mRNA
1018	13650	27010	1.06	5.0E-51	AL13204.1	NT	Homo sapiens 1 cell lymphoma protein and metastasis 1 (TAM1), mRNA
1030	14460	27023	1.06	5.0E-51	5031983	NT	Homo sapiens 1 cell lymphoma protein and metastasis 1 (TAM1), mRNA
2634	15532	28626	1.151	5.0E-51	AJ307555.1	NT	Homo sapiens 26S ribosomal protein L15 homolog (F0H1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Max Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1681	14711	27674	2.22	8.0E-52	11598028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
4080	14711	27673	8.4	8.0E-52	11598028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
4080	14711	27674	8.4	8.0E-52	11598028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
7940	20682	34170	1.36	8.0E-52	11416855	NT	Homo sapiens transforming growth factor beta-induced, 58D (TGFB3), mRNA
7940	20682	34171	1.36	8.0E-52	11416855	NT	Homo sapiens transforming growth factor beta-induced, 58D (TGFB3), mRNA
9386	22492	38564	1.01	7.0E-52	U65471.1	EST_HUMAN	transcript 1, Sarcos, postnatal-2d, Juncos, NHAPA Homo sapiens cDNA, clone IMAGE:326576 5' similar to
1216	14283		0.92	6.0E-52	U65471.1	EST_HUMAN	transcript 1, Sarcos, postnatal-2d, Juncos, NHAPA Homo sapiens cDNA, clone IMAGE:326576 5' similar to
1720	14748	27716	6.03	6.0E-52	AF408907.1	NT	OV18-17083/271229-049-437 BT0837 Homo sapiens cDNA
5929	18048	37116	2.45	6.0E-52	AF408907.1	EST_HUMAN	Homo sapiens, S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
11657	24693	39036	1.97	6.0E-52	BE048172.1	EST_HUMAN	124904.1 NCL_GCAP_Bm52 Homo sapiens cDNA clone IMAGE:183047.3
1859	14719	27680	1.1	4.0E-52	AF267316.1	NT	124904.1 NCL_GCAP_Bm52 Homo sapiens cDNA clone IMAGE:226167.1 5' similar to
1611	14836	27687	1.09	4.0E-52	4758943	NT	SW_FGBM_MOUSE_D06783 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE
4001	17028	20017	0.95	4.0E-52	4007500	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
4883	17855	30720	0.86	4.0E-52	AI796814.1	EST_HUMAN	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TAM1) mRNA
5409	16590	31392	1.26	4.0E-52	4506132	NT	wilms02.ct NCL_GCAP_Rd12 Homo sapiens cDNA clone IMAGE:2400459.3
8618	21547	34686	2.19	4.0E-52	BF027032.1	EST_HUMAN	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
9008	22027	36383	3.77	4.0E-52	AB022089.1	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
12485	25228		8.17	4.0E-52	AI118177	EST_HUMAN	00144069P1 NH_MGC_72 Homo sapiens cDNA, clone IMAGE:3916638 5'
4151	17201		13.74	3.0E-52	11470942	NT	Homo sapiens hydroxymethyl (17-beta) dehydrogenase 4 (HSD17B4), mRNA
594	13682	26557	1.34	2.0E-52	MI0976.1	NT	Homo sapiens DNA for Human P25M, complete cds
594	13612	26158	1.34	2.0E-52	MI0976.1	NT	Homo sapiens hypothetical protein FLJ10075 (FLJ10075), mRNA
2027	19044	28039	1.17	2.0E-52	AI030075.1	NT	Human endogenous retrovirus DNA (4-1), complete retroviral segment
2622	16523	26527	1.47	2.0E-52	BE207575.1	EST_HUMAN	Human endogenous retrovirus DNA (4-1), complete retroviral segment
2785	15776		11.94	2.0E-52	BF077892.1	EST_HUMAN	Homo sapiens mRNA for KIAA1249 protein, partial cds
							1248507.1 NH_MGC_9 Homo sapiens cDNA clone IMAGE:3056421 5' similar to gp.X19463 Mus musculus
							mRNA for Zfp-1 zinc finger protein (MGCUSE),
							002004710P1 NH_MGC_33 Homo sapiens cDNA clone IMAGE:3248897.5

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6008	19005	30942	4.83	2.0E-52	AL137168.3	NT	Novel human gene mapping to chromosome 20, similar to members of the
6138	19133	30975	1.83	2.0E-52	A141492.1	EST_HUMAN	q16505.51 Scores: N141492.1 ST Homo sapiens cDNA clone IMAGE:16505.51
6138	19133	30976	1.83	2.0E-52	A141492.1	EST_HUMAN	q16505.51 Scores: N141492.1 ST Homo sapiens cDNA clone IMAGE:16505.51
6502	18971	32089	1.33	2.0E-52	AY184604.1	EST_HUMAN	LC-C10244-20720-053-E12 C10244-20720-053 cDNA
6627	19007	32852	1.71	2.0E-52	U1141938	NT	Homo sapiens mRNA for KIAA1081, transcript variant 1
7011	20038	33271	0.95	2.0E-52	AB22804.1	NT	Homo sapiens cDNA clone IMAGE:165831.5
7273	20228	33474	0.78	2.0E-52	A19243.1	EST_HUMAN	U94812.93 NC1 CGAP_E22 Homo sapiens cDNA clone IMAGE:165831.5
8339	21244	34577	0.84	2.0E-52	U632188	NT	Homo sapiens cDNA clone IMAGE:165831.5
8339	21244	34578	0.84	2.0E-52	U632188	NT	Homo sapiens cDNA clone IMAGE:165831.5
8212	22140	34579	0.84	2.0E-52	A141398.1	NT	Homo sapiens cDNA clone IMAGE:165831.5
8471	22419	35781	0.92	2.0E-52	A1377398.1	EST_HUMAN	Human adult brain/blood mRNA, complete cds
10010	27820		1.38	2.0E-52	47820709	NT	Homo sapiens MADH dehydrogenase (ubiquinol) FcS protein 5 (16D) (NADH-coenzyme Q reductase)
10816	23602	38925	5.77	2.0E-52	6750038	NT	Human P-53 protein
10816	23602	38926	5.77	2.0E-52	6750038	NT	Human P-53 protein
11653	24589	38029	3.32	2.0E-52	A1831482.1	EST_HUMAN	THR repetitive element
11653	24599	38930	3.32	2.0E-52	A1831482.1	EST_HUMAN	THR repetitive element
11684	24670	39048	3.19	2.0E-52	A171837.1	EST_HUMAN	AV171837 DCB Homo sapiens cDNA clone DDBA E03 5'
11701	24713		1.44	2.0E-52	U70260.1	EST_HUMAN	z18g12.11 Scores: Jcat_18g12.11 Homo sapiens cDNA clone IMAGE:344038 5'
12043	24694		2.92	2.0E-52	U1147690	NT	Homo sapiens LIM domain kinase 2 (LUK2), mRNA
12317	26592	31359	14.39	2.0E-52	AW280297.1	EST_HUMAN	nt72657.1 NC1 CGAP_OAL1 Homo sapiens cDNA clone IMAGE:2700036 3' similar to contains Alu repetitive element/contains element LTR2 repetitive element
12894	29343		5.81	2.0E-52	A180898.1	EST_HUMAN	w16705.1 Scores: N141492.1 ST Homo sapiens cDNA clone IMAGE:2700036 3' similar to contains Alu repetitive element/contains element LTR2 repetitive element
659	13625	29534	1.82	1.0E-52	A1834446.1	EST_HUMAN	C16950 CARBOXYPESTERASE
1398	14439	27383	6.3	1.0E-52	4604028	NT	z176112.1 Scores: Jcat_176112.1 Homo sapiens cDNA clone IMAGE:2700036 3' similar to contains Alu repetitive element/contains element LTR2 repetitive element
2954	15903		2.01	1.0E-52	4602238	NT	Homo sapiens (glutathione-S-transferase) (GSTA), transcript variant 1, mRNA
3107	16188	29058	1.42	1.0E-52	SC1070.1	NT	pad-reverse transcriptase homolog (retroviral) (human, oncogenous retroviral element RTV-Hp1, Genbank, ccd nt)
5516	18959	31443	4.48	1.0E-52	U39426.1	NT	Human P-glycoprotein (MDR3) gene, exon 4
6897	19659	32892	2.18	1.0E-52	U39894.1	NT	Human P-glycoprotein (MDR3) gene, complete cds
7834	20782	34085	2.57	1.0E-52	X07292.1	NT	Human P-glycoprotein (MDR3) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8334	21288	34520	0.45	1.0E-52	U60071.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
9034	21063		1.2	1.0E-42	AL163277.2	NT	Homo sapiens chromosome 21 segment HS21C027
8730	22696	39038	1.05	1.0E-52	AF078779.1	NT	Human neurospiral protein for repeat on olivary mRNA, complete cds
11049	29353		0.95	1.0E-52	AY023701.1	EST_HUMAN	cdgag5y11 Marfan Fc11 Collagen Fc11 Homo sapiens chromosome 21 segment HS21C082
11059	29543		1.24	1.0E-52	AL163262.2	NT	Homo sapiens chromosome 21 segment HS21C082
11204	24130	37578	1.87	1.0E-52	U62562.1	NT	Homo sapiens protein growth factor 1 (pgf1) gene, complete cds
3565	16955	28739	0.82	9.0E-53	U500448.1	NT	Homo sapiens cAMP-dependent protein kinase regulatory subunit II, beta (PRKAR2B) mRNA
4469	17529	32975	1.35	9.0E-53	U500448.1	NT	Homo sapiens cAMP-dependent protein kinase regulatory subunit II, beta (PRKAR2B) mRNA
12532	22526		3.76	7.0E-53	BF22563.1	EST_HUMAN	60180471F1F1 NH MG-43 Homo sapiens cDNA clone IMAGE:433769.5
12626	25942		6.93	7.0E-53	AA421762.1	EST_HUMAN	644807.1 NCI C636 Fmoc3 Homo sapiens cDNA clone IMAGE:206077.9 similar to contains THR.H
4159	12159	32075	1.74	5.0E-53	AF078779.1	NT	THP regulatory domain
12579	26278		2.56	5.0E-53	AW183663.1	EST_HUMAN	Homo sapiens histoneproteins nuclear ribonucleoprotein C (C1123) (HNRPCL) mRNA
52	13159	26016	1.36	4.0E-53	AL163263.2	NT	RG3-370187-18109-011-q10 ST0197 Homo sapiens cDNA
52	13159	26017	1.39	4.0E-53	AL163263.2	NT	Homo sapiens chromosome 21 segment HS21C085
9940	22655		0.99	4.0E-53	AF013037.1	EST_HUMAN	N06104.1 NCI C636 Fmoc3 Homo sapiens cDNA clone IMAGE:277837.3
10276	23149		0.6	4.0E-53	FC3063.1	EST_HUMAN	HS21C0841 normalized infant brain cDNA Homo sapiens cDNA clone c-31084
11592	24598	38642	2.92	4.0E-53	BF128701.1	EST_HUMAN	601810599F1 NH MG-43 Homo sapiens cDNA clone IMAGE:405897.5
11602	24568	38643	2.92	4.0E-53	BF128701.1	EST_HUMAN	601810599F1 NH MG-43 Homo sapiens cDNA clone IMAGE:405897.5
2706	15703	25686	2.4	3.0E-53	AB203686.1	NT	Homo sapiens DNA DLEC1 to ORC1L4 gene region, section 12 (DLEC1, ORC1L4 genes, complete cds)
3794	16925	25712	1.06	3.0E-53	AY003636.1	EST_HUMAN	wc2207.1 X1 Sources: Dackiwaffe, colon, NHCO Homo sapiens cDNA clone IMAGE:285876.9
5510	19359	31665	1.08	3.0E-53	AF-021212.1	NT	Homo sapiens 20S proteasome subunit 9 mRNA, complete cds
5520	19802	32005	1.19	3.0E-53	11520297	NT	Homo sapiens MIL1 protein (MIL1), mRNA
8405	19462	32957	0.8	3.0E-53	BC169026.1	NT	QY-H110412-203030-123-c04 HTD412 Homo sapiens cDNA
7437	20357	33069	0.85	3.0E-53	Y10368.3	NT	H sapiens uraf gene
7437	20357	33070	0.89	3.0E-53	Y10368.3	NT	H sapiens uraf gene
8579	21619	35162	11.57	3.0E-53	S72043.1	NT	GIF growth inhibitory factor [human, brain, Genomic, 2015 nt]
9418	22645	35710	0.64	3.0E-53	10330092	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
8009	22635		10.83	3.0E-53	5001933	NT	Homo sapiens FGFRT oncogene partner (FOP), mRNA
12836	25406	31792	4.13	3.0E-53	11417998	NT	Homo sapiens SEC14 (S. coronavirus-like 2) (SEC14.2), mRNA
480	13651		5.6	2.0E-53	AA386556.1	EST_HUMAN	EST177625 Pancreas tumor III Homo sapiens cDNA 6 end

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2220	16230	25235	6.73	7.0E-54	N27177.1	EST_HUMAN	yw98012.1l Scores: placenta, B6H2w62a... 2h0UP-868W Homo sapiens cDNA clone IMAGE:257988 3' similar to contains LTR/58 LTR negative element.
10027	25513	95945	2.88	7.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (N. sapiens) (LOC25182), mRNA
11726	24698		3.8	7.0E-54	A100789.1	EST_HUMAN	q657602.1 Scores: fetal, heart, N2H110W Homo sapiens cDNA clone IMAGE:170524 5' similar to contains ORF11 ORF repetitive element.
12203	26038	38546	1.44	7.0E-54	AF111672.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfo gene, complete cds; and unknown gene
12203	26038	38541	1.44	7.0E-54	AF111672.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfo gene, complete cds; and unknown gene
24	13140	26038	1.73	6.0E-54	AB030813.3	NT	Homo sapiens DNA for MICE, exon 4, 5 and partial cds
405	13519	25440	1.04	6.0E-54	8022148	NT	Homo sapiens hypothetical protein DKFZp434M235 DKFZp434M235, mRNA
405	13519	25440	1.04	6.0E-54	8022148	NT	Homo sapiens hypothetical protein DKFZp434M235 DKFZp434M235, mRNA
5335	18373	20374	1.32	6.0E-54	8022148	NT	Homo sapiens hypothetical protein DKFZp434M235 DKFZp434M235, mRNA
5335	18373	20374	1.32	6.0E-54	8022148	NT	Homo sapiens hypothetical protein DKFZp434M235 DKFZp434M235, mRNA
3027	18373	20374	0.94	6.0E-54	AL183247.2	NT	Homo sapiens chromosome 21 segment H82TC047
3027	18373	20374	0.94	6.0E-54	AL183247.2	NT	Homo sapiens chromosome 21 segment H82TC047
3027	17115	20693	3.11	6.0E-54	4602872	NT	Homo sapiens chloride channel 5 (CLCN5) mRNA
4572	17681	30443	1.05	6.0E-54	AV754760.1	EST_HUMAN	AV754760 TP Homo sapiens cDNA clone TPQAC10 5'
4893	17692	30759	0.97	6.0E-54	AV724885.1	EST_HUMAN	AV724885 HTB Homo sapiens cDNA clone HTBACE52 5'
6121	17690		1.66	6.0E-54	Y09346.1	NT	H. sapiens also pseudogene, p26 isoform
6903	16339		1.24	6.0E-54	AL163262.2	NT	Homo sapiens chromosome 21 segment H82TC082
2105	15177	28163	1.2	5.0E-54	F01623	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
194	13222		47.94	4.0E-54	AF110103.1	NT	Tupakia balagant beta-actin mRNA, partial cds
502	14033	26976	46.51	4.0E-54	AA308764.1	EST_HUMAN	EST T177696 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
1827	14850	27827	2.37	4.0E-54	D38521.1	NT	Human mRNA for OAM0077 gene, partial cds
1827	14850	27827	2.37	4.0E-54	D38521.1	NT	Human mRNA for OAM0077 gene, partial cds
1827	14850	27829	2.37	4.0E-54	D38521.1	NT	Human mRNA for OAM0077 gene, partial cds
3248	16295		2.63	4.0E-54	AB163069.1	EST_HUMAN	w620311.1 Scores: NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:233209 3' similar to TRO02711
7095	20075		0.93	4.0E-54	BF554899.1	EST_HUMAN	O07711 PHO-POLYMERASE POLYMERASE
905	13305	29121	8.99	3.0E-54	AA313487.1	EST_HUMAN	B0107004F1 NH1 MGC, 12 Homo sapiens cDNA clone IMAGE:546107 5'
1593	14624		0.97	3.0E-54	AA161547.1	EST_HUMAN	EST1165717 Colon carcinoma (HCO) cell line Homo sapiens cDNA 5' end
2004	16602	28696	1.4	3.0E-54	AL110398.1	EST_HUMAN	h07908.1X1 NO1 CGAP, G00 Homo sapiens cDNA clone IMAGE:2810342 3'
2070	16602		1.49	3.0E-54	AL110398.1	EST_HUMAN	DKFZp404E0731.1 (1.434 (genom. files)) Homo sapiens cDNA clone DKFZp404E0731 5'
2670	16602		1.49	3.0E-54	AA06757.1	EST_HUMAN	IL-81185-100894-007 B1180 Homo sapiens cDNA
5122	19181	32316	1.4	3.0E-54	4902654	NT	Homo sapiens BDNF non-receptor tyrosine kinase (BNA) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7786	20715	34017	1.44	3.0E-54	AJ344059.1	EST_HUMAN	ad2208.1 Scars, parathyroid, liver, N18P1 Homo sapiens cDNA clone IMAGE:138270.3
7786	20715	34018	1.44	3.0E-54	AJ344061.1	EST_HUMAN	ad2209.1 Scars, parathyroid, liver, N18P1 Homo sapiens cDNA clone IMAGE:138270.3
8290	21165	34523	0.41	3.0E-54	AJ42222.1	EST_HUMAN	tg4001.L1 Scars, NSF, F3_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:235763.3
11454	24578		1.59	3.0E-54	U01454	NT	homo sapiens cDNA clone IMAGE:4156121.5
11527	24597	37865	4.38	3.0E-54	BF34560.1	EST_HUMAN	homo sapiens cDNA clone IMAGE:4156121.5
11607	24728	38220	2.78	3.0E-54	AA320382.1	EST_HUMAN	homo sapiens cDNA clone IMAGE:277777.5 similar to TR.G161315
11607	24728	38221	2.78	3.0E-54	AA320383.1	EST_HUMAN	homo sapiens cDNA clone IMAGE:277777.5 similar to TR.G161315
12406	26172	31978	2.17	3.0E-54	AW194589.1	EST_HUMAN	EST396529 MAGE measure, MAGEC Homo sapiens cDNA
12406	26222	32041	2.64	3.0E-54	AW178605.1	EST_HUMAN	RC1-370312-1159-011-409 B10313 Homo sapiens cDNA
695	13727	26337	21.60	2.0E-54	0031900	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRL3), mRNA
1392	14426	27377	1.23	2.0E-54	4607164	NT	Homo sapiens nuclear anion, Sp103 (SP103) mRNA
1598	14600	27559	1.14	2.0E-54	AA465008.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:1204600 similar to contains element L1 repetitive element;
2509	15507	28507	1.04	2.0E-54	AW163175.1	EST_HUMAN	ad2203.Y1 Schwann cell brain 00004 Homo sapiens cDNA clone IMAGE:2783764.5 similar to
2842	15638	28637	3.84	2.0E-54	AL163210.2	NT	SW-G03.1, HUMAN Q13916 CULLIN HOMOLOG 1;
2337	15690	28802	1.86	2.0E-54	AW057524.1	EST_HUMAN	Homo sapiens chromosome 21, segment H82/C010
3907	16544		1.79	2.0E-54	AA032925.1	EST_HUMAN	WY0012.1 Scars, NSF, F3_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2652627.5 similar to
4300	17374		1.6	2.0E-54	4502042	NT	TR-06284-06284 PHOSPHOLIPASE C NEIGHBORING
4580	17659		1.6	2.0E-54	AF208191.1	NT	homo sapiens cDNA clone IMAGE:995488 similar to gb:XS3777.60S
5692	18786	31644	7.2	2.0E-54	4750099	NT	RIBOSOMAL PROTEIN L23 (HUMAN);
5767	18808	31676	1.22	2.0E-54	BE04784.1	EST_HUMAN	Homo sapiens cytochrome precursor, mRNA, complete cds
5970	19036	32157	3.72	2.0E-54	11426857	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 14 (SCYA14) mRNA
6078	19137	32271	15.01	2.0E-54	AD048911.1	NT	homo sapiens KLOA0700 gene product (KLOA0700), mRNA
6078	19137	32272	15.01	2.0E-54	AD048911.1	NT	Homo sapiens KLOA0700 gene product (KLOA0700), mRNA
6951	19860	33234	0.78	2.0E-54	AF008915.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
7122	20326	33560	0.67	2.0E-54	AD022121.1	NT	Homo sapiens EY3 homolog mRNA, complete cds
7122	20326	33561	0.67	2.0E-54	AD022121.1	NT	Homo sapiens EY3 homolog mRNA, complete cds
7483	20423	33703	9.24	2.0E-54	11426544	NT	Homo sapiens recombination 1 (recombination), partial cds
10155	25046	36445	3.99	2.0E-54	AB001028.1	NT	Homo sapiens mRNA for brain phospholipase, complete cds
10514	25401	36812	1.18	2.0E-54	11426127	NT	Homo sapiens alpha class 2 (g protein gamma binding) (UGK2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top HitAccession No.	Top Hit Database Source	Top Hit Descriptor
10621	23907	398-11	0.89	2.0E-54	11416762	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
10621	23907	398-11	0.89	2.0E-54	11416762	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
12143	19680	332-04	1.41	2.0E-54	AF00819.1	NT	Homo sapiens ET19 (h-mc3) mRNA, complete cds
12148	21088	332-04	2.35	2.0E-54	703/484	NT	Homo sapiens p53 (p53) mRNA, complete cds
12698	25469	31761	1.91	2.0E-54	8507387	NT	Human PIP5K3 (PIP5K3) mRNA
4877	17695		1.48	1.0E-54	3F515418.1	EST_HUMAN	BC1092267 (h) MGC_19 Homo sapiens cDNA clone IMAGE:4126335
13021	25554		2.98	1.0E-54	AI077641.1	EST_HUMAN	AI077641, Sperm cDNA, human Homo sapiens cDNA clone Z163850 similar to 5'-end region of Human
13045	27371	37154	1.03	8.0E-55	AF030198.1	EST_HUMAN	Homo sapiens RING finger protein 30 (RNF30) mRNA, 5' end
13432	14375		2.77	8.0E-55	AF030198.1	EST_HUMAN	Homo sapiens RNF30 gene for RING finger protein
1346	14378		2.3	8.0E-55	AF030198.1	EST_HUMAN	Homo sapiens RNF30 gene for RING finger protein
11541	24547		1.85	8.0E-55	AW409744.1	EST_HUMAN	h0202-c1 Sraes, NTL_1, G8C_1 Homo sapiens cDNA clone IMAGE:2550907.5
9552	22920		0.81	7.0E-55	AW109339.1	EST_HUMAN	h0202-c1 Sraes, NTL_1, G8C_1 Homo sapiens cDNA clone IMAGE:2550907.5
9724	22949	9831-1	1.55	7.0E-55	AA85681.1	EST_HUMAN	Q93965 POS39554.1...
9768	22949	9836-5	1.74	7.0E-55	AI013806.1	EST_HUMAN	ai32811.1 Sraes, Indis, NHT Homo sapiens cDNA clone IMAGE:1407200.3
11698	24004	9831-5	10.35	7.0E-55	AI013806.1	EST_HUMAN	AI0138069 PLAC1 Homo sapiens cDNA clone PLACE1011576.9
11698	24004	9831-5	10.35	7.0E-55	AI013806.1	EST_HUMAN	ai32811.1 NCI CGAP_UH Homo sapiens cDNA clone IMAGE:2210249.3
11708	24594	38037	1.05	7.0E-55	AB510561.1	EST_HUMAN	ai32811.1 NCI CGAP_UH Homo sapiens cDNA clone IMAGE:2210249.3
12740	25732	31669	1.92	7.0E-55	BE370068.1	EST_HUMAN	7637071.1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284640.3
12009	25658		5.95	7.0E-55	H23359.1	EST_HUMAN	ym67907.1 Sraes infant brain (NB) Homo sapiens cDNA clone IMAGE:52444.5
11946	24790	35263	1.84	0.0E-55	AB040924.1	NT	Homo sapiens mRNA for KIAA1801 protein, partial cds
11946	24790	35263	1.84	0.0E-55	AB040924.1	NT	Homo sapiens mRNA for KIAA1801 protein, partial cds
1705	14821	27769	1.49	0.0E-55	AA701971.1	EST_HUMAN	256509.41 Sraes, fetal_liver_spleen, NHTLS, S1 Homo sapiens cDNA clone IMAGE:462617.3
1705	14821	27769	1.49	0.0E-55	AA701971.1	EST_HUMAN	256509.41 Sraes, fetal_liver_spleen, NHTLS, S1 Homo sapiens cDNA clone IMAGE:462617.3
4884	17693	30749	0.35	5.0E-55	AW26821.1	EST_HUMAN	UHHB-vf19y-09-LU1 NC_004362 Homo sapiens cDNA clone IMAGE:2725956.3
6519	19652	33214	1.32	6.0E-55	4606952	NT	Homo sapiens p53 (p53) mRNA, complete cds
6519	19652	33214	1.32	6.0E-55	4606952	NT	Homo sapiens p53 (p53) mRNA, complete cds
6991	26059	33215	1.82	6.0E-55	4606952	NT	Homo sapiens p53 (p53) mRNA, complete cds
6991	26059	33215	1.82	6.0E-55	4606952	NT	Homo sapiens p53 (p53) mRNA, complete cds
7348	21381	33050	0.91	6.0E-55	11434422	NT	Homo sapiens p53 (p53) mRNA, complete cds
7675	20009	33050	0.88	6.0E-55	11434422	NT	Homo sapiens p53 (p53) mRNA, complete cds
9596	22627	35866	2.83	5.0E-55	AB030498.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA), mRNA
9689	27774		1.69	6.0E-55	BC030498.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA), mRNA
10540	29426	98844	1.74	5.0E-55	AB014511.1	NT	BC1_010510:10500-016410 BT0310 Homo sapiens cDNA
10540	29426	98844	1.74	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0911 protein, partial cds
10540	29426	98844	1.85	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0911 protein, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	Q95 SEQ ID NO.	Expression Signal	Max Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10718	23904	37033	1.26	5.0E-56	5453795	NT	Homo sapiens rat (Rattus norvegicus) class 2 (HEL2), mRNA
12470	26223		3.46	5.0E-56	11417972	NT	Homo sapiens peroxisomal (peroxisomal) homolog 1, containing BLOC1 domain (PES1), mRNA
58	15065	26076	1.22	4.0E-56	AW957594.1	EST_HUMAN	EST170041 IMAGE resources, IMAGE Homo sapiens cDNA
605	13765	26672	37.86	4.0E-55	4855973	NT	Homo sapiens RNA binding motif protein 1, chromosome 1 family 1, member A1 (RBMY1A1), mRNA
14395	14995		1.06	4.0E-55	BF061411.1	EST_HUMAN	7526 (G3) Source: JRGF_P3_UOJ_P3_1 Homo sapiens cDNA clone IMAGE:5360443 3' similar to contig L118.1 repetitive element 1
2038	15065	26054	1.13	4.0E-56	4326180	NT	Homo sapiens proteasome (prosome, multicatalytic) subunit, alpha class 2 (PSMA2), mRNA
2038	15065	26053	1.13	4.0E-56	4326180	NT	Homo sapiens proteasome (prosome, multicatalytic) subunit, alpha class 2 (PSMA2), mRNA
2038	19112	26115	0.85	4.0E-56	4333314	NT	Homo sapiens deoxyribonuclease, nuclear (DNase I) (DNKG), mRNA
2038	19112	26116	0.85	4.0E-56	4333314	NT	Homo sapiens deoxyribonuclease, nuclear (DNase I) (DNKG), mRNA
2331	15339	25544	2.28	4.0E-55	4637791	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1), mRNA
2331	15337		1.38	4.0E-55	AA271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
2918	21546		1.14	4.0E-55	AF071852.1	NT	Homo sapiens chromosome 21 segment HS21C010
11978	21952		2.16	4.0E-55	U72818.2	EST_HUMAN	4355 Human telomeric cDNA randomly primed subclone 7 Homo sapiens cDNA
12407	25178		5.09	4.0E-55	BF030944.1	EST_HUMAN	801886752 NF1/MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5'
12407	25178		5.09	4.0E-55	BF030944.1	EST_HUMAN	801886752 NF1/MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5'
12407	25178	33129	0.79	3.0E-55	AA071581.1	EST_HUMAN	7890A09 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7890A09
13033	26143		2.13	3.0E-55	BE175191.1	EST_HUMAN	PM1-H10933-003000-001-008 H10933 Homo sapiens cDNA
13035	26073		5.4	3.0E-55	AL132542.1	NT	Homo sapiens chromosome 21 segment HS21C064
308	13469	26406	1.76	2.0E-55	X67147.1	NT	Human endogenous retrovirus pHE1 (ERV9)
673	13941		1.00	2.0E-55	U10076.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
672	13734	26040	2.14	2.0E-55	4607206	NT	Homo sapiens synuclein-binding protein 1 (STX2BP1), mRNA, and translated products
2598	10051	25955	0.86	2.0E-55	4507708	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angiogenin syndrome) (UBE3A), mRNA
6698	17657	30752	1.71	2.0E-55	BE170983.1	EST_HUMAN	CM1-H10576-159500-357-p03 H10576 Homo sapiens cDNA
7620	26000	34164	0.76	2.0E-55	AF150198.1	EST_HUMAN	UHP-BN0-445-7-05-0-UT1 NH/MGC_50 Homo sapiens cDNA clone IMAGE:3078275 5'
6517	22643	35913	0.82	2.0E-55	BF224482.1	EST_HUMAN	HF7603-11 NCI COGAP_P0471 Homo sapiens cDNA clone IMAGE:3134483 3'
6517	22643	35914	0.82	2.0E-55	BF224482.1	EST_HUMAN	HF7603-11 NCI COGAP_P0471 Homo sapiens cDNA clone IMAGE:3134483 3'
6517	22643	35914	0.82	2.0E-55	BF224482.1	EST_HUMAN	HF7603-11 NCI COGAP_P0471 Homo sapiens cDNA clone IMAGE:3134483 3'
9703	27628		5.6	2.0E-55	AA02365.1	EST_HUMAN	en6905.01 Staphylococcus aureus S11 Homo sapiens cDNA, clone IMAGE:1981186 3' similar to contains THR3.2 THR repetitive element 1
6783	22707		0.71	2.0E-55	BC307939.1	EST_HUMAN	QVC-BN147-259400-215-p06 BN0147 Homo sapiens cDNA
11386	24305	37752	1.71	2.0E-55	AF118941.1	EST_HUMAN	AUT118941 HEMBA1 Homo sapiens cDNA clone HEMBA1005933 5'
90	13212	26124	1.26	1.0E-55	4605000	NT	Homo sapiens inositol-3-phosphate receptor (cation dependent) (VSP-R), mRNA
202	13901	25219	29.8	1.0E-55	U06823.1	NT	Oryzias latipes carotid New Zealand white elongation factor 1 alpha (Rube1a2), complete cds

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590	19093	26665	0.96	1.0E-56	AB02718.1	EST_HUMAN	0x5590.4 Soares, testis, NBT Homo sapiens cDNA clone IMAGE:164410 3'
1177	14217	27166	3.76	1.0E-56	AB020719.1	NT	Homo sapiens mRNA for VMAO3 protein, partial cds
1905	14683	27665	2.32	1.0E-56	BE27766.1	EST_HUMAN	0112317181 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2691037 5'
1905	14683	27667	2.32	1.0E-56	BE27766.1	EST_HUMAN	0112317181 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2691037 5'
2347	19396		7.77	1.0E-56	AF030860.1	NT	Homo sapiens mRNA for GNAO1 protein, partial cds
2591	19398	28372	1.04	1.0E-56	AF030860.1	NT	Homo sapiens mRNA for GNAO1 protein, partial cds
2543	19543	28541	28.28	1.0E-56	K01111.1	NT	Homo sapiens mRNA for GNAO1 protein, partial cds
2538	19398	28630	5.22	1.0E-56	AB007663.2	NT	Homo sapiens mRNA for GNAO1 protein, partial cds
2538	19398	28531	5.22	1.0E-56	AB007663.2	NT	Homo sapiens mRNA for GNAO1 protein, partial cds
2034	19549	29018	2.38	1.0E-56	AF030860.1	NT	Homo sapiens mRNA for GNAO1 protein, partial cds
3409	19398	29110	1.38	1.0E-56	V739139.1	EST_HUMAN	43x3 Human retina cDNA, randomly primed sublibrary Homo sapiens cDNA
3542	19575	29573	1.38	1.0E-56	AF133267.2	NT	Homo sapiens DMPZ56651219 protein, DMPZ56651219, mRNA
4137	17450	29569	4.16	1.0E-56	AF133267.2	NT	Homo sapiens DMPZ56651219 protein, DMPZ56651219, mRNA
4337	17450	30276	0.98	1.0E-56	AF133267.2	NT	Homo sapiens DMPZ56651219 protein, DMPZ56651219, mRNA
4643	17844	30768	1.14	1.0E-56	NT261.1	EST_HUMAN	Homo sapiens DMPZ56651219 protein, DMPZ56651219, mRNA
4642	17844	30769	1.42	1.0E-56	AB037168.1	NT	Homo sapiens DMPZ56651219 protein, DMPZ56651219, mRNA
4942	17941	30769	1.42	1.0E-56	AB037168.1	NT	Homo sapiens DMPZ56651219 protein, DMPZ56651219, mRNA
5397	18340	31185	0.91	1.0E-56	BE07198.1	EST_HUMAN	HC5-B170605-190200-231-B11 B170605 Homo sapiens cDNA
5697	18700	31664	50.3	1.0E-56	AF119856.1	NT	Homo sapiens PRO1851 mRNA, complete cds
5623	19557	32760	6.54	1.0E-56	AF119856.1	NT	Homo sapiens PRO1851 mRNA, complete cds
5623	19557	32757	6.54	1.0E-56	AF119856.1	NT	Homo sapiens PRO1851 mRNA, complete cds
7435	20132		0.95	1.0E-56	AF159420.1	NT	Homo sapiens PRO1851 mRNA, complete cds
6013	20320	34249	0.46	1.0E-56	AF159420.1	NT	Homo sapiens PRO1851 mRNA, complete cds
8508	21469	34842	1.32	1.0E-56	AF159420.1	NT	Homo sapiens PRO1851 mRNA, complete cds
8508	21469	34843	1.32	1.0E-56	AF159420.1	NT	Homo sapiens PRO1851 mRNA, complete cds
8900	21691	34629	1.16	1.0E-56	AF224692.1	NT	Homo sapiens PRO1851 mRNA, complete cds
8900	21691	34630	1.16	1.0E-56	AF224692.1	NT	Homo sapiens PRO1851 mRNA, complete cds
11349	24267	37706	1.48	1.0E-56	AF159420.1	NT	Homo sapiens PRO1851 mRNA, complete cds
11349	24267	37708	1.48	1.0E-56	AF159420.1	NT	Homo sapiens PRO1851 mRNA, complete cds
11891	26541	37419	1.1	1.0E-56	U06950.1	NT	Homo sapiens PRO1851 mRNA, complete cds
11899	26959	37437	1.89	1.0E-56	T110046.1	EST_HUMAN	Homo sapiens PRO1851 mRNA, complete cds
12008	24650	38349	1.41	1.0E-56	U06950.1	EST_HUMAN	Homo sapiens PRO1851 mRNA, complete cds
7757	20387	33887	1.99	9.0E-56	BE277074.1	EST_HUMAN	Homo sapiens PRO1851 mRNA, complete cds

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2762	1573	28766	8.27	7.0E-56	H19934.1	EST_HUMAN	y62303.r1 Soares adult brain N25H4B57 Homo sapiens cDNA clone IMAGE:17004.5 similar to contains
6089	21001	34323	2.26	7.0E-56	AW361213.1	EST_HUMAN	TRN representative
6089	21001	34323	2.26	7.0E-56	AW361213.1	EST_HUMAN	RC1410232.2B1060433.407 CT0362 Homo sapiens cDNA
1718	14746	27714	3.14	5.0E-56	AW067712.1	EST_HUMAN	RC1410232.2B1060433.407 CT0362 Homo sapiens cDNA
6794	22029	35007	0.71	5.0E-56	AW015507.1	EST_HUMAN	U14306.10300011101 BN0363 Homo sapiens cDNA
10876	2762		1.63	5.0E-56	W21683.1	EST_HUMAN	U14306.10300011101 CT0362 Homo sapiens cDNA clone IMAGE:2710544.3
12594	25611	31368	3.32	5.0E-56	H50363.1	EST_HUMAN	U345 Musca domestica cDNA, embryonic, primed salivary Homo sapiens cDNA
29	13146	26032	7.23	4.0E-55	U14306.1	NT	CH220038 Chromosome 22, same Homo sapiens cDNA, clone G22.355
25	13146	26033	7.23	4.0E-55	AF141546.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2738	10740	28744	4.11	4.0E-56	AF141546.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2738	10740	28745	4.11	4.0E-56	AF141546.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2650	13618	26526	2.73	4.0E-56	AF03328.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2676	15063	28652	1.16	4.0E-56	AK23488.1	EST_HUMAN	Homo sapiens beta-tubulin mRNA, complete cds
2676	15063	28653	1.16	4.0E-56	AK23488.1	EST_HUMAN	Homo sapiens beta-tubulin mRNA, complete cds
6507	16551	32731	5.84	4.0E-56	AF121528.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
6507	16551	32732	5.84	4.0E-56	AF121528.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
10894	22603	37262	1.4	4.0E-56	AF043346.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
11300	24278	37719	8.51	4.0E-56	A468068.1	EST_HUMAN	Homo sapiens beta-tubulin mRNA, complete cds
11300	24278	37720	8.51	4.0E-56	A468068.1	EST_HUMAN	Homo sapiens beta-tubulin mRNA, complete cds
1370	14402	27356	2.44	3.0E-56	8524029	NT	Homo sapiens beta-tubulin mRNA, complete cds
1789	18115	27784	1.15	3.0E-56	8512743	NT	Homo sapiens beta-tubulin mRNA, complete cds
2164	19178	29182	0.93	3.0E-56	8512743	NT	Homo sapiens beta-tubulin mRNA, complete cds
3170	16220	29110	1.93	3.0E-56	A432920.1	EST_HUMAN	Homo sapiens beta-tubulin mRNA, complete cds
3170	16220	29111	1.93	3.0E-56	A432920.1	EST_HUMAN	Homo sapiens beta-tubulin mRNA, complete cds
3908	16337		1.44	3.0E-56	AF059066.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
3952	17019	29089	0.79	3.0E-56	B139512.1	EST_HUMAN	Homo sapiens beta-tubulin mRNA, complete cds
4495	17605	30371	0.97	3.0E-56	767042	NT	Homo sapiens beta-tubulin mRNA, complete cds
4531	17540	30402	5.37	3.0E-56	AL62068.2	NT	Homo sapiens beta-tubulin mRNA, complete cds
4688	17663	30560	2.3	3.0E-56	5902095	NT	Homo sapiens beta-tubulin mRNA, complete cds
8207	18243	31094	0.97	3.0E-56	6912593	NT	Homo sapiens beta-tubulin mRNA, complete cds

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Table 4
Antibodies Expressed in Adult Liver

Probes SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5951	18590	32065	1.08	3.0E-58	4750163	NT	Human sapiens sparcidomectin, cwox and kuzali-like domains proteoglycan (testican) [SPOCK] mRNA
5951	18590	32066	1.04	3.0E-58	4750163	NT	Human sapiens sparcidomectin, cwox and kuzali-like domains proteoglycan (testican) [SPOCK] mRNA
7207	20200	33446	7.54	3.0E-58	1124124	NT	Human sapiens lysosomal-associated membrane protein 2 (LAMP2) mRNA
7107	20200	33446	0.88	3.0E-58	4904070	NT	Human sapiens LIM binding domain 2 (LDB2) mRNA
7107	20200	33437	0.88	3.0E-58	4904070	NT	Human sapiens LIM binding domain 2 (LDB2) mRNA
6975	20535	33564	6.27	3.0E-58	1148704	NT	Human sapiens bone morphogenetic protein 3 (BMP3) mRNA
10328	23218	39552	0.89	3.0E-50	0343782	NT	Human sapiens mRNA for KIAA0456 protein, partial cds
10358	23843	39552	1.68	3.0E-58	11435969	NT	Human sapiens KIAA0317 gene product (KIAA0317) mRNA
11759	24600	37728	1.71	3.0E-58	5901031	NT	Human sapiens nuclear pore complex interacting protein (NPIP) mRNA
11759	24600	39116	1.71	3.0E-58	5901031	NT	Human sapiens nuclear pore complex interacting protein (NPIP) mRNA
12463	25198	31647	1.04	3.0E-58	11424876	NT	Human sapiens caveolin 3 (CAV3) mRNA
12463	25198	31648	1.44	3.0E-58	11434876	NT	Human sapiens caveolin 3 (CAV3) mRNA
10427	33510	41881	1.44	2.0E-56	A11698181	EST_HUMAN	Human sapiens SV40 transformant neuroepithelium (6637237) Homo sapiens cDNA clone IMAGE:544206 3'
7596	15853	26740	2.20	2.0E-56	E05043851	EST_HUMAN	RC4-BT01010-110000-01510 B T01010 Homo sapiens cDNA
7596	15853	26741	2.20	2.0E-56	E05043851	EST_HUMAN	RC4-BT01010-110000-01510 B T01010 Homo sapiens cDNA
3030	3030	22663	1.12	2.0E-56	A50375351	EST_HUMAN	Human sapiens mRNA for KIAA1141 protein, partial cds
3391	16405	151	1.21	2.0E-56	A50375351	NT	Human sapiens gene for activin receptor type Iib, complete cds
3955	16532	29837	1.75	2.0E-56	AV7031841	EST_HUMAN	AV7018184 ADB Homo sapiens cDNA clone ADBCF010 6'
7449	20330	33500	3.5	2.0E-56	57520318	EST_HUMAN	Human sapiens SET domain and marker transposase fusion gene (SETMAR) mRNA
10427	14456	3882	5.82	1.0E-56	AF190301	NT	Human sapiens SET domain and marker transposase fusion gene (SETMAR) mRNA
3742	16714	28920	1.68	1.0E-56	AF190301	NT	Human sapiens SET domain and marker transposase fusion gene (SETMAR) mRNA
3742	16714	29091	1.68	1.0E-56	AF190301	NT	Human sapiens SET domain and marker transposase fusion gene (SETMAR) mRNA
8355	18738	31183	0.94	1.0E-56	AF190301	NT	Human sapiens SET domain and marker transposase fusion gene (SETMAR) mRNA
7131	20242	33403	0.5	1.0E-56	AF190301	NT	Human sapiens SET domain and marker transposase fusion gene (SETMAR) mRNA
10427	23550	3882	0.76	1.0E-56	AF190301	NT	Human sapiens SET domain and marker transposase fusion gene (SETMAR) mRNA
10591	24317	38558	1.75	1.0E-56	AF190301	NT	Human sapiens SET domain and marker transposase fusion gene (SETMAR) mRNA
649	13710	38558	1.44	1.0E-56	AF190301	NT	Human sapiens SET domain and marker transposase fusion gene (SETMAR) mRNA
11699	24573	39049	1.83	9.0E-57	AF2294971	NT	Human sapiens serine protease 17 (KLK4) gene, complete cds
11699	24573	39050	1.83	9.0E-57	AF2294971	NT	Human sapiens serine protease 17 (KLK4) gene, complete cds
14	13120	20015	1.61	8.0E-57	8923346	EST_HUMAN	Human sapiens hypothetical protein FLJ20371 (FLJ20371) mRNA
317	19459	20327	2.22	8.0E-57	AV8184051	EST_HUMAN	QV43510284-181199-037-406 370234 Homo sapiens cDNA

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Table 4
Probes Expressed in Adult Liver

Probe ID SEQ ID NO.	Exon ID NO.	QRF SEQ ID NO.	Expression Signal	Meat Similar (BLAST E Value)	Top Hit Accession No.	Top Hit Distance Score	Top Hit Description
900	13061	26008	5.62	8.0E-57	AW26500.1	EST_HUMAN	cd6510.41 NCBI GAP_Bms5 Homo sapiens cDNA clone IMAGE:2759261 3' similar to gb:U0387.6
1358	14521	27843	2.95	8.0E-37	AA056109.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR HUMAN;
1359	14522	27844	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1360	14523	27845	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1361	14524	27846	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1362	14525	27847	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1363	14526	27848	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1364	14527	27849	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1365	14528	27850	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1366	14529	27851	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1367	14530	27852	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1368	14531	27853	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1369	14532	27854	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1370	14533	27855	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1371	14534	27856	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1372	14535	27857	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1373	14536	27858	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1374	14537	27859	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1375	14538	27860	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1376	14539	27861	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1377	14540	27862	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1378	14541	27863	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1379	14542	27864	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1380	14543	27865	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1381	14544	27866	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1382	14545	27867	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1383	14546	27868	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1384	14547	27869	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1385	14548	27870	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1386	14549	27871	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1387	14550	27872	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1388	14551	27873	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1389	14552	27874	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1390	14553	27875	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1391	14554	27876	2.95	8.0E-37	AA056109.1	EST_HUMAN	p21512.11 Soares, Jesta, NIH Homo sapiens cDNA clone IMAGE:767151 5'
1392	14555						

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Table 4
Probes Expressed in Adult Liver

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NC	Exon SEQ ID NO	ORF SEQ ID: NO	Emission Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2245	16255	26261	3.88	1.0E-57	AW50208.1	EST_HUMAN	UHF-BN0-adj-0-4-UIT NH_MGC_50 Homo sapiens cDNA clone IMAGE:3078948.5
8416	21319	34951	0.461	1.0E-57	H09076.1	EST_HUMAN	BT020015 Chromosome 22 exon Homo sapiens cDNA clone c22-28.5
8281	22179		2.62	1.0E-57	BE040831.1	EST_HUMAN	h033068.1 NC1 CGAP L201 Homo sapiens cDNA clone IMAGE:3039032.5 similar to TR000246 O00246 HYPOHECTAL 0.3 NO PROTEIN.
12395	22096		9.43	1.0E-57	AW47091.1	EST_HUMAN	h033068.1 NC1 CGAP L201 Homo sapiens cDNA clone IMAGE:3037493.3 similar to contains 1HR.33
8574	18944	32060	0.97	8.0E-58	AA297347.1	EST_HUMAN	EST_HUMAN Homo sapiens cDNA 5' end
12638	25431	31777	2.89	8.0E-58	BE33066.1	EST_HUMAN	EST_HUMAN Homo sapiens cDNA 5' end
610	13575		4.48	8.0E-58	BE309716.1	EST_HUMAN	h01330495 NH_MGC_44 Homo sapiens cDNA clone IMAGE:303100.5
677	13739	26662	3.76	8.0E-58	AI790376.1	EST_HUMAN	h01330495 NH_MGC_44 Homo sapiens cDNA clone IMAGE:303211.5
677	13739	26662	3.76	8.0E-58	AI790376.1	EST_HUMAN	UNNAMED NERV-H PROTEIN.
677	13739	26663	3.76	8.0E-58	AI790376.1	EST_HUMAN	UNNAMED NERV-H PROTEIN.
1881	14003	27886	2.25	8.0E-58	11434821	NT	Homo sapiens relative protein O-mannosyl transferase (POMT2), mRNA
1881	14002	27886	2.25	8.0E-58	11434821	NT	Homo sapiens relative protein O-mannosyl transferase (POMT2), mRNA
3016	16048		3.15	8.0E-58	7708132	NT	Homo sapiens DHHC1 protein (LOC31304), mRNA
7698	20543	33834	0.84	7.0E-58	BE201911.1	EST_HUMAN	h01346704 NH_MGC_38 Homo sapiens cDNA clone IMAGE:305737.5
11200	24210		5.09	7.0E-58	5174542	NT	Homo sapiens MAD5 box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B) (MEF2B), mRNA
11367	24285	37729	3.15	7.0E-58	AW504109.1	EST_HUMAN	UHF-BN0-adj-2-10-0-UIT NH_MGC_50 Homo sapiens cDNA clone IMAGE:3078667.5
11367	24285	37730	3.15	7.0E-58	AW504109.1	EST_HUMAN	UHF-BN0-adj-2-10-0-UIT NH_MGC_50 Homo sapiens cDNA clone IMAGE:3078667.5
2270	15200	26257	1.48	6.0E-58	BE330631.1	EST_HUMAN	h01330495 NH_MGC_44 Homo sapiens cDNA clone IMAGE:303100.5
2398	15403	29407	5.2	6.0E-58	AI103899.1	EST_HUMAN	AT103899 NT2R3P3 Homo sapiens cDNA clone NT2R3P301203.5
2345	15957	26886	1.28	6.0E-58	BE242130.1	EST_HUMAN	TOAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Bcl-2-HGSC progenitor-TCAA Homo sapiens cDNA clone TOAAP1219
2345	15957	26886	1.28	6.0E-58	BE242130.1	EST_HUMAN	TOAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Bcl-2-HGSC progenitor-TCAA Homo sapiens cDNA clone TOAAP1219
8411	19459	32933	1.81	6.0E-58	AF100911.1	NT	Homo sapiens chemokine MIP-2 gamma (MIP-2 gamma) mRNA, complete cds
10769	20883	37115	1.02	6.0E-58	11454746	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPRT2), mRNA
330	13412	26329	3.29	5.0E-58	4607334	NT	Homo sapiens synaptophysin 1 (SYN1), mRNA
733	13791	26715	4.74	5.0E-58	BE769384.1	EST_HUMAN	RC4NT0057-16000-015-005 NT0057 Homo sapiens cDNA
1222	14200	27201	2.33	5.0E-58	AW77948.1	EST_HUMAN	C08-UM0003-24000-127-407 UM0003 Homo sapiens cDNA
1222	14200	27202	2.33	5.0E-58	AW77948.1	EST_HUMAN	C08-UM0003-24000-127-407 UM0003 Homo sapiens cDNA
1223	14200	27201	1.89	5.0E-58	AW77948.1	EST_HUMAN	C08-UM0003-24000-127-407 UM0003 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top 5) Hit Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1223	14200	27802	1.93	5.0E-56 A/1707493.1	EST_HUMAN	EST_HUMAN	CHL-UM0043:340303:127-407 UM0043 Homo sapiens cDNA
3398	16112	28319	5.27	5.0E-56 A/0681983.1	EST_HUMAN	EST_HUMAN	cr69007.x1 NC1 CGAP_Lut Homo sapiens cDNA clone IMAGE:168668 3'
4357	17371	30236	0.74	5.0E-56 A/539745.1	EST_HUMAN	EST_HUMAN	hs6907.x1 NC1 CGAP_G08 Homo sapiens cDNA clone IMAGE:233908 3' similar to SW:FR02_ACACA P18884 PROPLIN 11:
5090	18087		0.66	5.0E-56 A/934894.1	EST_HUMAN	EST_HUMAN	LC-C1024:040303:051-F56 C1024 Homo sapiens cDNA
5823	18894		1.9	5.0E-56 T146292	NT	NT	Homo sapiens pacific-specific T1 (PLC1), mRNA
6419	19468	32640	6.18	5.0E-56 H2072.1	EST_HUMAN	EST_HUMAN	Homo sapiens pacific-specific T1 (PLC1), mRNA
6658	19697	32953	1.1	5.0E-56 A/10235.2	NT	NT	Ynt1007.71 Soares infant brain T1B Homo sapiens cDNA clone IMAGE:43071 5'
6744	19778	32951	0.84	5.0E-56 T1421930	EST_HUMAN	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C08 Ynt1007.71 Soares infant brain T1B Homo sapiens cDNA clone IMAGE:43071 5'
7085	20291	33550	1.03	5.0E-56 A/561334.1	NT	NT	Homo sapiens alpha 1 (HSA) mRNA, complete cds
7485	20475	33551	0.73	5.0E-56 A/781334.1	NT	NT	Homo sapiens alpha 1 (HSA) mRNA, complete cds
8517	21478	34320	8.94	5.0E-56 A85500	EST_HUMAN	EST_HUMAN	Homo sapiens alpha 1 (HSA) mRNA, complete cds
8626	21635	35212	0.75	5.0E-56 B22263	NT	NT	Homo sapiens alpha 1 (HSA) mRNA, complete cds
10371	22350	35851	0.83	5.0E-56 U304833	NT	NT	Homo sapiens alpha 1 (HSA) mRNA, complete cds
10571	23309	36918	0.42	5.0E-56 A/492112	NT	NT	Homo sapiens alpha 1 (HSA) mRNA, complete cds
10858	23711	37106	0.64	5.0E-56 A/801451.1	NT	NT	Homo sapiens alpha 1 (HSA) mRNA, complete cds
12419	25830	37187	0.64	5.0E-56 A/801451.1	NT	NT	Homo sapiens alpha 1 (HSA) mRNA, complete cds
12419	25830		2.28	5.0E-56 1162623	NT	NT	Homo sapiens alpha 1 (HSA) mRNA, complete cds
324	13478	26907	4.5	4.0E-56 4902302	NT	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O) mRNA
823	13878	26915	1.54	4.0E-56 4940364	NT	NT	Homo sapiens intercalin 10 receptor, beta (IL10RB), mRNA
1487	14518	27479	3.55	4.0E-56 4603548	NT	NT	Homo sapiens intercalin 10 receptor, beta (IL10RB), mRNA
2613	15611	28906	1.27	4.0E-56 AF266056.1	NT	NT	Homo sapiens intercalin 10 receptor, beta (IL10RB), mRNA
2676	15974	29672	2	4.0E-56 U36251.1	NT	NT	Homo sapiens intercalin 10 receptor, beta (IL10RB), mRNA
3370	16414	29315	1.81	4.0E-56 D16470.1	NT	NT	Homo sapiens intercalin 10 receptor, beta (IL10RB), mRNA
3903	18534	29720	1.11	4.0E-56 9061900	NT	NT	Homo sapiens intercalin 10 receptor, beta (IL10RB), mRNA
5123	18119	30861	1.08	4.0E-56 S75284.1	NT	NT	Homo sapiens intercalin 10 receptor, beta (IL10RB), mRNA
8338	21243	34676	0.57	4.0E-56 BE469587	EST_HUMAN	EST_HUMAN	WT1-WT1 tumor suppressor protein (human, fetal kidney) (WT1), mRNA, 821 nt
11793	24982	39172	6.37	4.0E-56 BE469587	EST_HUMAN	EST_HUMAN	WT1-WT1 tumor suppressor protein (human, fetal kidney) (WT1), mRNA, 821 nt
335	13442		1.61	3.0E-56 11424059	NT	NT	Homo sapiens 11B-580De-associated protein 5 (E1B-AP5), mRNA
1418	14447	27401	1.73	3.0E-56 RT879.1	EST_HUMAN	EST_HUMAN	Ynt10402.1 Soares infant brain T1B Homo sapiens cDNA clone IMAGE:31693 5'
3071	16123		0.86	3.0E-56 RT879.1	EST_HUMAN	EST_HUMAN	Ynt10402.1 Soares infant brain T1B Homo sapiens cDNA clone IMAGE:31693 5'

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3321	10239	29167	2.98	3.0E-58	BF55848.1	EST_HUMAN	002185789Ft NHF_MGC_45 Homo sapiens cDNA clone IMAGE:500843.5
3321	10239	29168	2.98	3.0E-58	BF55848.1	EST_HUMAN	002185789Ft NHF_MGC_45 Homo sapiens cDNA clone IMAGE:500843.5
8611	10566	32735	0.95	3.0E-58	AF058069.1	EST_HUMAN	U94010702-174400-19409.0107021 Homo sapiens cDNA
6714	10700	32954	2.78	3.0E-58	AF07095.1	EST_HUMAN	U94010702-174400-19409.0107021 Homo sapiens cDNA
6532	18401	33182	1.8	3.0E-58	AF171297.1	EST_HUMAN	AF171297.1 DCA Homo sapiens cDNA clone IMAGE:500843.5
998	14019	25993	8.48	2.0E-58	AF058024.1	NT	Homo sapiens 5' untranslated region 2 (UTS2) gene, complete cds
1318	14349		13.31	2.0E-58	DE220532.1	EST_HUMAN	h00867.01 NHF_MGC_7 Homo sapiens cDNA clone IMAGE:500843.5 similar to g0265931.80S
5519	18598	31447	0.81	2.0E-58	AF107463.1	EST_HUMAN	RIBOSOMAL PROTEIN L7 (RPL18A); g0261807.1 Mitochondrial mRNA for TXA response element binding protein 30.1 kDa; NBF_1, cDNA, S1 Homo sapiens cDNA clone IMAGE:2687704.3
5542	25028	31471	3.35	2.0E-58	DE307186.1	EST_HUMAN	g0261807.1 Mitochondrial mRNA for TXA response element binding protein 30.1 kDa; NBF_1, cDNA, S1 Homo sapiens cDNA clone IMAGE:2687704.3
5542	25028	31485	3.35	2.0E-58	DE307186.1	EST_HUMAN	g0261807.1 Mitochondrial mRNA for TXA response element binding protein 30.1 kDa; NBF_1, cDNA, S1 Homo sapiens cDNA clone IMAGE:2687704.3
5521	18933	32511	1.38	2.0E-58	BF571468.1	EST_HUMAN	g0261807.1 Mitochondrial mRNA for TXA response element binding protein 30.1 kDa; NBF_1, cDNA, S1 Homo sapiens cDNA clone IMAGE:2687704.3
6601	18410	32575	2	2.0E-58	AF124974.1	EST_HUMAN	U94010702-174400-19409.0107021 Homo sapiens cDNA clone IMAGE:500843.5
6536	18410	32612	0.89	2.0E-58	AF025607.1	EST_HUMAN	U94010702-174400-19409.0107021 Homo sapiens cDNA clone IMAGE:500843.5
7069	20168	33402	0.89	2.0E-58	AF129407.1	EST_HUMAN	g0261807.1 Mitochondrial mRNA for TXA response element binding protein 30.1 kDa; NBF_1, cDNA, S1 Homo sapiens cDNA clone IMAGE:2687704.3
7618	20457	33743	2.69	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7618	20457	33743	2.69	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
11192	24108	37556	14.38	2.0E-58	BF307746.1	EST_HUMAN	g0261807.1 Mitochondrial mRNA for TXA response element binding protein 30.1 kDa; NBF_1, cDNA, S1 Homo sapiens cDNA clone IMAGE:500843.5
11402	24338	37765	1.95	2.0E-58	AF157264.1	EST_HUMAN	h00867.01 NHF_MGC_7 Homo sapiens cDNA clone IMAGE:500843.5 similar to g0265931.80S
745	13803	28727	6.88	1.0E-58	M55194.1	NT	Human complement component C5 mRNA, 3' end
1005	14138	27075	4.52	1.0E-58	6274549	NT	Homo sapiens MADH dehydrogenase (ubiquinol) 1 beta subcomplex, 9 (22D, E22) (NDUF9), mRNA
13355	14337	27340	1.25	1.0E-58	AF1957182.1	EST_HUMAN	ES11500232 MADGE, resequenced, MAGD Homo sapiens cDNA
13355	14337	27341	1.25	1.0E-58	AF1957182.1	EST_HUMAN	ES11500232 MADGE, resequenced, MAGD Homo sapiens cDNA
14233	14454	27418	0.29	1.0E-58	AJ238058.1	NT	Homo sapiens partial A1-1 gene, exons 2 to 7 and A1 repeat elements
2840	15538	28335	1.95	1.0E-58	4159108	NT	Homo sapiens Alu repeat element binding transcription factor 2 (SREBF2) mRNA
3784	18515	29702	0.66	1.0E-58	4607628	NT	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNP1) mRNA
4549	18747	30715	0.95	1.0E-58	IV86038.1	NT	Homo sapiens nucleosome core particle (NCP) mRNA, exon 4
5051	18098	30938	9.03	1.0E-58	AF141063.1	EST_HUMAN	h00867.01 NHF_MGC_7 Homo sapiens cDNA clone IMAGE:500843.5 similar to g0265931.80S
6035	19177	32248	1.02	1.0E-58	BF001830.1	EST_HUMAN	RC1-B10254-200100-015-401 170251 Homo sapiens cDNA
7187	20187	33430	1.04	1.0E-58	11422031	NT	Homo sapiens hypopharyngeal protein (LOC51260), mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Eno SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8091	21622		0.61	1.0E-58 AW675337.1	EST_HUMAN	EST	EST385537 MAGE resequencing, MAGE Homo sapiens cDNA
8092	22235	33720	0.61	1.0E-58 AW675337.1	EST_HUMAN	EST	Homo sapiens myosin (M protein) 2 (16Sk) (MYO16), mRNA
8093	22430	33927	1.23	1.0E-58 AW71001.1	EST_HUMAN	EST	AW71001 NPO Homo sapiens cDNA clone NP04-109.5
8094	22430	33927	0.60	1.0E-58 AW71001.1	EST_HUMAN	EST	AW71001 NPO Homo sapiens cDNA clone MAGE-730467.5
8095	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8096	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8097	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8098	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8099	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8100	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8101	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8102	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8103	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8104	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8105	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8106	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8107	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8108	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8109	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8110	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8111	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8112	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8113	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8114	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8115	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8116	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8117	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8118	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8119	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8120	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8121	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8122	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8123	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8124	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-730467.5
8125	22563	35922	0.62	1.0E-58 AA112397.1	EST_HUMAN	EST	AB206347 Source, testis, NHT Homo sapiens cDNA clone MAGE-7

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	ORF BEQ ID NO.	Expression Signal	Most Similar BLAST [†] E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12546	26796	5.78	4.0E-56	AF5720.1	NT	Homo sapiens 17-oxide-hydroxy-steroid dehydrogenase H (HSD17B4) gene, promoter region and exon 1
10	13126	4.23	3.0E-59	AW46582.1	EST_HUMAN	ES137/1582 IMAGE resequencing, MAGI Homo sapiens cDNA
244	14341	26293	3.0E-59	765224.1	EST_HUMAN	Homo sapiens KIAA0490 gene product (KIAA0490), mRNA
1735	14761	27736	8.38	4903690	NT	Homo sapiens plasminogen activator, tissue (PLAT) mRNA
1739	14760	27737	8.38	4903690	NT	Homo sapiens plasminogen activator, tissue (PLAT) mRNA
2143	16150	28157	6.78	3.0E-59	AB202036.1	Homo sapiens plaminogen activator, tissue (PLAT) mRNA
2143	16150	28158	6.78	3.0E-59	AB202036.1	Homo sapiens plaminogen activator, tissue (PLAT) mRNA
3268	16197	29033	1.21	3.0E-59	118995.1	NT
3086	16197	29034	1.21	3.0E-59	118995.1	EST_HUMAN
3174	16224	29117	4.58	492031.4	NT	H202071 Testis 1 Homo sapiens cDNA clone M20317 5' end
3174	16224	29118	4.0	3.0E-59	492031.4	EST_HUMAN
3388	16567	29615	1.35	492004.4	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
4788	17600	30608	7.2	3.0E-59	492004.4	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
4985	17603	30812	1.48	3.0E-59	AL16594.2	Homo sapiens zinc polypeptide glucocorticoid 2 (zperm receptor) (ZP2) mRNA
6465	19011	32695	1.91	742752.1	NT	Homo sapiens chromosome 21 segment H521034
7781	20351	32695	1.91	742752.1	NT	Homo sapiens chromosome 21 segment H521034
8510	21441	34752	1.31	3.0E-59	Y15661.1	Homo sapiens hypoxanthine phosphoribosyl transferase (HGPRT), mRNA
8510	21441	34753	1.31	3.0E-59	Y15661.1	Homo sapiens hypoxanthine phosphoribosyl transferase (HGPRT), mRNA
10347	24783	36785	0.76	3.0E-59	Y15661.1	Homo sapiens hypoxanthine phosphoribosyl transferase (HGPRT), mRNA
10347	24783	36785	0.76	3.0E-59	Y15661.1	Homo sapiens hypoxanthine phosphoribosyl transferase (HGPRT), mRNA
13237	26261	36855	1.82	3.0E-59	Y15661.1	H. sapiens GKI-like gene
13237	26261	36855	1.82	3.0E-59	Y15661.1	H. sapiens GKI-like gene
12648	26268	36855	1.82	11417869.1	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
6700	19161	32294	0.53	11417869.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
6700	19161	32294	0.53	11417869.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
6700	19161	32295	0.53	11417869.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
7118	20322	33295	0.49	2.0E-59	BF53683.1	U14844-ayp-02-0.11.1 NQ1 OGAP, 3.0x8 Homo sapiens cDNA clone IMAGE 2086522 3'
7424	20723	33320	0.59	2.0E-59	AF15817.1	U14844-ayp-02-0.11.1 NQ1 OGAP, 3.0x8 Homo sapiens cDNA clone IMAGE 2086522 3'
8261	21865	33504	0.41	2.0E-59	AF15817.1	U14844-ayp-02-0.11.1 NQ1 OGAP, 3.0x8 Homo sapiens cDNA clone IMAGE 2086522 3'
10163	23554	33554	0.72	2.0E-59	BF73928.1	U14844-ayp-02-0.11.1 NQ1 OGAP, 3.0x8 Homo sapiens cDNA clone IMAGE 2086522 3'
11005	23500	33554	0.72	2.0E-59	BF73928.1	U14844-ayp-02-0.11.1 NQ1 OGAP, 3.0x8 Homo sapiens cDNA clone IMAGE 2086522 3'
11270	24162	37612	1.77	2.0E-59	AW140088.1	U14844-ayp-02-0.11.1 NQ1 OGAP, 3.0x8 Homo sapiens cDNA clone IMAGE 2086522 3'
11270	24162	37643	1.77	2.0E-59	AW140088.1	U14844-ayp-02-0.11.1 NQ1 OGAP, 3.0x8 Homo sapiens cDNA clone IMAGE 2086522 3'
24269	25196	31881	7.18	2.0E-59	AB18109.1	U14844-ayp-02-0.11.1 NQ1 OGAP, 3.0x8 Homo sapiens cDNA clone IMAGE 2086522 3'

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar (Top) HI BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1263	26822	31482	1.83	2.0E-50	L16465.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
173	13274		6.93	1.0E-49	BE29441.1	EST_HUMAN	0911670777 NH: JACQ-17 Homo sapiens cDNA clone IMAGE:3531027 8'
2450	15440	28441	1.71	1.0E-50	D11466.2	NT	Homo sapiens Xist mRNA for xarline chromosome, complete cds
2450	15440	28441	1.71	1.0E-50	D11466.2	NT	Homo sapiens Xist mRNA for xarline chromosome, complete cds
2692	16596		3.97	1.0E-50	AA74949.8	EST_HUMAN	060811.1 NC: CGM-7303 Homo sapiens cDNA clone IMAGE:3532902 8' (similar to TRQ13837 C13837/MC307 TRANSPOSABLE ELEMENT), complete consensus sequence.
6078	19715	32511	0.43	1.0E-59	1142724	NT	Homo sapiens phosphatidylinositol transfer protein (PTPN), mRNA
6078	19715	32512	0.43	1.0E-59	1142724	NT	Homo sapiens phosphatidylinositol transfer protein (PTPN), mRNA
7655	20913	34229	1.32	1.0E-50	AJ100654.1	EST_HUMAN	Homo sapiens RNA polymerase I subunit 1 (POLR1A), mRNA
8178	21005	34413	0.94	1.0E-50	BE23051.1	EST_HUMAN	0911110451 NH: JACQ-16 Homo sapiens cDNA clone IMAGE:3532902 8'
8178	21005	34413	0.94	1.0E-50	BE23051.1	EST_HUMAN	0911110451 NH: JACQ-16 Homo sapiens cDNA clone IMAGE:3532902 8'
8622	22910	35245	0.83	1.0E-50	11426920	NT	Homo sapiens zinc finger protein 278 (ZNF278), mRNA
10131	23022	36416	0.83	1.0E-50	11426920	NT	Homo sapiens hydroxymethylglutaryl-Coenzyme A lyase (HMGH), mRNA
10131	23022	36416	0.83	1.0E-50	11426920	NT	Homo sapiens hydroxymethylglutaryl-Coenzyme A lyase (HMGH), mRNA
11289	20913	34229	0.97	1.0E-50	AJ100654.1	EST_HUMAN	Homo sapiens RNA polymerase I subunit 1 (POLR1A), mRNA
11289	20913	34229	0.97	1.0E-50	AJ100654.1	EST_HUMAN	Homo sapiens RNA polymerase I subunit 1 (POLR1A), mRNA
14231	14535	30334	0.35	0.0E-40	AF064530.1	NT	Homo sapiens cyclin-D binding, MAF-like protein mRNA, complete cds
759	13945	26779	1.86	0.0E-40	AY16776.5	EST_HUMAN	EST:856549 IMAGE: ressequens, MAGO Homo sapiens cDNA
1420	14521	27482	1.82	0.0E-40	4769169	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (180D) (SNRPD3) mRNA
2185	15109	26201	2.12	0.0E-40	5174656	NT	Homo sapiens differentiation-related gene 1 (molar-specific induction protein) (RTP) mRNA
2185	15109	26202	2.12	0.0E-40	5174656	NT	Homo sapiens differentiation-related gene 1 (molar-specific induction protein) (RTP) mRNA
8211	10320	32417	1.12	0.0E-40	AB220044.1	NT	Homo sapiens mRNA for KIAA1081 protein, Fertilis cds
6781	10514	33029	2.92	0.0E-40	S63182.1	NT	Hydrolase-binding protein-hepatocyte growth factor activator homolog (human, plasma, mRNA, 2405 nt)
8151	21060	34351	0.98	0.0E-40	11420941	NT	Homo sapiens phosphatidylinositol 3-kinase 1, choline, beta isoform (POT1B), mRNA
8543	21474	34616	3.95	0.0E-40	X17033.1	NT	Human mRNA for the protein in alpha-2 subunit
5455	22423	35766	3.17	0.0E-40	11438949	NT	Homo sapiens S-allylglutathione transferase (GSTA3), mRNA
10004	22621	36206	0.85	0.0E-40	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10004	22621	36206	0.85	0.0E-40	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11146	22620	37370	0.76	0.0E-40	5403697	NT	Homo sapiens RNN binding protein 7 (RNNBP7), mRNA
11272	24164	37645	5.04	8.0E-40	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21004
11272	24164	37646	5.04	8.0E-40	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21004
776	18345	26769	6.89	7.0E-40	AF106006.1	NT	Homo sapiens MHC class 1 region
776	18345	26769	6.89	7.0E-40	AF106006.1	NT	Homo sapiens MHC class 1 region
840	13655	26832	1.36	7.0E-40	4504634	NT	Homo sapiens inhibition 10 receptor, beta (IL10RB), mRNA

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Table 4

Single Exon Probes Expressed in Adult Liver

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1448	14477	27436	2.16	2.0E-60	Z11094.1	NT	H.sapiens, f10D1 protein kinase related to rat ERK2
1790	14777	27436	1.18	2.0E-60	M34603.1	NT	Human bar protein mRNA, 3' end
1790	14787	27797	0.04	2.0E-60	A100286.1	NT	Homo sapiens soluble carrier (SC)25A19 mRNA, complete cds; nuclear gene for mitochondrial product
2649	15644	26944	0.91	2.0E-60	7657226	NT	Homo sapiens nucleon 17 (NOL17) mRNA
3059	16275	28073	0.07	2.0E-60	4757967	NT	Homo sapiens cell cycle protein 110 (CCP110) mRNA
3958	17015	28504	0.72	2.0E-60	AF231918.1	NT	Homo sapiens chromosome 21 (HSA21) mRNA
4221	17257		0.66	2.0E-60	BF512438.1	EST_HUMAN	U14-BW1 Homo sapiens cDNA clone IMAGE3070627.3
6556	16507	33786	0.9	2.0E-60	A1701652.1	EST_HUMAN	pro112.25 NCL CGAP_C20 Homo sapiens cDNA clone IMAGE107448.5 similar to contains THR.L1 THR repetitive domain
6788	16002	33786	1.08	2.0E-60	AF200472.1	NT	Homo sapiens pro-alpha 2(I) collagen (COL1A2) gene, complete cds
7013	20140	33742	1.03	2.0E-60	AF163476.1	NT	Homo sapiens DNA polymerase subunit 10 (POL10) mRNA, complete cds
7103	19140	31542	2.11	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
7108	18440	31543	2.11	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
7489	25409	33686	6.72	2.0E-60	A4331188.1	EST_HUMAN	EST1181519 Juxtal T-cells V Homo sapiens cDNA 5' end similar to prothyrostat, alpha
7489	25409	33687	5.72	2.0E-60	A4331188.1	EST_HUMAN	EST1181519 Juxtal T-cells V Homo sapiens cDNA 5' end similar to prothyrostat, alpha
7593	20526	33820	0.44	2.0E-60	A008124.1	EST_HUMAN	h23209.1 NCL CGAP_KH12 Homo sapiens cDNA clone IMAGE205188.3 similar to SV:GALR_FAT
8680	20622		1.19	2.0E-60	BF512083.1	EST_HUMAN	Q12905 GALANIN RECEPTOR
8684	21615	34959	1.07	2.0E-60	X85507.1	EST_HUMAN	U14-BW1 Homo sapiens adult testis Homo sapiens cDNA clone CAM_EST15
8425	22503	35710	4.02	2.0E-60	L36033.1	NT	Human pre-B cell stimulating factor homologous (SDF1b) mRNA, complete cds
10484	23372	36786	2.47	2.0E-60	11691659	NT	Homo sapiens serum domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 9A (SEM9A), mRNA
10484	23372	36787	2.47	2.0E-60	11691659	NT	Homo sapiens serum domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 9A (SEM9A), mRNA
12627	25393		2.08	2.0E-60	11418192	NT	Homo sapiens non histone chromosome protein 2 (S. cerevisiae-like) (NHP2L1), mRNA
12631	26140		1.84	2.0E-60	11418038	NT	Homo sapiens similar to HSPC22 protein (H. sapiens) (TC083524), mRNA
12635	26450		1.79	2.0E-60	A0011306.1	NT	Homo sapiens gene for AL-2, complete cds
545	1384	26522	1.03	1.0E-60	BF16596.1	EST_HUMAN	PM2-H1006-270200-001-408 H10655 Homo sapiens cDNA
3074	17002	29889	1.56	1.0E-60	AU143399.1	EST_HUMAN	AUT1-6389 770A1 Homo sapiens cDNA clone Y7A01.100159.5
5071	17008	30916	1.75	1.0E-60	AL16328.2	NT	Homo sapiens chromosome 21 segment H321035
8527	21448	34901	0.86	1.0E-60	BF064410.1	EST_HUMAN	RC4241031-141769-011-406 510311 Homo sapiens cDNA
9316	22243		3.32	1.0E-60	A424941.1	EST_HUMAN	nc04442.71 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE1007182 similar to contains L1.1 L1 repetitive element

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Emission Signal	Most Similar (Top 3) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
521	13931	26003	1.23	2.0E-61	8802329	NT	Homo sapiens hypothetical protein FLJ1026 (FLJ1026), mRNA
1240	14278	27219	2.07	2.0E-61	BE169410.1	EST_HUMAN	CY3-H10615-06040-147-40T H10615 Homo sapiens cDNA
1240	14278	27220	2.07	2.0E-61	BE169410.1	EST_HUMAN	CY3-H10615-06040-147-40T H10615 Homo sapiens cDNA
1692	14722	27699	1.6	2.0E-61	N53091.1	EST_HUMAN	Y63H11.40S feline liver spleen TNL33 Homo sapiens cDNA clone IMAGE246453 3' similar to pL2944.40S REDUCED-DIMENSIONAL PROTEIN L284 (HUMAN);
2698	16983		1.06	2.0E-61	N53091.1	EST_HUMAN	Y63H11.40S feline liver spleen TNL33 Homo sapiens cDNA clone IMAGE270189 5'
6664	19730	32936	0.97	2.0E-61	11426168	NT	Homo sapiens AT184, H ⁺ transporting, lysosomal (vacuolar proton pump) ion-catalytic accessory protein 1A (H11180) (A1PONTA), human cDNA clone GGC51 G05 5'
9507	22494	33577	1.74	2.0E-61	AV594317.1	EST_HUMAN	Y63H11.40S feline liver spleen TNL33 Homo sapiens cDNA clone GGC51 G05 5'
10051	22894		0.89	2.0E-61	AD01108.1	EST_HUMAN	Y63H11.40S feline liver spleen TNL33 Homo sapiens cDNA clone GGC51 G05 5'
10433	23322	35740	2.01	2.0E-61	AV592293.1	EST_HUMAN	Y63H11.40S feline liver spleen TNL33 Homo sapiens cDNA clone IMAGE307074 5'
10744	25300	37062	2.81	2.0E-61	11421778	EST_HUMAN	Homo sapiens thymosin (RNA) III (DNA directed) (354d) (RPG39), mRNA
11321	25340		3.49	2.0E-61	11421778	EST_HUMAN	Homo sapiens thymosin (RNA) III (DNA directed) (354d) (RPG39), mRNA
13602	26598	31741	0.91	2.0E-61	AV595326.1	EST_HUMAN	CY3-SN0423-17030-16210 BNC042 Homo sapiens cDNA
453	33530		0.91	1.0E-61	AL163203.2	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog) Hsa ORC2L mRNA
178	14630	29792	1.26	1.0E-61	5463829	NT	Human polymorphic nucleotide repeat in X-linked retinitis pigmentosa (RPS) gene region
178	14630		1.07	1.0E-61	U32957.1	NT	Homo sapiens alpha poliovirus glycoprotein 3A (saccharin receptor) (2F3A), mRNA
1833	14634	27885	3.39	1.0E-61	5055933	NT	Y63H11.40S feline liver spleen TNL33 Homo sapiens cDNA clone IMAGE269365 5' similar to contains element
2212	18223	26226	1.35	1.0E-61	AV1827981.1	EST_HUMAN	MSR1 repetitive element
4549	17598	30418	0.87	1.0E-61	4739249	NT	Homo sapiens T2AF family member-associated NFkB activator (TANK) mRNA
4649	17598	30419	0.87	1.0E-61	4739249	NT	Homo sapiens T2AF family member-associated NFkB activator (TANK) mRNA
4657	17605	30923	10.94	1.0E-61	AV126181.1	EST_HUMAN	U1-HSWQ-01-b09-Q-U1 at NCL CGAP Sub6 Homo sapiens cDNA clone IMAGE272671 3'
4657	17605	30924	10.94	1.0E-61	AV126181.1	EST_HUMAN	U1-HSWQ-01-b09-Q-U1 at NCL CGAP Sub6 Homo sapiens cDNA clone IMAGE272671 3'
5578	18606	31933	0.87	1.0E-61	MT6423.1	NT	H sapiens carboxin entylase VII (CA VII) gene, exons 4,5,6, and 7, and complete cds
5578	18606	32073	0.87	1.0E-61	7692203	NT	Homo sapiens KIA0703 gene product (KIA0703), mRNA
6029	19100	32203	1.52	1.0E-61	11418891	NT	Homo sapiens survival of motor neuron 1, isoform 2 (SMN1), mRNA
7229	20138	33577	12.06	1.0E-61	MD135.1	NT	Human P-0 T-cell and mast cell growth factor (hP-0) gene, complete cds
7430	20391	33951	0.71	1.0E-61	475917.1	NT	Homo sapiens SCG5-interacting protein 1 (SHRIP125), mRNA
7595	20492	33791	1.37	1.0E-61	6623130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
7595	20492	33792	1.37	1.0E-61	6623130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8710	21641	34695	3.04	1.0E-61	11034949	NT	Homo sapiens growth hormone releasing hormone (GRH), mRNA
8898	21618	35189	3.49	1.0E-61	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MAN5A) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D) genes, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9922	22728	3.19	1.0E-61	AW996726.1	EST_HUMAN	MRQ-BN0070-0400-010-507 BN0070 Homo sapiens cDNA
9985	22810	99169	0.87	1.0E-61	11416290	Homo sapiens cathepsin B1 (CDH16), mRNA
10332	22418	59833	5.12	1.0E-61	11429982	Homo sapiens KIAA0871 protein (KIAA0871), mRNA
11080	24012	37453	1.88	1.0E-61	11425978	Homo sapiens actinin, alpha 4 (ACTN4), mRNA
11509	24419	37874	1.72	1.0E-61	AB007830.1	Homo sapiens mRNA for CSF2, complete cds
12362	26831	31489	3.97	1.0E-61	11430490	Homo sapiens low density lipoprotein receptor protein 2 (LDLR), mRNA
12802	26831	31489	3.97	1.0E-61	11430490	Homo sapiens low density lipoprotein receptor protein 2 (LDLR), mRNA
12705	25360	31797	2.7	1.0E-61	M23609.1	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
12852	26841	31791	10.21	1.0E-61	11418127	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
10943	23729	37162	1.94	9.0E-63	BE064368.1	FC-33105-119300-015410 B1 (FC310) Homo sapiens cDNA
4697	17072	30945	1.24	8.0E-62	AA394393.1	CG8841.x1 NCI CGAP CG81 Homo sapiens cDNA clone IMAGE:1347283.3 similar to SW_P0L_JALVRK
13102	26812	27113	2.72	8.0E-62	AA394393.1	PG1708 POL POL PROTEIN
1134	14718	27113	2.72	7.0E-62	AW148341.1	nc75901.x1 NCI CGAP CG81 Homo sapiens cDNA clone IMAGE:1301328.3
3983	16920	26504	1.02	7.0E-62	P17490	AV174381 CG81 Homo sapiens cDNA clone DCBAMA08.6
6138	19197	33336	1.04	7.0E-62	P17490	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) (AUTOANTIGEN NOR-40)
11789	24711	39202	1.81	7.0E-62	AI209391.1	Homo sapiens hypothetical protein (F120295), mRNA
3042	16004	16004	1.88	6.0E-62	U09410.1	O15103 HYPOTHETICAL 27.3 KD PROTEIN ;
3445	16494	34322	6.38	6.0E-62	11118235	Human zinc finger protein ZNF191 mRNA, partial cds
8073	20968	34302	3.88	6.0E-62	AI762301.1	Homo sapiens G31-56 protein (G31-56), mRNA
8073	20968	34303	3.88	6.0E-62	AI762301.1	wb4402.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2389291.3
8684	21635	39110	0.84	6.0E-62	AW501194.1	wb4402.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2389291.3
8833	21763	39110	1.82	6.0E-62	11431138	UHF-EP04-wb4402-U11 NIT_MGC_51 Homo sapiens cDNA clone IMAGE:3072833.6
9932	22807	39195	3.49	6.0E-62	AW514383.1	Homo sapiens G31-18 protein (G31-18), mRNA
4309	18310	26434	1.44	5.0E-62	AI000028.1	MR3-510203-130100-025-409 ST0203 Homo sapiens cDNA
2430	18434	28434	0.98	5.0E-62	AJ277351.1	wb51607.x1 NCI CGAP Luc8 Homo sapiens cDNA clone IMAGE:2641704.3 similar to SW_GG98_HUMAN
2430	18434	28434	0.98	5.0E-62	AJ277351.1	CG8379 GCG139del, contains element MER22 repetitive element ;
20401	16434	28435	0.98	5.0E-62	AJ277351.1	Homo sapiens Xq pseudobulbar region, segment 1/2
20401	16434	28435	0.98	5.0E-62	AJ277351.1	Homo sapiens Xq pseudobulbar region, segment 1/2
2031	16628	28623	1.79	5.0E-62	U09487.1	Homo sapiens Xq pseudobulbar region, complete cds
2031	16628	28623	1.79	5.0E-62	U09487.1	Homo sapiens Xq pseudobulbar region, complete cds
3480	16920	28419	2.41	5.0E-62	4800796	Homo sapiens tyrosine receptor 3 (RYR3), mRNA

Table 4

Probe SEQ ID No.	Exon SEQ ID No.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
267600.01	4435	30306	2.23	6.0E-02	AA931093.1	EST - HUMAN	267600.01 Scores: <i>hmla</i> , <i>NHT</i> Homo sapiens cDNA clone IMAGE162344 3' similar to SW NRDC_RAT P47245 NR010153.N
46714	17679		1.16	6.0E-02	AV100887.1	EST - HUMAN	RCF-NT10592-100560-021-H35 NT10589 Homo sapiens cDNA
10143	226.41	33598	0.72	6.0E-02	4560759	NT	Homo sapiens <i>gamma</i> -interleukin receptor 3 (RYR1S) mRNA
91048	225.64	30633	6.76	6.0E-02	AV1140837.1	EST - HUMAN	707/gdabx.NT_MSC_17 Homo sapiens cDNA clone IMAGE2091616 5'
895	139.19	29893	3.34	4.0E-02	AV1161479.1	EST - HUMAN	wt14603.y1 Schneider cell brain 00004 Homo sapiens cDNA clone IMAGE2091616 5'
805	139.19	29894	3.34	4.0E-02	AV1161479.1	EST - HUMAN	ATP SYNTHASE COUPLING FACTOR 8, MITOCHONDRIAL PRECURSOR (HUMAN);
886	139.19	29893	3.58	4.0E-02	AV1161479.1	EST - HUMAN	wt14603.y1 Schneider cell brain 00004 Homo sapiens cDNA clone IMAGE2091616 5'
886	139.19	29894	3.99	4.0E-02	AV1161479.1	EST - HUMAN	ATP SYNTHASE COUPLING FACTOR 8, MITOCHONDRIAL PRECURSOR (HUMAN);
886	139.19	29894	3.99	4.0E-02	AV1161479.1	EST - HUMAN	wt14603.y1 Schneider cell brain 00004 Homo sapiens cDNA clone IMAGE2091616 5'
2482	16484	28488	1.74	4.0E-02	M87900.1	EST - HUMAN	wt2603.01 Scores: <i>NHL</i> , <i>NHLT</i> , <i>1586.3</i> S1 Homo sapiens cDNA clone IMAGE2350369 3' similar to
3459	16500		8.31	4.0E-02	4557893	NT	g0357139.y1 HST11001 Homo sapiens cDNA clone IMAGE2350369 3' similar to
6147	16296	32344	1.64	4.0E-02	4460878	NT	Homo sapiens <i>hmla</i> (carc) family 15 (sodium-dependent deoxyribonucleic transporter), member 2 (SLC19A2) mRNA
6551	16993	32791	3.62	4.0E-02	11429056	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9P), mRNA
7535	24.14	37192	1.76	4.0E-02	1142104.1	NT	Homo sapiens phosphoenolpyruvate synthase 2 (PRP32), mRNA
8082	20084	34316	2.41	4.0E-02	7857057	NT	Homo sapiens polyubiquitin translation initiation factor 2B, adult 2 (b2a, 39AD) (EIF2B32), mRNA
8082	20084	34316	2.41	4.0E-02	7857057	NT	Homo sapiens polyubiquitin translation initiation factor 2B, adult 2 (b2a, 39AD) (EIF2B32), mRNA
8082	20084	34316	2.41	4.0E-02	11428079	NT	Homo sapiens 20S proteasome-associated pseud 1 homolog (POM1), mRNA
8082	20084	34316	2.41	4.0E-02	45003395.1	NT	Homo sapiens mRNA for KIAA1263 protein, partial cds
8082	20084	34316	2.41	4.0E-02	717685.1	NT	Homo sapiens flow-sorted chromosome 6 HindIII fragment, SCQpA1603
8082	20084	34316	2.41	4.0E-02	276766.1	NT	Homo sapiens flow-sorted chromosome 6 HindIII fragment, SCQpA1603
8082	20084	34316	2.41	4.0E-02	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
8082	20084	34316	2.41	4.0E-02	11418322	NT	Homo sapiens cyclin-like EGF-LAG serpin-pa2 G-type receptor 1 (CLLSR1), mRNA
8082	20084	34316	2.41	4.0E-02	11417852	NT	Homo sapiens calcitonin binding protein 1 (KIAA0330), mRNA
8082	20084	34316	2.41	4.0E-02	11417852	NT	Homo sapiens calcitonin binding protein 1 (KIAA0330), mRNA
8082	20084	34316	2.41	4.0E-02	11434050	NT	Homo sapiens low density lipoprotein-related protein 2 (LDLR2), mRNA
8082	20084	34316	2.41	4.0E-02	11434050	NT	Homo sapiens low density lipoprotein-related protein 2 (LDLR2), mRNA

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Probe SEQ ID NO:	Exon ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
77	13101	26102	1.03	3.0E-62	4527794	NT	Homo sapiens neurofilament 2 (beta) (NF2) mRNA
3068	13104	26040	0.74	3.0E-62	AB040608.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
3093	16144	26041	0.74	3.0E-62	AB040608.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
3743	16795	26064	2.21	3.0E-62	X02953.1	NT	Human optic tinnit-related processed pseudogene
5002	18079	30526	1.22	3.0E-62	AF222910.1	NT	Homo sapiens alpha-mannosidase semaphorin 3A synthase mRNA, complete cds
9104	22032	35387	0.81	3.0E-62	AB027735.1	EST_HUMAN	W63104.41 NC1_GGAP_NMT1 Homo sapiens cDNA clone IMAGE:226669.8 similar to contains TIR-12 TIR negative element 1
1289	14284	27240	1.74	2.0E-62	AL162844.2	NT	Homo sapiens chromosome 21 segment H521C084
8305	12109	34603	0.42	2.0E-62	AA307460.1	EST_HUMAN	EST117874 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8634	22422	35626	6.06	2.0E-62	BF329911.1	EST_HUMAN	RC2-BN284-30060-031-408 BNC284 Homo sapiens cDNA
8634	22422	35626	5.00	2.0E-62	BF329911.1	EST_HUMAN	RC2-BN284-30060-031-408 BNC284 Homo sapiens cDNA
10688	20985		4.56	2.0E-62	A1724698.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
12113	24634		8.4	2.0E-62	BF330976.1	EST_HUMAN	OV17B0287-031102017-403 BT0287 Homo sapiens cDNA
1070	14174	27044	1.2	1.0E-62	AF248563.1	NT	Homo sapiens intracrin 2 (SRD18) mRNA, complete cds
1588	14677	27567	16.22	1.0E-62	L17810.1	NT	Homo sapiens DGP41A TP carrier protein (ANT-2) gene, complete cds
2657	16059	28069	1.24	1.0E-62	AL038444.1	EST_HUMAN	DKF2569F104.1T 566 (yprym. h62) Homo sapiens cDNA clone DNF2p66910.4 5'
4480	17471		0.60	1.0E-62	BE169433.1	EST_HUMAN	OV14-T0492-35000-135-112 H10483 Homo sapiens cDNA
4644	17690	30515	1.47	1.0E-62	692320	NT	Homo sapiens lysozymal protein FL39212 (FL20212) mRNA
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 5 (CUSP9), fibronectin protein L18a (R14.18a), Cse2/Cadmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT18), COM protein (COM), adrenomedullary thyro protein >
6542	18595	32770	1.01	1.0E-62	U82111.2	NT	COM protein (COM), adrenomedullary thyro protein >
7494	20433	32710	0.98	1.0E-62	AA40260.1	EST_HUMAN	450502.31 Stralagans fetal vitra 937202 Homo sapiens cDNA clone IMAGE:388904 3'
7503	20434	32710	2.54	1.0E-62	AA72678.1	EST_HUMAN	26910.11 Source, fetal, heart, N84H15W Homo sapiens cDNA clone IMAGE:406771 3'
7933	20414	32726	2.64	1.0E-62	AA72678.1	EST_HUMAN	26910.11 Source, fetal, heart, N84H15W Homo sapiens cDNA clone IMAGE:406771 3'
8010	20536	33006	1.79	1.0E-62	7682268	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
8010	20536	33007	1.79	1.0E-62	7682268	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
8948	23572	35943	2.32	1.0E-62	X15533.1	NT	H sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Ecom 9
9948	23572	35943	2.32	1.0E-62	X15533.1	NT	H sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Ecom 9
10086	27819	39095	3.28	1.0E-62	AA489170.1	EST_HUMAN	aa33406.51 NC1_G3AP (S-81 Homo sapiens cDNA clone IMAGE:810955 3'
11855	24726	39218	2.2	1.0E-62	Z78698.1	NT	H sapiens: flow-sorted chromosome 6 HindIII fragment, SC04P1429
12276	28073	39561	1.41	1.0E-62	11142035	NT	Homo sapiens cohesin component Rtp-16 (LOC98915), mRNA
12802	28427		3.45	1.0E-62	11148322	NT	Homo sapiens cohesin EGF-LAG seven-pass G-type receptor 1 (CELSR1), mRNA
12802	28427		2.78	1.0E-62	11148322	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP-2), mRNA

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390	13446	26357	2.34	9.0E-63	AI1616405.1	EST_HUMAN	Q143T022-161180-337-653 S10234 Homo sapiens cDNA
2398	13374		1.56	9.0E-63	CB18196.1	EST_HUMAN	C19189 Human placenta cDNA (1746mers) Homo sapiens cDNA clone GEN-58810.6
4176	17148	30022	11.76	9.0E-63	AB002346.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
8424	18421	50095	4.19	9.0E-63	AB002343.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
9632	16720	31531	1.49	9.0E-63	Y15053.1	NT	Homo sapiens nuclear ribonucleoproteins (RNP2), mRNA
7548	24484	33773	3.89	9.0E-63	U1428895	NT	Homo sapiens mRNA for 789 bp
3352	22266	34361	0.93	9.0E-63	4653344	NT	Homo sapiens nucleoside diphosphate kinase 3 (NDPK3), mRNA
6601	21631	35165	1.63	9.0E-63	11421103	NT	Homo sapiens Rho-associated (RhoGDI-like) domain family 2 (RASSF2), mRNA
2697	16376	26376	1.86	9.0E-63	4657734	NT	Homo sapiens inositol carboxyl transferase 1 (INCA), nuclear gene encoding mitochondrial protein, mRNA
2327	15302	26340	1.93	9.0E-63	5021810	NT	Homo sapiens L2-inducible c-fos (L2), nuclear gene
3323	19463	20463	3.97	9.0E-63	AF193348.1	NT	Gallus gallus DnaH2 protein (DnaH2) mRNA, complete cds
3322	19560	20463	3.97	9.0E-63	AF193348.1	NT	Gallus gallus DnaH2 protein (DnaH2) mRNA, complete cds
4395	17378	30243	3.76	9.0E-63	AL163268.2	NT	Homo sapiens chromosome 21 segment H32:10583
997	14007		2.12	7.0E-63	41971937.1	EST_HUMAN	wm5651.1 NCI_GCAP_L2 Homo sapiens cDNA clone IMAGE2459008.3
5523	18002		84.77	6.0E-63	AA420603.1	EST_HUMAN	nc5502.1 NCI_GCAP_P11 Homo sapiens cDNA clone IMAGE2459008.3
8432	22300	35729	0.7	6.0E-63	11528494	NT	RIBOSOMAL PROTEIN L16 (RPL16), mRNA
3300	16410	25012	0.85	4.0E-63	AL163278.2	NT	Homo sapiens G-protein-coupled receptor 81 (GPR81), mRNA
3678	16006	25765	1.66	4.0E-63	AB014607.1	NT	Homo sapiens chromosome 21 segment H32:1078
3676	16005	25766	1.66	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
9716	16751	32955	2.22	4.0E-63	AW176072.1	EST_HUMAN	CHS-5T0585-190100-672-408 BT0593 Homo sapiens cDNA
9715	16751	32956	2.22	4.0E-63	AW176072.1	EST_HUMAN	CHS-5T0585-190100-672-408 BT0593 Homo sapiens cDNA
11572	24481	37648	1.76	4.0E-63	AW147004.1	EST_HUMAN	UHH-BT-aba-a-920-QJ-1 NCI_GCAP_S343 Homo sapiens cDNA clone IMAGE271462.3
11672	24481	37649	1.76	4.0E-63	AW147004.1	EST_HUMAN	UHH-BT-aba-a-920-QJ-1 NCI_GCAP_S343 Homo sapiens cDNA clone IMAGE271462.3
1650	14670	27049	1.24	3.0E-63	AB018200.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
2630	16019	28814	1.43	3.0E-63	J00310.1	NT	Human T-cell leukemia virus type 1
2699	14301	27249	8.62	3.0E-63	0003903	NT	Human telomerase RNA gene 1
6748	19762	33984	30.82	3.0E-63	11146910	NT	Homo sapiens zinc finger protein 144 (ZNF144), mRNA
10228	23119	59621	0.92	3.0E-63	BE186188.1	EST_HUMAN	Homo sapiens leucocyte-specific carcinoma antigen gene 52 (LOC639528), mRNA
10228	23119	59622	0.92	3.0E-63	BE186188.1	EST_HUMAN	UHH-BT-aba-a-920-QJ-1 NCI_GCAP_S343 Homo sapiens cDNA clone IMAGE271462.3
204	15303	26219	1.22	2.0E-63	U07804.1	NT	Human DNA topoisomerase 1 mRNA, partial cds
211	13310	26227	1.47	2.0E-63	4685226	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA

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Probe SEQ ID No.	Exon SEQ ID No.	ORF SEQ ID	Expression Signal	Modi SizeR (Top) HT BLAST E Value	Top HT Accession No.	Top HT Database Source	Top HT Descriptor
6042	16104	32234	0.75	0.0E+00	11422180	NT	Homo sapiens calcitriol receptor (CALR), mRNA
7693	35640	33828	0.54	1.1E-07	11529070	NT	Homo sapiens mesorhynchus homo box 1 (MEOX1), mRNA
7693	35640	33828	2.54	0.0E+00	11529070	NT	Homo sapiens mesorhynchus homo box 1 (MEOX1), mRNA
8697	22792	39171	8.48	0.0E+00	11420558	NT	Homo sapiens acyl-CoA synthetase (LACS5602), mRNA
10037	22837	35258	1.17	0.0E+00	114274763	1	Homo sapiens progressive ataxia-like protein (A-N1), mRNA, complete cds
10249	10249	27131	2.23	0.0E+00	5764751	NT	HIC1 human, brain, mRNA, 2715 nt
11298	21134	37652	4.89	0.0E+00	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
11438	16217	37695	4.89	0.0E+00	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
11438	16217	37695	1.07	0.0E+00	AW0264451	EST_HUMAN	wt13033.v1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:3526433 5'
12462	23309	31553	3.71	0.0E+00	AW0264451	EST_HUMAN	wt13033.v1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:3526433 5'
845	13020	28835	2.55	0.0E+00	11420189	NT	Homo sapiens chromosome 21 unknown mRNA
845	13020	28835	2.55	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1396	13969	27532	2.55	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1396	13969	27532	2.55	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1444	1444	27433	1.71	0.0E+00	420933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMFR) gene, complete cds
1444	1444	27433	1.71	0.0E+00	420933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMFR) gene, complete cds
1444	1444	27433	1.71	0.0E+00	420933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMFR) gene, complete cds
1740	1740	27738	1.35	0.0E+00	U83698.1	NT	Human (3) mt protein homolog mRNA, complete cds
2874	14830	27463	3.68	0.0E+00	7862205	NT	Homo sapiens KIA00818 gene product (KIA00818), mRNA
2874	14830	27463	3.68	0.0E+00	7862205	NT	Homo sapiens KIA00818 gene product (KIA00818), mRNA
4043	17010	26968	6.61	0.0E+00	AF017433.1	NT	Homo sapiens putative transcription factor CHS3 (CHES3) mRNA, partial cds
4197	17215	30082	1.08	0.0E+00	AF017433.1	NT	Homo sapiens mRNA for KIA00603 protein, partial cds
8344	21245	36962	0.95	0.0E+00	AF074207.1	EST_HUMAN	001850352F NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3543507 5'
11262	21245	36962	2.14	0.0E+00	AF074207.1	EST_HUMAN	RCS-370167-120200-015-403 S10179 Homo sapiens cDNA
1252	21245	37053	2.14	0.0E+00	AF074207.1	EST_HUMAN	RCS-370167-120200-015-403 S10179 Homo sapiens cDNA
1252	21245	37053	2.14	0.0E+00	AF074207.1	EST_HUMAN	TC1895 Homo sapiens placenta cDNA (Tf1895) Homo sapiens cDNA
21413	15224	28227	10.14	0.0E+00	AF074207.1	EST_HUMAN	001850352F NIH_MGC_7 Homo sapiens cDNA clone GEN546209 5'
3209	16349	26250	0.93	0.0E+00	AF074207.1	EST_HUMAN	AV1717174 DCA Homo sapiens cDNA clone DCAAMC01 5'
3504	16342	28412	1.54	0.0E+00	AF11714.1	EST_HUMAN	AV1717174 DCA Homo sapiens cDNA clone DCAAMC01 5'
3504	16342	28412	1.54	0.0E+00	AF11714.1	EST_HUMAN	H sapiens isoform 1 gene for L-type calcium channel, exon 28
6318	19738	32537	1.42	0.0E+00	220737.1	NT	U49F-6P49c-05-05-DJ117 NIH_MGC_81 Homo sapiens cDNA
6660	19805	32819	0.95	0.0E+00	AF000861.1	EST_HUMAN	RCS-FN001C-200900-011-511 FN0018 Homo sapiens cDNA
6760	18033	32014	0.95	0.0E+00	BF170893.1	EST_HUMAN	Homo sapiens p67 mdr1a protein OMT39 (GOLGA2) mRNA, complete cds
9035	21954	35523	1.85	0.0E+00	AF248953.1	NT	Homo sapiens p67 mdr1a protein OMT39 (GOLGA2) mRNA, complete cds
9035	21954	35523	1.89	0.0E+00	AF248953.1	NT	Homo sapiens p67 mdr1a protein OMT39 (GOLGA2) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar Database Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6092	21891	35345	2.84	3.0E-64	BE20621.1	EST_HUMAN	h07x12.1Y1 NH_MGC_15 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb.L08030 DNA
6092	21891	35344	2.81	3.0E-64	BE20621.1	EST_HUMAN	PROTEIN HOMOLOG 2 (HUMAN)
6091	22699	92353	1.78	3.0E-64	AL103240.2	NT	h07x12.1Y1 NH_MGC_15 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb.L08030 DNA
6091	22699	92354	1.78	3.0E-64	AL103240.2	NT	PROTEIN HOMOLOG 2 (HUMAN)
10046	22691	92349	0.76	3.0E-64	AF187394.1	EST_HUMAN	Homo sapiens chromosome 21 segment H8210348
10046	22691	92350	0.76	3.0E-64	AF187394.1	EST_HUMAN	Homo sapiens chromosome 21 segment H8210348
12115	24696	39489	2.03	3.0E-64	AL103227.2	NT	EST1358493 IMAGE: rescapases, MAGO Homo sapiens cDNA
11115	11197	27095	0.60	2.0E-64	AF005941.1	EST_HUMAN	EST1358493 IMAGE: rescapases, MAGO Homo sapiens cDNA
1424	14493	27409	1.96	2.0E-64	4157701	NT	462303.1 Source: testis, NBT Homo sapiens cDNA clone IMAGE:1031161 3'
2502	15592	28566	2.34	2.0E-64	AF027030.1	EST_HUMAN	Homo sapiens p27E12.1a2 cap-binding protein (4EHP) mRNA
2502	15592	28567	2.34	2.0E-64	AF027030.1	EST_HUMAN	1.1 repetitive element
2503	15597	28567	4.95	2.0E-64	AF153246.2	NT	Homo sapiens chromosome 21 segment H8210348
2503	15597	28567	4.95	2.0E-64	AF153246.2	NT	Homo sapiens chromosome 21 segment H8210348
2508	19232	32452	2.09	2.0E-64	AF113307.1	EST_HUMAN	Homo sapiens chromosome 21 segment H8210348
4460	19534	32712	1.08	2.0E-64	AF113307.1	NT	EST1358493 IMAGE: rescapases, MAGO Homo sapiens cDNA
6760	19764	33036	5.25	2.0E-64	BF965637.1	EST_HUMAN	60212347.1 NH_MGC_06 Homo sapiens cDNA clone IMAGE:4250306 5'
6877	19648	33123	1.35	2.0E-64	AF175837.1	EST_HUMAN	022603.1 Source: testis, NBT Homo sapiens cDNA clone IMAGE:1079717 3'
6968	20075	33766	3.9	2.0E-64	MT7185.1	NT	H. sapiens dopaminergic receptor D5 pseudogene 1, partial cds
8320	21225	34560	0.48	2.0E-64	11451054	NT	H. sapiens stem 2-binding protein 1 (A25P1), mRNA
8405	21306	34641	0.83	2.0E-64	AF169575.1	EST_HUMAN	QV1-H10413-010200-050-h12 H10413 Homo sapiens cDNA
8226	22154	35505	0.80	2.0E-64	11454008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plestin) (LCP1), mRNA
8226	22154	35505	0.80	2.0E-64	11454008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plestin) (LCP1), mRNA
9772	22699	36062	1.20	2.0E-64	AF1132507.1	EST_HUMAN	EST1357070 HRP4 Homo sapiens cDNA clone NT2P-400109 5'
10445	23373	36766	0.56	2.0E-64	T03997.1	EST_HUMAN	EST1357070 HRP4 Homo sapiens cDNA clone NT2P-400109 5'
10445	23373	36766	0.56	2.0E-64	T03997.1	EST_HUMAN	EST1357070 HRP4 Homo sapiens cDNA clone NT2P-400109 5'
11201	24127	37574	2.3	2.0E-64	BF928114.1	EST_HUMAN	EST1357070 HRP4 Homo sapiens cDNA clone NT2P-400109 5'
11489	24401	37951	4.81	2.0E-64	AF022911.1	EST_HUMAN	60212347.1 NH_MGC_06 Homo sapiens cDNA clone IMAGE:4250306 5'
11489	24401	37951	4.81	2.0E-64	AF022911.1	EST_HUMAN	60212347.1 NH_MGC_06 Homo sapiens cDNA clone IMAGE:4250306 5'
11682	24593	38053	1.71	2.0E-64	AF169473.1	EST_HUMAN	Wnt1006.1 NCI_OGAP_UH Homo sapiens cDNA clone IMAGE:2452211 3'
12351	25167	31873	2	2.0E-64	6997397	NT	Wnt1006.1 NCI_OGAP_UH Homo sapiens cDNA clone IMAGE:2452211 3'
12718	25424		1.80	2.0E-64	HE5162.1	EST_HUMAN	PK2-SN0016-226000-002-e12 SN018 Homo sapiens cDNA
277	13372	20266	1.52	1.0E-64	AF231919.1	NT	Homo sapiens period (Drosophila) homolog 3 (PER-3), mRNA
277	13372	20266	1.52	1.0E-64	AF231919.1	NT	CHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22_133 5'

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Probe SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
7194	33438	0.63	6.0E-05	4504003	NT	-c-mo sapiens interferon-related developmental regulator 1 (IFRD1), mRNA	
10946	23520	37256	1.2E-05	AF036061	NT	Multiple adjacent associated retrovirus polyprotein (pol) mRNA, partial cds	
206	26222	1.36	4.0E-05	AF110419.1	EST_HUMAN	DNAI2/2707/G108.1770 (synonym: hamy2). Homo sapiens cDNA, clone DKFZ2767G108.5	
709	13320	20756	1.18	4.0E-05	AB294408.1	EST_HUMAN	gri66001.x1 Scores_placenta_Budweisses_ZNHHP800W Homo sapiens cDNA, clone IMAGE:181900.3
709	13826	20757	1.18	4.0E-05	AB294408.1	EST_HUMAN	gri66001.x1 Scores_placenta_Budweisses_ZNHHP800W Homo sapiens cDNA, clone IMAGE:181900.3
11038	14148	27085	0.96	4520738	NT	-c-mo sapiens fingrin X mental retardation, autosomal homolog 1 (FXR1), mRNA	
1604	14535	27486	1.18	4.0E-05	4500933	EST_HUMAN	-c-mo sapiens ribosomal protein L34 (RPL34) mRNA
2359	15050	29360	1.1	4.0E-05	BE221460.1	EST_HUMAN	NZ5604.041 NC: CGAP_Mer16 Homo sapiens cDNA, clone IMAGE:3171102.3
2359	15050	29360	1.1	4.0E-05	BE221460.1	EST_HUMAN	NZ5604.041 NC: CGAP_Mer16 Homo sapiens cDNA, clone IMAGE:3171102.3
4029	17009	29945	1.39	4.0E-05	AF1031195.1	EST_HUMAN	RGZ-BN0033.110200-G13-a03 BN0033 Homo sapiens cDNA
6368	18444	32613	4.62	4.0E-05	AF4533093.1	NT	Homo sapiens mRNA for KIAA1237 protein, partial cds
6368	18444	32613	4.62	4.0E-05	AF4533093.1	NT	Homo sapiens mRNA for KIAA1237 protein, partial cds
7478	20141	33684	0.39	4.0E-05	AF030372.1	NT	Homo sapiens cytoskeletal binding protein-related protein 3 (ORP3) mRNA, complete cds
7478	20141	33684	0.39	4.0E-05	AF030372.1	NT	Homo sapiens cytoskeletal binding protein-related protein 3 (ORP3) mRNA, complete cds
7598	20524	33813	2.01	4.0E-05	U18078.1	NT	Human ubiquitin 27 gene, exons 10 and 11, and L1 and L2 repeats
7990	20501	34218	0.67	4.0E-05	U40372.1	NT	Homo sapiens hypothetical protein FLJ22037 (FLJ22037), mRNA
7990	20501	34217	0.67	4.0E-05	U40372.1	NT	Homo sapiens hypothetical protein FLJ22037 (FLJ22037), mRNA
8335	21240	34572	0.56	4.0E-05	U36565.1	NT	Human 3'5' cyclic nucleotide phosphodiesterase (PDE3C) mRNA, partial cds
8424	21369	34983	0.74	4.0E-05	U45795.1	NT	Human MOP- annexin A5 (MOP-AN), complete cds
8424	21369	34983	0.74	4.0E-05	U45795.1	NT	Human MOP- annexin A5 (MOP-AN), complete cds
8424	21369	34983	0.74	4.0E-05	U45795.1	NT	Human MOP- annexin A5 (MOP-AN), complete cds
6688	22814	35957	0.77	4.0E-05	U142512	NT	Homo sapiens nrl (Chick) cDNA, 2.2 kb (NELL3), mRNA
6688	22814	35957	0.77	4.0E-05	U142512	NT	Homo sapiens nrl (Chick) cDNA, 2.2 kb (NELL3), mRNA
11053	29937	1.62	4.0E-05	U275746.2	NT	Homo sapiens WEE1, gene for protein kinase and partial ZNF-143 gene for zinc finger transcription factor	
11542	24423	37915	1.63	4.0E-05	AF118450.1	NT	Homo sapiens WEE1, gene for protein kinase and partial ZNF-143 gene for zinc finger transcription factor
100	13214	26127	2.79	3.0E-05	AF031076.1	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
101	13214	26127	2.79	3.0E-05	AF031076.1	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1260	13840	4.63	3.0E-05	Z79832.1	NT	Homo sapiens H2F3 mRNA for zinc finger protein	
8445	27850	1.63	3.0E-05	AF00092.1	EST_HUMAN	gri63873.1 Scores_testis_NHT Homo sapiens cDNA, clone IMAGE: 63873.3 similar to zinc element	
3321	15307	22265	1.13	4.0E-05	45044903	EST	NSR1 repetitive element:
3321	15307	22265	1.13	4.0E-05	45044903	EST	NSR1 repetitive element:
3295	22703	1.54	3.0E-05	AF00092.1	EST_HUMAN	gri63873.1 Scores_testis_NHT Homo sapiens cDNA, clone IMAGE: 63873.3 similar to zinc element	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top 5) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4780	17795	30628	1.22	3.0E-56	6912383	NT	Homo sapiens 140b GTPase activating protein (GAP and centrosome associated) (GAPCEV1), mRNA
11871	29467	96977	1.63	3.0E-55	BE767366.1	EST_HUMAN	9147/06087 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3822403 5'
10677	23662	37398	10.67	3.0E-65	AA430006.1	EST_HUMAN	265500671 Soares, Jents, NIH Homo sapiens cDNA clone IMAGE:101042 5'
3454	16504	29409	8.88	2.0E-56	BF660284.1	EST_HUMAN	0021600257 NIH_MGC_33 Homo sapiens cDNA clone IMAGE:426860 5'
4035	17062	25951	0.75	2.0E-55	AF114683.1	NT	Homo sapiens Interleukin 2 and Interleukin 12 (IL2/IL12) mRNA, complete cds
8515	16948		5.77	2.0E-56	BE26373.1	EST_HUMAN	6011933537 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3841012 5'
7492	25432	33711	22.99	2.0E-60	BF576222.1	EST_HUMAN	6012343597 NIH_MGC_31 Homo sapiens cDNA clone IMAGE:4262293 5'
8404	22332	35955	1.17	2.0E-56	AC024483.1	NT	Homo sapiens mRNA for FLJ30356 protein, partial cds
9404	22332	35958	1.17	2.0E-55	AC024483.1	NT	Homo sapiens mRNA for FLJ30356 protein, partial cds
12204	25124		5.37	2.0E-55	AA307604.1	EST_HUMAN	EST1174755 Cowan carcinoma (HCC) cell line Homo sapiens cDNA, 5' end similar to endogenous
12704	25728		2.48	2.0E-55	BE452363.1	EST_HUMAN	6018403357 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4072769 5'
93	13206		0.80	2.0E-55	BE72554.1	EST_HUMAN	6017554987 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4028501 5'
952	13031	28540	1.48	1.0E-55	7627495	NT	Homo sapiens putative RAB GTP/GTP exchange factor homologue (RABEX3), mRNA
1686	14688	27859	1.11	1.0E-55	AB028933.1	NT	Homo sapiens DLEC1 to ORC1L4 gene region, section 12 (DLEC1, ORC1L4, ORC1L4 gene, complete cds)
2324	18071	26072	0.97	1.0E-56	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
3430	18471	29375	0.77	1.0E-55	BE46681.1	EST_HUMAN	162440521 NCI CGAP_G33 Homo sapiens cDNA clone IMAGE:328898 5'
4034	17109	20687	1.76	1.0E-55	4504032	NT	Homo sapiens glycocalyx 4 (GPC4) mRNA
4034	17109	20686	1.76	1.0E-55	4504032	NT	Homo sapiens glycocalyx 4 (GPC4) mRNA
4502	17316	30183	2.3	1.0E-56	AV1023340.1	EST_HUMAN	w008006.x1 NCI CGAP_G34 Homo sapiens cDNA c clone IMAGE:2543752 3'
4502	17316	30183	2.3	1.0E-56	AV1023340.1	EST_HUMAN	w008006.x1 NCI CGAP_G34 Homo sapiens cDNA c clone IMAGE:2543752 3'
5498	18249	31389	0.58	1.0E-55	BE089559.1	EST_HUMAN	Q10-8170702-170400-194-409 B10702 Homo sapiens cDNA
5498	18249	31390	0.58	1.0E-55	BE089559.1	EST_HUMAN	Q10-8170702-170400-194-409 B10702 Homo sapiens cDNA
5595	18739	31646	0.83	1.0E-56	A0249738.1	EST_HUMAN	Q88807.x1 Soares, NFL_T_OEC_31 Homo sapiens cDNA clone IMAGE:1854109 3' similar to TR_007823
8829	21769	35104	1.85	1.0E-56	AV1520481.1	EST_HUMAN	QV2-370286-140200-942-F12 ST0298 Homo sapiens cDNA
8829	21769	35105	1.85	1.0E-56	AV1520481.1	EST_HUMAN	QV2-370286-140200-942-F12 ST0298 Homo sapiens cDNA
8857	21787	36136	0.87	1.0E-56	BE732118.1	EST_HUMAN	6016661247 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012 5'
8857	21787	36136	0.87	1.0E-56	BE732118.1	EST_HUMAN	6016661247 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012 5'
8854	21824	35175	2.44	1.0E-56	AV141296.1	EST_HUMAN	AU1412395 THYROT1 Homo sapiens cDNA clone THY2100056 5'
8854	21824	35176	2.44	1.0E-56	AV141296.1	EST_HUMAN	AU1412395 THYROT1 Homo sapiens cDNA clone THY2100056 5'
9365	22327	35859	0.83	1.0E-56	BF669707.1	EST_HUMAN	0021362037 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:4263319 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9571	22468	33891	2.05	1.0E-45	AF120040.1	EST_HUMAN	AL125040 N22RP27 Homo sapiens cDNA clone N22RP20474.9
9571	22468	33892	2.05	1.0E-45	AF120040.1	EST_HUMAN	AL125040 N22RP27 Homo sapiens cDNA clone N22RP20474.9
9582	22820		3.43	1.0E-45	11431994	NT	Homo sapiens insulin 1.4.2-dephosphatase receptor, type 1 (TIRP1), mRNA
10010	22827	33214	6.50	1.0E-45	AF107161.1	EST_HUMAN	q55602.x1 Sores, testis, NMT Homo sapiens cDNA clone IMAGE:1753460.3 similar to gb:U25961.ZINC
10397	23286	36708	1.5	1.0E-45	AF153783.1	EST_HUMAN	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
10781	23677	37107	0.72	1.0E-46	AA09559.1	EST_HUMAN	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
11043	23927	37398	1.14	1.0E-45	AB037832.1	NT	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
11054	24025	37468	2.2	1.0E-45	AB037832.1	NT	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
11218	24142	37924	2.62	1.0E-46	AB037832.1	NT	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
11570	24479	37945	2.58	1.0E-45	B-532707.1	EST_HUMAN	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
11899	24606	38038	2.82	1.0E-46	AB210171.1	EST_HUMAN	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
12283	25154		0.51	1.0E-46	11148041	NT	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
12458	25208	31850	2.4	1.0E-46	11148041	NT	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
13189	26068	32068	2.8	1.0E-46	AF140311.1	NT	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
1327	14333	20086	5.81	0.0E-46	AF140311.1	NT	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
1602	14333	20886	0.8	0.0E-46	AF140311.1	NT	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
3071	15059	20886	0.8	0.0E-46	AF140311.1	NT	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
3071	15059	20886	0.8	0.0E-46	AF140311.1	NT	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
4472	17453	30341	1.30	0.0E-46	AF24655.1	EST_HUMAN	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
4472	17453	30342	1.36	0.0E-46	AF24655.1	EST_HUMAN	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
4472	17453	30343	1.36	0.0E-46	AF24655.1	EST_HUMAN	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
9003	21932		0.53	0.0E-46	BC178553.1	EST_HUMAN	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
11599	24598	37075	3.24	0.0E-46	X09181.1	NT	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
11944	14425	27375	1.81	0.0E-46	BC044410.1	EST_HUMAN	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
5264	18240	31051	0.98	0.0E-46	BC093844.1	EST_HUMAN	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
5264	18240	31051	0.98	0.0E-46	BC093844.1	EST_HUMAN	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
9534	22740	36121	1.31	0.0E-46	11420567	EST_HUMAN	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
817	13872	28669	1.31	0.0E-46	9970916	NT	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9
1785	14781	27701	0.92	0.0E-46	AF07788.1	EST_HUMAN	PHOGER PROTEIN 5 (HUMAN) cDNA clone N22RP20474.9

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Probe SEQ ID NO.	Exon SEQ ID NO.	Q95 SEQ ID NO.	Expression Signal	Mean Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2300	15378	28814	4.89	4.0E-66	X98211.1	NT	H sapiens DNA for endogenous ribosomal like element
2405	15497		5.05	4.0E-66	AJ223364.1	NT	Homo sapiens germ-line DNA upstream of Aicardi like
4898	17895		2.61	4.0E-66	BC55497	NT	Human endogenous retrovirus, complete genome
5742	18815	31911	3.4	4.0E-66	U1428643	NT	Homo sapiens myeloblasts (myeloblasts) dehydrogenase (NAD+ dependent), malonyl/ethyl/ethyl oleate
5848	19015	32135	0.77	4.0E-66	AJ19259118.1	EST_HUMAN	cytochrome P-450 2C9 (CYP2C9), mRNA
7071	21432	30990	1.50	4.0E-66	U19259118.1	EST_HUMAN	CYP2C9-1 (CYP2C9-1) mRNA
11817	24738	38226	1.83	4.0E-66	AJ19254731.1	EST_HUMAN	EST177546 IMAGE read, sequence, human Homo sapiens cDNA
7491	25451	33710	7.60	4.0E-66	U978168.1	NT	Homo sapiens cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
8077	18815	31911	0.9	4.0E-66		NT	Homo sapiens methyl/lysine tetrahydrofolate dehydrogenase (NAD+ dependent), malonyl/ethyl/ethyl oleate
8055	21432	30990	7.27	4.0E-66	U1428643	NT	cytochrome P-450 2C9 (CYP2C9), mRNA
9121	21432	30990	1.50	4.0E-66	X97147.1	NT	Homo sapiens myeloblasts (myeloblasts) dehydrogenase (NAD+ dependent), malonyl/ethyl/ethyl oleate
11817	24738	38226	1.83	4.0E-66	AJ202315.1	NT	Human endogenous retrovirus PHE-1 (ERV6)
1448	14479	27439	6.99	3.0E-66	4502066	NT	Homo sapiens retinoblastoma protein (p107), partial cds
1448	14479	27439	8.99	3.0E-66	4502066	NT	Homo sapiens retinoblastoma protein (p107), partial cds
1559	15017	28007	1.08	3.0E-66	N55323.1	EST_HUMAN	Homo sapiens retinoblastoma protein (p107), partial cds
1909	15017	28008	1.08	3.0E-66	N55323.1	EST_HUMAN	Homo sapiens retinoblastoma protein (p107), partial cds
1909	15017	28009	1.08	3.0E-66	N55323.1	EST_HUMAN	Homo sapiens retinoblastoma protein (p107), partial cds
2767	15748	29743	2.83	3.0E-66	U1141890	NT	Homo sapiens retinoblastoma protein (p107), partial cds
3102	18212	25102	6.3	3.0E-66	AB020660.1	NT	Homo sapiens retinoblastoma protein (p107), partial cds
5993	18127	31632	0.79	3.0E-66	U1141890	NT	Homo sapiens retinoblastoma protein (p107), partial cds
5789	18942	31644	0.77	3.0E-66	U1141890	NT	Homo sapiens retinoblastoma protein (p107), partial cds
5941	19046	32169	2.50	3.0E-66	U1141890	NT	Homo sapiens retinoblastoma protein (p107), partial cds
5931	19046	32170	2.50	3.0E-66	U1141890	NT	Homo sapiens retinoblastoma protein (p107), partial cds
7530	20760	34063	0.52	3.0E-66	X62211.1	NT	Homo sapiens retinoblastoma protein (p107), partial cds
10095	23917	36960	0.52	3.0E-66	AJ2024483.1	NT	Homo sapiens retinoblastoma protein (p107), partial cds
10241	23132	36936	0.79	3.0E-66	U1141718	NT	Homo sapiens retinoblastoma protein (p107), partial cds
10575	23451	36963	0.9	3.0E-66	U1141718	NT	Homo sapiens retinoblastoma protein (p107), partial cds

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Protein Accession NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Tup-Hit Descriptor	
11877	26481	39059	2.0E-07	BE26741.1	EST_HUMAN	00175762P1.NH_MGC_17 Homo sapiens cDNA clone IMAGE:3537038 5'	
11886	26482	37428	2.3E-07	BFF37749.1	EST_HUMAN	NL2-1203-00090-001~c02 TN0103 Homo sapiens cDNA	
12573	25702	31570	1.6E-07	11414818	EST_HUMAN	Homo sapiens thyroid autoantigen TM04 (Ku antigen) (C22P1), mRNA	
12850	26461	31780	1.4E-07	11471877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA	
272	13367	26283	1.7E-07	AA024199	NT	Homo sapiens apoli (A4) precursor protein (protease nexin-1l, Alzheimer disease) (APP), mRNA	
731	13769	26713	1.7E-07	AJ702784.1	EST_HUMAN	z6B004.01 Soybean "edam" fme, soybean, NFLS_51 Homo sapiens cDNA clone IMAGE:448015 3'	
2169	15200	28205	1.3	E0E-08	BE870732.1	00144955P1.NH_MGC_05 Homo sapiens cDNA clone IMAGE:3852254 5'	
3638	16068	29848	6.6E-08	EA290446.1	EST_HUMAN	z42201.01 Striatagene NT neuron (6637233) Homo sapiens cDNA clone IMAGE:948163 3' similar to SW.SAV_SULAC 007590 SAV PROTEIN; 1	
3830	16066	28849	6.6E-08	EA290446.1	EST_HUMAN	z42201.01 Striatagene NT neuron (6637233) Homo sapiens cDNA clone IMAGE:948163 3' similar to SW.SAV_SULAC 007590 SAV PROTEIN; 1	
8048	21611	34492	0.6E-08	AA304005.1	EST_HUMAN	w660303.01 NCI-QOMP_P208 Homo sapiens cDNA clone IMAGE:2512660 3'	
7976	20866	34208	0.47	E1E-08	AJ795543.1	EST_HUMAN	EST3386573.MAGE_resuspensions_MAGE Homo sapiens cDNA
7975	20866	34209	0.47	E1E-08	AJ795543.1	EST_HUMAN	EST3386573.MAGE_resuspensions_MAGE Homo sapiens cDNA
10920	23815	37244	2.47	E0E-08	11422608	NT	Homo sapiens brainpan A-subunit guanine nucleotide-exchange protein 2 (B/C2), mRNA
11588	24468	37590	1.9E-08	E0E-08	F1593001.1	NT	Homo sapiens latrunculin inhibitory receptor 2-61 (LRX221) and other members (receptor 2-3-2 (NR222) genes, part 1)
12852	25403	2044	6.0E-08	BE272554.1	EST_HUMAN	pat 145305P1.NH_MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5'	
844	13859	28837	3.8E-08	EA273191.1	NT	Homo sapiens chromosome 31 unknown mRNA	
844	13859	28838	3.8E-08	EA273191.1	NT	Homo sapiens chromosome 31 unknown mRNA	
2831	18320	28515	0.003	E0E-08	AJ231911.1	NT	Homo sapiens chromosome 31 unknown mRNA
3190	12330	29734	1.9E-08	E0E-08	AJ537319.1	NT	Homo sapiens mRNA for KIAA1461 protein, partial cds
4277	71291	30296	0.71	E0E-08	AB282967	NT	Homo sapiens retinoldehydrogenase-binding protein 2 (RBP2), mRNA
7028	30341	32396	0.71	E0E-08	7019912.1	NT	Homo sapiens RABA3 "interacting protein (rab33) iso1 (RAB33L1), mRNA
7128	30341	32396	0.71	E0E-08	7019912.1	NT	Homo sapiens RABA3 "interacting protein (rab33) iso1 (RAB33L1), mRNA
14554	15554	26551	3.77	E0E-08	7019912.1	NT	Homo sapiens transcription factor NRF (NRF1), mRNA
2554	15554	26551	1.31	E0E-08	11421388	NT	Homo sapiens transcription factor NRF (NRF1), mRNA
8093	18093	26862	1.31	E0E-08	11421388	NT	Homo sapiens transcription factor NRF (NRF1), mRNA
6191	16248	32394	1.81	E0E-08	P04406	SWISSPROT	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE, LIVER
7980	20265	33544	6.72	E0E-08	AJ157003.1	NT	Homo sapiens selenin (SED), gene, exon 4
7040	20265	33545	6.72	E0E-08	11055591	NT	Homo sapiens selenin carboxypeptidase 1 precursor protein (HCSP1), mRNA
8135	21044	34374	0.78	E0E-08	11055591	NT	Homo sapiens selenin carboxypeptidase 1 precursor protein (HCSP1), mRNA
9882	25118	35680	6.07	E0E-08	DG470.2	NT	Homo sapiens KMT7P-S6L0724 protein (DKTP-FP568.0724), mRNA
9882	25118	35680	6.07	E0E-08	DG470.2	NT	Homo sapiens mRNA for KIAA07145 protein, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Exon Signal	Most Similar BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9592	225/18	35881	6.07	4.0E-68	D63476.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9627	226/46	35028	2.82	4.0E-68	AD0409.8.1	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
11441	243/67	37805	2.32	4.0E-68	4500282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
11441	243/67	37806	2.32	4.0E-68	4500282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
11603	245/12	37860	1.41	4.0E-68	AD0409.8.1	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
12780	263/88	31804	4.73	4.0E-68	11477998	NT	Homo sapiens SEC24L2 (SEC24L2) mRNA
3729	167/81	28648	2.71	3.0E-68	AF290082.1	NT	Mac musculus C-peptide coupled receptor, CPT2 (CPT2) mRNA, complete cds
9989	213/47		4.86	3.0E-68	AB242323.1	EST_HUMAN	Q48R02241 Soes, full, long, NIH, 1976 Homo sapiens cDNA clone IMAGE:1800291 3' similar to contains
10580	236/64	37291	1.12	3.0E-68	37291.1	EST_HUMAN	Q48R02241 Soes, full, long, NIH, 1976 Homo sapiens cDNA clone IMAGE:1800291 3' similar to contains
2904	19/408		6.99	2.0E-68	D05222.1	NT	Q48R02241 Soes, full, long, NIH, 1976 Homo sapiens cDNA clone IMAGE:1800291 3' similar to contains
4106	171/93	30008	0.79	2.0E-68	BE77768.1	EST_HUMAN	Q48R02241 Soes, full, long, NIH, 1976 Homo sapiens cDNA clone IMAGE:1800291 3' similar to contains
4753	171/93	30055	2.81	2.0E-68	BE77768.1	EST_HUMAN	Q48R02241 Soes, full, long, NIH, 1976 Homo sapiens cDNA clone IMAGE:1800291 3' similar to contains
7231	220/1		9.51	2.0E-68	BA3088.1	EST_HUMAN	Q48R02241 Soes, full, long, NIH, 1976 Homo sapiens cDNA clone IMAGE:1800291 3' similar to contains
7417	201/18	33332	4.34	2.0E-68	BF030516.1	EST_HUMAN	Q48R02241 Soes, full, long, NIH, 1976 Homo sapiens cDNA clone IMAGE:1800291 3' similar to contains
7884	205/20		0.51	2.0E-68	11525737	NT	Homo sapiens UDP-N-acetylglucosamine-6-phosphate polypeptide N-acetylglucosaminyltransferase 8 (GlcNAc-6T) (GALNT8), mRNA
7762	205/20	33597	0.71	2.0E-68	BF2307.6.1	EST_HUMAN	Q48R02241 Soes, full, long, NIH, 1976 Homo sapiens cDNA clone IMAGE:1800291 3' similar to contains
5526	224/31	35704	0.63	2.0E-68	BF05869	SWISSPROT	Q48R02241 Soes, full, long, NIH, 1976 Homo sapiens cDNA clone IMAGE:1800291 3' similar to contains
18901	245/33	38071	1.93	2.0E-68	BF230594.1	EST_HUMAN	Q48R02241 Soes, full, long, NIH, 1976 Homo sapiens cDNA clone IMAGE:1800291 3' similar to contains
12901	256/38		2.83	2.0E-68	BF302738.1	EST_HUMAN	Q48R02241 Soes, full, long, NIH, 1976 Homo sapiens cDNA clone IMAGE:1800291 3' similar to contains
13950	256/37		1.63	2.0E-68	AW106803.1	EST_HUMAN	Q48R02241 Soes, full, long, NIH, 1976 Homo sapiens cDNA clone IMAGE:1800291 3' similar to contains
82	131/95	25108	0.78	1.0E-68	AW181605.1	EST_HUMAN	Q48R02241 Soes, full, long, NIH, 1976 Homo sapiens cDNA clone IMAGE:1800291 3' similar to contains
3106	134/95	26320	8.85	1.0E-68	AW181605.1	EST_HUMAN	Q48R02241 Soes, full, long, NIH, 1976 Homo sapiens cDNA clone IMAGE:1800291 3' similar to contains
2298	182/78	26284	1.11	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0077 protein, complete cds
2298	182/78	26284	1.11	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0077 protein, complete cds
2806	167/95	29705	1.16	1.0E-68	AW491632.1	EST_HUMAN	Q48R02241 Soes, full, long, NIH, 1976 Homo sapiens cDNA clone IMAGE:1800291 3' similar to contains
2806	167/95	29705	1.16	1.0E-68	BE790332.1	EST_HUMAN	Q48R02241 Soes, full, long, NIH, 1976 Homo sapiens cDNA clone IMAGE:1800291 3' similar to contains
5105	181/52	30008	1.03	1.0E-68	AA087343.1	EST_HUMAN	Q48R02241 Soes, full, long, NIH, 1976 Homo sapiens cDNA clone IMAGE:1800291 3' similar to contains
5509	185/54	31453	1.56	1.0E-68	7982240	EST_HUMAN	Homo sapiens cell recognition molecule Cmap2 (KIA0869), mRNA
8129	210/39	34398	0.65	1.0E-68	11439716	NT	Homo sapiens centrin/SMO-specific protease (SENP1), mRNA
10678	236/65	36965	0.63	1.0E-68	11479420	NT	Homo sapiens similar to cytochrome pyrophosphatase/cytochrome c oxidase (LOC63214), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11287	21208	37656	1.51	1.0E-68	11418959	NT	Homo sapiens phosphodiesterase 7b (PDE7B), mRNA
11287	21208	37656	1.51	1.0E-68	11418959	NT	Homo sapiens phosphodiesterase 7b (PDE7B), mRNA
11341	24200	37700	1.51	1.0E-63	178416.1	NT	Homo sapiens NF2 suppressor (NF2) cDNA, complete cds
11341	24200	37700	2.03	1.0E-68	11430277	NT	Homo sapiens myosin IC (MYO1C), mRNA
11746	24647	38127	1.72	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80C4 (PRKGSH) gene, exon 4-5
11746	24647	38128	1.72	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80C4 (PRKGSH) gene, exon 4-5
12091	24632	38438	1.45	1.0E-68	11418481	NT	Homo sapiens G3176 protein (LOC51632), mRNA
12091	24632	38438	1.45	1.0E-68	11418481	NT	Homo sapiens G3176 protein (LOC51632), mRNA
12836	13195	26708	1.88	1.0E-68	4405922	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MNT), mRNA
12836	13195	26708	1.88	1.0E-68	4405922	NT	Homo sapiens low density lipoprotein receptor protein 2 (LRP2), mRNA
13033	25878	31476	1.75	1.0E-68	11430465	NT	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA
13072	25668		1.74	1.0E-68	11418213	NT	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA
21	13137	26023	1.159	9.2E-60	5031970	NT	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA
21	13137	26024	1.100	9.0E-60	5031970	NT	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA
1054	14038	27036	1.58	9.0E-60	5031930	NT	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA
1054	14038	27037	1.58	9.0E-60	5031930	NT	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA
11377	24248		4.82	9.0E-60	U11724.1	EST_HUMAN	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA
3405	15048		1.67	9.0E-60	A22174.1	EST_HUMAN	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA
6010	18651	32835	4.03	7.0E-68	5036012	EST_HUMAN	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA
8444	21376	34716	4.78	6.0E-60	A162704.1	EST_HUMAN	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA
8444	21376	34717	4.78	6.0E-60	A162704.1	EST_HUMAN	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA
8525	24452	35816	1.17	5.0E-60	A162704.1	EST_HUMAN	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA
8525	24452	35816	1.32	4.0E-60	A162704.1	EST_HUMAN	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA
5998	25636	32146	1.56	4.0E-60	BE59103.1	EST_HUMAN	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA
8037	18118	32248	5.90	4.0E-60	A162704.1	EST_HUMAN	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA
6918	19948	33169	2.5	4.0E-60	4587752	NT	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA
6918	19948	33169	2.5	4.0E-60	4587752	NT	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA
9471	23260	32762	0.52	4.0E-60	A111634.1	EST_HUMAN	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA
407	13522	29442	3	3.0E-60	BE259012.1	EST_HUMAN	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA
635	13696	29801	1.39	3.0E-60	A172112.1	NT	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA
2359	13104		1.11	3.0E-60	5728610	EST_HUMAN	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA
4169	17190	30062	1.05	3.0E-60	A176868.1	EST_HUMAN	Homo sapiens APC-5 cell colony-stimulating factor (CSF5) mRNA

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5423	16420	38594	1.92	3.0E-69	11418156	NT	Homo sapiens acylase 2, mitochondrial (AC02), mRNA
5625	18890	32005	0.51	3.0E-69	U14781.1	NT	Human type II IL-1 receptor gene, clone 1B
7113	20317		0.05	3.0E-69	AJ277651.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
7179	16451	31320	0.56	3.0E-69	11420786	NT	Homo sapiens acylase 2, mitochondrial (AC02), mRNA
7794	20504	33093	0.6	3.0E-69	AF094703.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
7821	20730	32055	1.35	3.0E-69	U23251.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
7822	20730	32055	1.35	3.0E-69	U23251.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
8642	21224	32223	0.8	3.0E-69	AF139646.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
8643	21224	32223	0.8	3.0E-69	AF139646.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
9327	21295		0.82	3.0E-69	AA373395.1	EST_HUMAN	Homo sapiens TRAFA-binding protein 16BP, mRNA, complete cds
9538	22455	33817	0.54	3.0E-69	AA373395.1	EST_HUMAN	U14781.1 Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
9647	22455	33817	0.54	3.0E-69	AA373395.1	EST_HUMAN	U14781.1 Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
9647	22455	33817	0.54	3.0E-69	AA373395.1	EST_HUMAN	U14781.1 Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
10052	22978	33839	3.86	3.0E-69	X13223.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
10344	20233	30051	0.83	3.0E-69	X13223.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
11088	24018	37469	2.12	3.0E-69	11432220	NT	Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
11279	24201		14.26	3.0E-69	AA373395.1	EST_HUMAN	U14781.1 Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
12370	25109		6.23	3.0E-69	AA373395.1	EST_HUMAN	U14781.1 Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
1333	13498	25421	1.03	2.0E-69	AF160252.1	NT	Homo sapiens KIA00553 protein gene, complete cds, and apolipoprotein protein gene, partial cds
1333	13498	25422	1.03	2.0E-69	AF160252.1	NT	Homo sapiens KIA00553 protein gene, complete cds, and apolipoprotein protein gene, partial cds
427	13498	25421	3.54	2.0E-69	AF160252.1	NT	Homo sapiens KIA00553 protein gene, complete cds, and apolipoprotein protein gene, partial cds
427	13498	25422	3.54	2.0E-69	AF160252.1	NT	Homo sapiens KIA00553 protein gene, complete cds, and apolipoprotein protein gene, partial cds
1805	14626	27005	1.23	2.0E-69	BE257697.1	EST_HUMAN	U14781.1 Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
2889	19843		3.17	2.0E-69	AA431157.1	EST_HUMAN	U14781.1 Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
817	22045	34002	0.84	2.0E-69	AA114270.1	EST_HUMAN	U14781.1 Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
1730	14757	27272	1.82	1.0E-69	AF053768.1	NT	U14781.1 Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
5151	18144		0.82	1.0E-69	BE400094.1	EST_HUMAN	U14781.1 Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
6285	19338	32502	0.84	1.0E-69	BE02501.1	EST_HUMAN	U14781.1 Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
6285	19338	32503	0.84	1.0E-69	BE02501.1	EST_HUMAN	U14781.1 Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
6890	19920	33135	3.67	1.0E-69	AF160252.1	EST_HUMAN	U14781.1 Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
7131	20335	33390	1.37	1.0E-69	7602263	NT	U14781.1 Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
7131	20335	33390	1.37	1.0E-69	7602263	NT	U14781.1 Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5
7130	20258	33511	3.87	1.0E-69	A0302973.1	NT	U14781.1 Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythymidylase (dNT-2 gene), exons 1-5

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Exon SEQ ID NO.	Most Similar (Top) Hit BLAST E Value	Top Hit Accession	Top Hit Database Source	Top Hit Descriptor
10181	20722	38472	0.57	7.0E-70	AB57824	NT	Homo sapiens glutamate-cysteine lyase (gamma-glutamylcysteine synthetase), catalytic (72 kDa) (GLCLC)
10187	28673	37101	0.62	7.0E-70	AB583428.1	NT	Homo sapiens NDS174 mRNA for N-disuccinylase/N-sulfotransferase 4, complete cds
10187	28673	37102	0.62	7.0E-70	AB583428.1	NT	Homo sapiens NDS174 mRNA for N-disuccinylase/N-sulfotransferase 4, complete cds
11513	24423	37880	1.64	7.0E-70	U1439385	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant spastic) (SPG4), mRNA
11513	24423	37881	1.64	7.0E-70	U1439385	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant spastic) (SPG4), mRNA
12027	24659	38371	1.6	7.0E-70	U1526319	NT	Homo sapiens HR (Hiborne cell cycle regulation defective, S. cerevisiae) homolog A (HRA), mRNA
12027	24659	38372	1.6	7.0E-70	U1526319	NT	Homo sapiens HR (Hiborne cell cycle regulation defective, S. cerevisiae) homolog A (HRA), mRNA
13060	25022	31751	2.17	7.0E-70	Z00345.1	NT	Human kappa-immunoglobulin germ line pseudogene, variable region (isotype J kappa 1)
896	13240	28836	2.07	8.0E-70	AF02168	NT	Homo sapiens amyloid beta (A4) precursor protein (precursor neuron-11, Alzheimer disease) (APP), mRNA
2151	18163	28166	1.68	6.0E-70	M30383.1	EST	Human K1 (P70-80) subunit mRNA, complete cds
2854	19535	28635	1.01	6.0E-70	85283899	NT	Homo sapiens CMP-N-acetylneuraminic acid synthase (LOC56507), mRNA
4629	17635	30489	0.87	6.0E-70	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
2855	19527	28670	2.07	5.0E-70	7682307	NT	Homo sapiens KIAA0762 gene product (KIAA0762), mRNA
2585	19527	28671	6.82	6.0E-70	7682307	NT	Homo sapiens KIAA0762 gene product (KIAA0762), mRNA
12330	25128	28718	6.82	5.0E-70	BE106040.1	EST	HUMAN VR3-10487-1 (20200-115-406 T1047) Homo sapiens cDNA
7059	20308	33517	3.67	4.0E-70	T0037.1	EST	HUMAN EST103928 Fetal brain, Shiga toxin (Gibbs30207) Homo sapiens cDNA clone HFSN22
7102	23318	33508	1.47	4.0E-70	AW76328.1	EST	HUMAN KIAA10000-105-908 UHM003 Homo sapiens cDNA
7102	23318	33509	1.47	4.0E-70	AW76328.1	EST	HUMAN KIAA10000-105-908 UHM003 Homo sapiens cDNA
1812	14642	27602	3.94	3.0E-70	BE017665.1	EST	HUMAN RQ-617052-071299-011-4128 T0322 Homo sapiens cDNA
1912	14642	27603	3.94	3.0E-70	BE017665.1	EST	HUMAN RQ-617052-071299-011-4128 T0322 Homo sapiens cDNA
5312	18236	31149	1.33	3.0E-70	A271736.1	NT	Homo sapiens X4 pseudodisulfide isomerase, segment 22
8514	18365	31995	0.97	3.0E-70	U143868	NT	Homo sapiens plectrophilin 4 (PPL4), mRNA
8514	18365	31997	0.97	3.0E-70	U143868	NT	Homo sapiens plectrophilin 4 (PPL4), mRNA
1812	14642	27602	3.94	3.0E-70	BE017665.1	EST	HUMAN RQ-617052-071299-011-4128 T0322 Homo sapiens cDNA
9533	19873	33840	3.05	3.0E-70	FB85833.1	EST	HUMAN RQ3419041 F1 NH MG5-46 Homo sapiens cDNA clone IMAGE433260 5'
10069	24925	39625	1.17	2.0E-70	BE020722.1	EST	HUMAN hM192.1 (1) KIA5-1124 Homo sapiens cDNA clone IMAGE324419.3'
40	13156	29627	1.17	2.0E-70	BE020722.1	EST	Homo sapiens fibronectin type-1, Lysine 230, (645/230) cDNA clone IMAGE324419.3'

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Value	Mean Similar (Top) HM BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3452	16493		2.92	1.0E-70	4657476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine gamma-glutamyltransferase) (TGMD)
9820	22726		0.94	1.0E-70	W057251	EST_HUMAN	h55955.11 Soares fetal liver splice_1 INFLS, S1 Homo sapiens cDNA clone IMAGE:46024 5'
10315	23234		0.61	1.0E-70	AA42292.1	EST_HUMAN	TC46033.1 Soares fetal liver splice_1 NT Homo sapiens cDNA clone IMAGE:73744 5'
11373	24299	37735	2.80	1.0E-70	AY78538.1	EST_HUMAN	AY785383.1 CB Homo sapiens cDNA clone IMAGE:73744 5'
6166	19226	32970	7.7	9.0E-71	AI43370.1	EST_HUMAN	sp491141.1 Soares fetal liver splice_1 NT Homo sapiens cDNA clone IMAGE:1736009 3' similar to TR-O14045
6166	19226	32970	7.7	9.0E-71	AI43370.1	EST_HUMAN	sp491141.1 Soares fetal liver splice_1 NT Homo sapiens cDNA clone IMAGE:1736009 3' similar to TR-O14045
6166	19226	32970	7.7	9.0E-71	AI43370.1	EST_HUMAN	sp491141.1 Soares fetal liver splice_1 NT Homo sapiens cDNA clone IMAGE:1736009 3' similar to TR-O14045
7841	20376	33544	2.07	9.0E-71	AF54903.1	EST_HUMAN	U4446.11 Soares fetal liver splice_1 NT Homo sapiens cDNA clone IMAGE:1736009 3' similar to TR-O14045
11935	20376	33544	3.80	9.0E-71	AI554903.1	EST_HUMAN	U4446.11 Soares fetal liver splice_1 NT Homo sapiens cDNA clone IMAGE:1736009 3' similar to TR-O14045
9921	22547		2.73	8.0E-71	AA17451.1	EST_HUMAN	TR-G1143651 G1143651 STRAIN XA34 POL:
11089	23563	37385	0.57	8.0E-71	AI273820.1	EST_HUMAN	NG4480.11 Soares fetal liver splice_1 NT Homo sapiens cDNA clone IMAGE:2814049 3' similar to TR-O54730
7768	20558	33998	8.30	7.0E-71	AA44230.1	EST_HUMAN	NG4480.11 Soares fetal liver splice_1 NT Homo sapiens cDNA clone IMAGE:2814049 3' similar to TR-O54730
9239	22154	35517	1.26	7.0E-71	AA705457.1	EST_HUMAN	NG4480.11 Soares fetal liver splice_1 NT Homo sapiens cDNA clone IMAGE:2814049 3' similar to TR-O54730
11774	24078	38162	1.03	7.0E-71	AL18320.2	NT	NG4480.11 Soares fetal liver splice_1 NT Homo sapiens cDNA clone IMAGE:2814049 3' similar to TR-O54730
2225	15235	26242	6.03	5.0E-71	AF05532.2	NT	Homo sapiens chromosome 21 segment H821010
4215	17232	30101	1.16	6.0E-71	AI781605.1	EST_HUMAN	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
6096	19157	32290	1.52	5.0E-71	4523740	NT	DV4-S10234-18119-037-405 ST0234 Homo sapiens cDNA
6096	19157	32290	1.52	5.0E-71	11641408	NT	Homo sapiens cytochrome-dependent kinase 6 (CDK6) mRNA
6596	19495	33029	1.05	6.0E-71	7602208	NT	Homo sapiens keratin, hair, acidic, 7 (KRT47), mRNA
7249	20195	35397	0.95	5.0E-71	AB033106.1	NT	Homo sapiens KIA00823 gene product (KIA00823), mRNA
7314	18462	31905	0.42	5.0E-71	AB033106.1	NT	Homo sapiens mRNA for KIA1290 protein, partial cds
7505	20146	33729	0.82	5.0E-71	11615800	NT	Homo sapiens protein kinase C, beta 1 (PRKCβ1), mRNA
7603	20555	34165	1.7	6.0E-71	M89106.1	NT	Homo sapiens neurofilament protein type 1 (NF1), mRNA
8196	21073	34403	0.89	5.0E-71	11534448	NT	Homo sapiens MAGUK protein p571, Protein Associated with Lys 2 (LOC51670), mRNA
8196	21104	34436	22.52	5.0E-71	AF072810.1	NT	Homo sapiens transcription factor W517, Protein Associated with Lys 2 (LOC51670), mRNA
0087	22016	35371	0.85	5.0E-71	5463777	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKB), mRNA
0087	22016	35371	0.85	5.0E-71	5463777	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKB), mRNA
10422	23311		2.34	5.0E-71	X13467.1	NT	Human TRCA gene for Alzheimer's disease A1 amyloid protein precursor (clone 2)

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	Q95 SEQ ID NO:	Expression Signal	Most Similar (Top) Ht BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
11418	24534	37763	5.21	6.0E-71	11435914	NT	Homo sapiens predicted basic protein (includes predicted basic protein, basic fibroblast growth factor, connective tissue-activating protein III, neurokinin A receptor, and proteinase-3) (PPSP7) mRNA
11637	24543	39077	2.73	5.0E-71	11435909	NT	Homo sapiens similar to hypothetical protein FL22193 (F14488) (LOC333295) mRNA
12264	25068	39574	1.48	5.0E-71	11417662	NT	Homo sapiens calcium binding protein (C12533) mRNA
107	13220	26733	1.14	4.0E-71	4507892	NT	Homo sapiens similar to hypothetical protein FL22193 (F14488) (LOC333295) mRNA
370	13497	26371	55.47	4.0E-71	AF157626.1	NT	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
370	13497	26372	59.47	4.0E-71	AF157626.1	NT	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
2628	15637	25973	2.47	4.0E-71	4505890	NT	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
4535	17544	33405	2.84	4.0E-71	AF056322	EST_HUMAN	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
6708	19155	33952	7.02	4.0E-71	AF056322	EST_HUMAN	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
8672	21643	33952	1.3	3.0E-71	AF135744.1	EST_HUMAN	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
11134	24093	37509	4	3.0E-71	AA557653.1	EST_HUMAN	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
12569	14203	37229	3.15	2.0E-71	AF133203.2	NT	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
8503	19992	31431	6.85	2.0E-71	AF14623.1	NT	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
8503	19992	31432	6.85	2.0E-71	AF14623.1	NT	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
7505	18474	31295	0.84	2.0E-71	AF049439.1	EST_HUMAN	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
6395	21190	34627	0.43	2.0E-71	AF061179.1	EST_HUMAN	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
6557	22484	35944	0.82	2.0E-71	BF065565.1	EST_HUMAN	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
11098	23542	37378	3.02	2.0E-71	AF065703.1	NT	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
11098	23542	37379	3.02	2.0E-71	AF065703.1	NT	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
11130	24095	37510	1.84	2.0E-71	BE018477.1	EST_HUMAN	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
12014	24866	36365	2.43	2.0E-71	R05926.1	EST_HUMAN	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
12360	25106		3.49	2.0E-71	T05499.1	EST_HUMAN	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
691	18173	26834	1.42	1.0E-71	AF077027.1	EST_HUMAN	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
959	14020	25854	1.43	1.0E-71	7762981	NT	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
1127	14169	27106	9.66	1.0E-71	AF235960.1	NT	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
1398	14400	27154	9.50	1.0E-71	AF078721.1	NT	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA
2065	15109	28112	1.75	1.0E-71	AB077007.1	NT	Human proteinase-3 (PR3) (P05000) member 10 (TNFSF10) mRNA

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Extension Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4206	17223	30089	1.39	7.0E-72	4601868	NT	Homo sapiens acylase 2, mitochondrial (AC02), nuclear gene encoding mitochondrial protein, mRNA
4208	17223	30090	1.39	7.0E-72	4601869	NT	Homo sapiens acylase 2, mitochondrial (AC02), nuclear gene encoding mitochondrial protein, mRNA
17484	26424	33704	2.67	7.0E-72	541641.1	NT	[uncharacterized] RPLP220707, nuclear gene encoding mitochondrial protein, mRNA
12840	26424	33704	2.12	7.0E-72	526259.1	EST_HUMAN	hsp471370 Hsp Homo sapiens cDNA clone IMAGE:2782664 5' similar to
6905	21683	26089	5.71	6.0E-72	AC103246.2	NT	hsp471370 Hsp Homo sapiens cDNA clone IMAGE:2782664 5' similar to
66	13162	26089	0.8	5.0E-72	BF333707.1	EST_HUMAN	hsp471370 Hsp Homo sapiens cDNA clone IMAGE:2782664 5' similar to
67	13162	26089	0.9	5.0E-72	BF333707.1	EST_HUMAN	hsp471370 Hsp Homo sapiens cDNA clone IMAGE:2782664 5' similar to
67	13162	26089	4.78	5.0E-72	BF333707.1	EST_HUMAN	hsp471370 Hsp Homo sapiens cDNA clone IMAGE:2782664 5' similar to
67	13162	26089	4.78	5.0E-72	BF333707.1	EST_HUMAN	hsp471370 Hsp Homo sapiens cDNA clone IMAGE:2782664 5' similar to
1195	14207	22595	1.95	8.0E-72	LI1045.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
7282	22235	33485	1.42	5.0E-72	AF123644.1	EST_HUMAN	hsp471370 Hsp Homo sapiens cDNA clone IMAGE:2782664 5' similar to
6208	22264	34828	4.11	5.0E-72	AF11274.1	EST_HUMAN	hsp471370 Hsp Homo sapiens cDNA clone IMAGE:2782664 5' similar to
10407	23365	36770	0.68	8.0E-72	AF124632.1	EST_HUMAN	hsp471370 Hsp Homo sapiens cDNA clone IMAGE:2782664 5' similar to
11859	24591	39096	2.84	5.0E-72	BF333167.1	EST_HUMAN	hsp471370 Hsp Homo sapiens cDNA clone IMAGE:2782664 5' similar to
11859	24591	39096	2.84	5.0E-72	BF333167.1	EST_HUMAN	hsp471370 Hsp Homo sapiens cDNA clone IMAGE:2782664 5' similar to
12070	24611	36413	1.82	6.0E-72	BE208546.1	EST_HUMAN	hsp471370 Hsp Homo sapiens cDNA clone IMAGE:2782664 5' similar to
12070	24611	36414	1.82	6.0E-72	BE208546.1	EST_HUMAN	hsp471370 Hsp Homo sapiens cDNA clone IMAGE:2782664 5' similar to
12454	26910	34514	3.12	5.0E-72	BE208546.1	EST_HUMAN	hsp471370 Hsp Homo sapiens cDNA clone IMAGE:2782664 5' similar to
4855	17894	31630	1.57	4.0E-72	AF170035.1	NT	Homo sapiens hypoxanthine phosphoribosyl transferase 1, complete cds
5031	18725	31630	0.65	4.0E-72	AF170035.1	NT	Homo sapiens hypoxanthine phosphoribosyl transferase 1, complete cds
6538	19870	33095	0.85	4.0E-72	T07947.1	EST_HUMAN	Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternative spliced, complete cds
7608	20737	34040	0.48	4.0E-72	572867.1	EST_HUMAN	Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternative spliced, complete cds
10333	23193	33604	1.17	4.0E-72	8923059	NT	Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternative spliced, complete cds
10033	23788	37210	0.56	4.0E-72	AI248798.1	EST_HUMAN	Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternative spliced, complete cds
11731	24633	38114	1.52	4.0E-72	AA185838.1	EST_HUMAN	Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternative spliced, complete cds

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	OFF SEQ ID NO.	Emission Signal	Best Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
11731	24633	38115	1.52	4.0E-72	AA405988.1	EST_HUMAN	h03030.1 NCL G2AR_C8B1 Homo sapiens cDNA clone IMAGE814191.3 similar to SW G2TR_FUAPR
11950	24802	38500	7.7	4.0E-72	HF9421.1	EST_HUMAN	P49131 CHONDROPLAST THIOSE PHOSPHATE TRANSFERRIN CONTAINING RECEPTOR
12105	24648	38449	2.25	4.0E-72	781901.1	EST_HUMAN	Y42803.71 Soares fetal liver spleen INCL3 Homo sapiens cDNA clone IMAGE28934.6
12786	25415	31768	6.47	4.0E-72	AJ277462.2	NT	Y42803.71 Soares fetal liver spleen INCL3 Homo sapiens cDNA clone IMAGE109948.3
20	13136	26222	3.4	3.0E-72	5031978	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
628	13860		1.46	3.0E-72	AJ173823.1	EST_HUMAN	Homo sapiens pnc-B-cell colony-enriching factor (PBEF) mRNA
1192	14222	27159	4.37	3.0E-72	U16306.1	NT	h03030.31 Soares_testis_NHT Homo sapiens cDNA clone 1310250.3
1192	14222	27160	4.37	3.0E-72	U16306.1	NT	Homo chondroin sulfate proteoglycan version V0 splice-variant precursor peptide mRNA, complete cds
1201	14259	27136	3.81	3.0E-72	U02226.1	NT	Human gamma aminobutyric acid transaminase mRNA, partial cds
1221	14259	27200	3.81	3.0E-72	U02226.1	NT	Human gamma aminobutyric acid transaminase mRNA, partial cds
1541	14871	27630	0.88	3.0E-72	BE24216.1	EST_HUMAN	TOA4PIE1263 Pediatric acute myelogenous leukemia cell (FAB M1) Bayleir-HQSC project-TCAA Homo sapiens cDNA clone TCAPI.252
3124	16175	26070	15.66	3.0E-72	AJ22904.1	NT	Homo sapiens 959 to 1019 region between AML1 and CBR1 on chromosome 21q22, segment 33
3323	16369	26270	2.74	3.0E-72	8623648	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
3898	18025	28802	2.48	3.0E-72	S7769.1	NT	TOR Y delta 2-C alpha 1 -cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction) (human, precursor B-cell line REH, mRNA Partial, 211 nt)
4021	17658	30854	3.32	3.0E-72	S7769.1	NT	(human, precursor B-cell line REH, mRNA Partial, 211 nt)
5710	18763		1.15	3.0E-72	4750009.1	NT	Homo sapiens hypothetical protein (FLJ11127), mRNA
6209	19264	32414	1.98	3.0E-72	AF073367.1	NT	Homo sapiens thrombin W (SEIWA) mRNA
6209	19264	32415	1.98	3.0E-72	AF073367.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6407	19435	32828	4.54	3.0E-72	AJ5029004.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 6
6899	19925	33146	4.54	3.0E-72	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
8002	20938	34283	2.47	3.0E-72	U6017.1	NT	Homo sapiens ribosome protein L3-Mit (RPL3L) mRNA
8754	21694	35027	1.39	3.0E-72	8031892	NT	Homo sapiens basic transcription factor 2 p44 (b2p44) gene, partial cds, neuronal apoptosis inhibitory protein (napi) and survival motor neuron protein (smn) genes, complete cds
10013	23798	37227	1.23	3.0E-72	X08280.1	NT	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3), mRNA
12708	28391	31798	2.20	3.0E-72	AB011380.1	NT	Homo sapiens STON242 gene for Calgranulin C, exon 2 and joined cds
6184	19241	32388	1.3	2.0E-72	1142667.1	NT	Homo sapiens solid cancer family 13 (solid-tumor-dependent factor/late transposon), member 2 (SLC1A3), mRNA

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Probe SEQ ID NO:	Seq ID	ORF SEQ ID NO:	Expression Signal	Mean Similarity (BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9641	22567	35937	1.01	2.0E-73	BF506600.1	EST_HUMAN	601600-138F1.NH1.MGC.7 Homo sapiens cDNA clone IMAGE:431451.9
9641	22567	35938	1.01	2.0E-72	BF506600.1	EST_HUMAN	011600-118F1.NH1.MGC.7 Homo sapiens cDNA clone IMAGE:431451.9
11181	24107	37694	2.46	2.0E-72	AF189777.1	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
12762	25411	31785	3.94	2.0E-72	AF182744.1	EST_HUMAN	011600-118F1.NH1.MGC.7 Homo sapiens cDNA clone IMAGE:431451.9
2085	25103	29103	1.04	1.0E-72	AF440223.1	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
6978	16040	32182	3.82	1.0E-72	7687026	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
6940	16772	33085	1.11	1.0E-72	1321915	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
6940	16772	33087	1.11	1.0E-72	1321915	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
6923	26593	33172	1.19	1.0E-72	U781918.1	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
7732	23294	33652	0.43	1.0E-72	BF519178.1	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
8685	20565	34518	3.7	1.0E-72	BF7454.1	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
8685	20565	34518	3.7	1.0E-72	BF7454.1	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
10118	23100	34408	8.3	1.0E-72	AF22742.1	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
10118	23100	34407	9.3	1.0E-72	AF22742.1	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
1438	14111	27471	0.91	8.0E-73	AF374968.1	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
6273	19124	32499	0.83	9.0E-73	11525983	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
11390	24004		13.13	8.0E-73	11424066	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
11390	24004		13.13	8.0E-73	11424066	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
1004	14107	27045	2.01	8.0E-73	AF071755.1	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
3333	18382	23281	0.74	8.0E-73	11435180	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
5772	18346	31648	0.84	8.0E-73	4800798	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
8584	19865	33100	4.57	8.0E-73	11429465	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
8574	21065	31647	2.13	8.0E-73	AF113126.1	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
9881	22805	36194	4.46	8.0E-73	BE019800.1	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
10262	23160	39457	1.54	8.0E-73	11520337	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
10262	23160	39566	1.54	8.0E-73	11520337	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
12939	25447	31716	4.36	8.0E-73	11418868	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
1161	14302	27140	0.94	7.0E-73	8925200	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9
3344	15860	28290	0.51	7.0E-73	AF116390.2	EST_HUMAN	42609-41 Source: testis; NIH1 Homo sapiens cDNA clone IMAGE:431451.9

Table 4

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466
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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
11484	24408	37859	3.28	2.0E-71	4576912	NT	Homo sapiens galactoseyltransferase (GalT), mRNA
11484	24408	37859	3.28	2.0E-71	4576912	NT	Homo sapiens galactoseyltransferase (GalT), mRNA
11522	24432	37860	1.83	2.0E-73	AB02986.1	NT	Homo sapiens mRNA for KIAA1018 protein, partial cds
12635	14980	27903	2.74	2.0E-73	AF186966.1	EST_HUMAN	KC3-1180G5-27003-471 cDNA: Homo sapiens cDNA
1607	14653	27903	4.82	1.0E-73	AU121895.1	EST_HUMAN	AU121895.1 Homo sapiens cDNA: KIAA1018/100460.5
2507	15008	28101	1.08	1.0E-73	AF116348.1	NT	Human DDX33, mRNA (BC232), mRNA, complete cds
6919	19959	32643	1.91	1.0E-73	BE157483.1	EST_HUMAN	GH-170283.31158-02-3130 HT0283 Homo sapiens cDNA
10031	22631	38317	1.88	1.0E-73	AF147437.1	EST_HUMAN	AF147437.1 Homo sapiens cDNA: IMAGE:138937.5 similar to contains element MB2-2, multiple element
11004	23694	37422	1.85	1.0E-73	BE35477.1	EST_HUMAN	BE35477.1 Homo sapiens cDNA: IMAGE:39177.03.5
7094	13521	28780	2.83	8.0E-74	457426	NT	Homo sapiens, CD38-like 2 (CD38L2), mRNA
6138	9189	32532	1.80	8.0E-74	BE3194.1	NT	C20-calcimulin-dependent protein kinase IV kinase isoform [rat, brain, mRNA, 3,429 nt]
6138	9189	32532	1.80	8.0E-74	BE3194.1	NT	C20-calcimulin-dependent protein kinase IV kinase isoform [rat, brain, mRNA, 3,429 nt]
1118	24234	32533	1.47	8.0E-74	NC2276.1	EST_HUMAN	Y16610.1 Scores fast liver screen INFL3 Homo sapiens cDNA: IMAGE:248829.3
1624	14682	27985	8.12	7.0E-74	A101669.1	NT	Homo sapiens NK2D2 gene, exon 10
3378	18419	28231	2.2	7.0E-74	AL183248.2	NT	Homo sapiens chromosome 21 segment HS21048
6765	27749	34131	2.77	7.0E-74	BE367142.1	EST_HUMAN	BE367142.1 Homo sapiens cDNA: IMAGE:333260.5
12638	25446	31774	5.6	7.0E-74	BE263065.1	EST_HUMAN	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds, and S171 gene, partial cds
1146	14181	27130	4.16	6.0E-74	AF10907.1	NT	AF10907.1 Scores, NFL_T_GSC_S1 Homo sapiens cDNA: IMAGE:270036.3
1650	14691	27643	0.88	6.0E-74	AV1203177.1	EST_HUMAN	AV1203177.1 Homo sapiens cDNA: IMAGE:369548.3
2337	15345	28349	8.31	6.0E-74	BE386280.1	EST_HUMAN	BE386280.1 Homo sapiens cDNA: IMAGE:369548.3
2337	15345	28349	8.31	6.0E-74	BE386280.1	EST_HUMAN	BE386280.1 Homo sapiens cDNA: IMAGE:369548.3
2206	15559	28860	1.13	6.0E-74	AV1074038.1	EST_HUMAN	UHH-BBC-uk-h-03-0-JL-nt1 NC1 CGAP_S471 Homo sapiens cDNA: IMAGE:270088.3
2006	15949	28861	1.13	6.0E-74	AV1074038.1	EST_HUMAN	UHH-BBC-uk-h-03-0-JL-nt1 NC1 CGAP_S471 Homo sapiens cDNA: IMAGE:270088.3
3718	16807	28864	1.43	6.0E-74	BEQ48449.1	EST_HUMAN	IR15411.1 NC1 CGAP_KURT1 Homo sapiens cDNA: IMAGE:313232.3
3718	16807	28864	1.43	6.0E-74	BEQ48449.1	EST_HUMAN	IR15411.1 NC1 CGAP_KURT1 Homo sapiens cDNA: IMAGE:313232.3
5550	18807	31505	3.1	6.0E-74	11090013	NT	Homo sapiens actin filament associated protein (AFAP), mRNA
5930	13928	28927	1.89	5.0E-74	AV1000868.1	EST_HUMAN	AF170001.1 Marton Field Cochise Homo sapiens cDNA: IMAGE:2483704.5
2733	15744	292	2.92	5.0E-74	AV362785.1	EST_HUMAN	PH0-070289-27094001-H07 C10289 Homo sapiens cDNA
6592	18693	31546	2.06	5.0E-74	11425417	NT	Homo sapiens phosphotyrosine oxidase, class I (P-GO), mRNA
0000	19005	32192	11.99	5.0E-74	Y08070.1	NT	H. sapiens mRNA for TPST16 protein
0032	18114	32243	10.24	5.0E-74	4907898	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (350d) (VAPPA) mRNA, and translated products

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Eno SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1618	14648	27610	2.74	2.0E-74	4895198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-b-b) oncogene homolog) (EGFR) mRNA
1618	14648	27611	2.74	2.0E-74	4895198	EST	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-b-b) oncogene homolog) (EGFR) mRNA
2044	16040	28059	2.02	2.0E-74	A577820	EST_HUMAN	P121_1_G11T1 tumor? Homo sapiens cDNA 3'
2044	16040	28059	2.02	2.0E-74	A577820	EST	P121_1_G11T1 tumor? Homo sapiens cDNA 3'
5127	18126	30045	3.33	2.0E-74	AL350592.1	NT	Novel human gene mapping to chromosome 22
5127	18126	30045	3.33	2.0E-74	AL350592.1	NT	Novel human gene mapping to chromosome 22
5127	18126	30045	3.33	2.0E-74	U029383	EST	Human placenta glycoprotein IIb-mRNA, 3' end
5133	18126	30071	4.78	2.0E-74	BAC00464.1	EST_HUMAN	R01303606P NH1 MGC_21 Homo sapiens cDNA clone IMAGE:3838344 5'
5133	18126	30071	4.78	2.0E-74	BAC00464.1	EST	R01303606P NH1 MGC_21 Homo sapiens cDNA clone IMAGE:3838344 5'
5353	18376	31218	0.99	2.0E-74	BE010464.1	EST_HUMAN	R03-H1067-6-220605-011-C03 HTc078 Homo sapiens cDNA
5353	18376	31218	0.99	2.0E-74	BE010464.1	EST_HUMAN	R03-H1067-6-220605-011-C03 HTc078 Homo sapiens cDNA
6059	26337	32107	1.75	2.0E-74	B11134.1	EST_HUMAN	Homo sapiens PDZ-F3 protein (PDZ-TANT-DO-38), mRNA
6114	26400	32303	1.97	2.0E-74	U11439687	NT	Homo sapiens PDZ-F3 protein (PDZ-TANT-DO-38), mRNA
6114	26400	32303	1.97	2.0E-74	U11439687	NT	Homo sapiens PDZ-F3 protein (PDZ-TANT-DO-38), mRNA
8114	26540	32307	2.87	2.0E-74	U11439687	NT	Homo sapiens PDZ-F3 protein (PDZ-TANT-DO-38), mRNA
8114	26540	32307	2.87	2.0E-74	U11439687	NT	Homo sapiens PDZ-F3 protein (PDZ-TANT-DO-38), mRNA
8193	26540	32307	2.87	2.0E-74	U11439687	NT	Homo sapiens PDZ-F3 protein (PDZ-TANT-DO-38), mRNA
7462	20462	33671	1.22	2.0E-74	BC030781.1	EST_HUMAN	HT157525P4P NH1 MGC_38 Homo sapiens cDNA clone IMAGE:3827548 5'
7462	20462	33671	1.22	2.0E-74	BC030781.1	EST_HUMAN	HT157525P4P NH1 MGC_38 Homo sapiens cDNA clone IMAGE:3827548 5'
8519	21460	34792	1.93	2.0E-74	BF030781.1	EST_HUMAN	Homo sapiens mRNAs for KIAA1960 protein, partial cds
8519	21460	34792	1.93	2.0E-74	BF030781.1	EST_HUMAN	Homo sapiens mRNAs for KIAA1960 protein, partial cds
9220	22608	36287	0.09	2.0E-74	AF18304.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C034
9220	22608	36287	0.09	2.0E-74	AF18304.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C034
12821	29677	39287	2.33	2.0E-74	AA168184.1	EST_HUMAN	Z22606.6 1 Stragglems muscle 337250 Homo sapiens cDNA clone IMAGE:436018 5'
12821	29677	39287	2.33	2.0E-74	AA168184.1	EST_HUMAN	Z22606.6 1 Stragglems muscle 337250 Homo sapiens cDNA clone IMAGE:436018 5'
13065	26051	31742	2.38	2.0E-74	BF026058.1	EST_HUMAN	D212142d8P NH1 MGC_35 Homo sapiens cDNA clone IMAGE:4371569B 5'
13065	26051	31742	2.38	2.0E-74	BF026058.1	EST_HUMAN	D212142d8P NH1 MGC_35 Homo sapiens cDNA clone IMAGE:4371569B 5'
26594	26594		1.5	2.0E-74	BF026055.1	EST_HUMAN	7950308.1 NGI CGM_F109 Homo sapiens cDNA clone IMAGE:3506916 5'
26594	26594		1.5	2.0E-74	BF026055.1	EST_HUMAN	7950308.1 NGI CGM_F109 Homo sapiens cDNA clone IMAGE:3506916 5'
66	13376	28073	1.27	1.0E-74	T057334.1	EST_HUMAN	Homo sapiens Musashi1/Ng2 mRNA (NM_017000)
367	13444	28369	3.35	1.0E-74	AW816406.1	EST_HUMAN	QY45310234-101T04-037 S1S1 10821 Homo sapiens cDNA
367	13444	28369	3.35	1.0E-74	AW816406.1	EST_HUMAN	QY45310234-101T04-037 S1S1 10821 Homo sapiens cDNA
822	13892	29581	0.91	1.0E-74	8072823	NT	Homo sapiens type III nuclear P1J 1020 (FLJ1020), mRNA
822	13892	29581	0.91	1.0E-74	8072823	NT	Homo sapiens type III nuclear P1J 1020 (FLJ1020), mRNA
559	13956	29569	6.61	1.0E-74	U02344.1	NT	Homo sapiens beta 2 gene
559	13956	29569	6.61	1.0E-74	U02344.1	NT	Homo sapiens beta 2 gene
1027	13879	29590	2.31	1.0E-74	U068020.1	NT	Homo sapiens beta 2 gene
1027	13879	29590	2.31	1.0E-74	U068020.1	NT	Homo sapiens beta 2 gene

3 Expression

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Probe SEQ ID NO:	Exon SEQ ID NO:	OPF SEQ ID NO:	Expression Signal	Next Smaller (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11127	24057	37503	16.27	4.0E-75	7639505	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
10301	14079	27019	3.17	3.0E-75	AF167023.1	NT	Homo sapiens HTRA serine protease (PROS17) gene, complete cds
10311	14079	27019	2.26	3.0E-75	AF167023.1	NT	Homo sapiens HTRA serine protease (PROS17) gene, complete cds
10961	14882	27662	2.12	3.0E-75	AB011163.1	NT	Homo sapiens mRNA for KIAA0351 protein, partial cds
21241	19137	28143	1.97	3.0E-75	4507334	NT	Homo sapiens synaptotagmin 1 (SYN1), mRNA, 2450 (SNAP29) mRNA
24681	15450	28445	2.87	3.0E-75	4759153	NT	Homo sapiens synapocome 21 segment HS21C091
30671	19119	28020	0.80	3.0E-75	AL153071.2	NT	Homo sapiens mRNA for KIAA0351 protein, partial cds
32321	15280	29100	1.16	3.0E-75	AL153071.1	NT	Human calcineurin-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
33991	16441	28345	0.84	3.0E-75	AF167023.1	NT	Homo sapiens mRNA for KIAA0351 protein, partial cds
35991	16441	28345	0.84	3.0E-75	AF167023.1	NT	Homo sapiens mRNA for KIAA0351 protein, partial cds
45431	17821	30172	0.21	3.0E-75	7892421	NT	Human calcineurin-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
46231	18514	31238	0.82	3.0E-75	11420960	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1B2), mRNA
49231	18514	31238	0.82	3.0E-75	11420960	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1B2), mRNA
67881	15810	33031	0.71	3.0E-75	AF123074.1	NT	Homo sapiens cytoplasmic dyane intermediate chain 1 mRNA, complete cds
67881	15810	33032	0.71	3.0E-75	AF123074.1	NT	Homo sapiens cytoplasmic dyane intermediate chain 1 mRNA, complete cds
70761	20282	33358	1.87	3.0E-75	11523519	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
70761	20282	33359	1.87	3.0E-75	11523519	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
70651	20435	33714	4.51	3.0E-75	7992209	NT	Homo sapiens KIAA0023 gene product (KIAA0023), mRNA
74951	20435	33715	4.61	3.0E-75	7992209	NT	Homo sapiens KIAA0023 gene product (KIAA0023), mRNA
80701	20393	34207	3.08	3.0E-75	4898932	NT	Homo sapiens Oncogene TIM (TIM) mRNA
80701	20393	34208	3.08	3.0E-75	4898932	NT	Homo sapiens Oncogene TIM (TIM) mRNA
93581	22693	33629	1.39	3.0E-75	11420904	NT	Homo sapiens small 1 (disocipin homolog), zinc finger protein (SNA1), mRNA
102331	22694	349494	0.62	3.0E-75	11420222	NT	Homo sapiens Oncogene Kohn like protein (DKELCH), mRNA
122031	25059	39535	1.91	3.0E-75	6715984	NT	Homo sapiens bircadin A inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
122031	25059	39536	1.91	3.0E-75	6715984	NT	Homo sapiens bircadin A inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
58701	16541		1.48	2.0E-75	AF194800.1	EST HUMAN	AF194800.1 NC_004047 Homo sapiens cDNA clone IMAGE:263207 3' similar to TRC60836 C60839
93101	22298	35506	2.53	2.0E-75	AF11783.1	EST HUMAN	X69402.1 NC_004047 Homo sapiens cDNA clone IMAGE:263207 3' similar to contains P17R.17
23221	15330	28333	13.14	1.0E-75	AF168195.1	EST HUMAN	P-197, rapamycin domain
25681	10040	29545	2.2	1.0E-75	U03221.1	EST HUMAN	S. sapientis ERCC2 gene, clone 1 8.5 (partial)
80271	20549	34258	0.64	1.0E-75	BE062526.1	EST HUMAN	BC5-517640-52050-531-F05 DT0560 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4478	17488	30549	6.17	7.0E-78	4507184	NT	Human sapiens caspase1inhibitor 7 (8.5 kilobases) to MALP2, ectoderm (cDNA) (SFR) mRNA
1282	14288		6.16	6.0E-78	03532033.1	EST - HUMAN	03532033.1 HMG-44 Homo sapiens cDNA clone IMAGE:368767 5'
11897	28597	37435	2.86	5.0E-78	01627320.1	EST - HUMAN	01627320.1 HMG-14 Homo sapiens cDNA clone IMAGE:350029 5'
11953	14877	27839	4.81	6.0E-78	033874.1	NT	Human mRNA for HMG-1, complete cds
11958	14877	27900	4.81	6.0E-78	033874.1	NT	Human mRNA for HMG-1, complete cds
19581	14677	27901	4.81	6.0E-78	033874.1	NT	Human mRNA for HMG-1, complete cds
32521	16500	26205	1.93	3.0E-78	0384528.1	EST - HUMAN	QV3-B0047.270700-288-c01 BN90.7 Homo sapiens cDNA
94621	18333	31259	1.93	3.0E-78	0384528.1	EST - HUMAN	87-17125F1 NHT MAG-87 Homo sapiens cDNA clone IMAGE:3874470 5'
10527	28473	31259	1.93	3.0E-78	0384528.1	EST - HUMAN	HUM176501B Human fetal brain (Fujivara) Homo sapiens cDNA clone GEN176501 5'
10527	28473	31259	1.93	3.0E-78	0384528.1	EST - HUMAN	HUM176501B Human fetal brain (Fujivara) Homo sapiens cDNA clone GEN176501 5'
10527	28473	31259	1.93	3.0E-78	0384528.1	EST - HUMAN	UHH-BW1-ano2-b-04-DULS1 NCJ CGAP SUB7 Homo sapiens cDNA clone IMAGE:3083862 3'
10527	28473	31259	1.93	3.0E-78	0384528.1	EST - HUMAN	UHH-BW1-ano2-b-04-DULS1 NCJ CGAP SUB7 Homo sapiens cDNA clone IMAGE:3083862 3'
8581	13714	28620	2.1	3.0E-78	0384528.1	EST - HUMAN	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
8581	13714	28620	2.1	3.0E-78	0384528.1	EST - HUMAN	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
8581	13714	28620	2.1	3.0E-78	0384528.1	EST - HUMAN	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
14922	14852	27615	4	3.0E-78	4503476	NT	RC5-3 103300-180100-033-A03 S10300 Homo sapiens cDNA
14922	14852	27615	4	3.0E-78	4503476	NT	RC5-3 103300-180100-033-A03 S10300 Homo sapiens cDNA
3460	18528	28426	6.66	3.0E-78	0375559.1	EST - HUMAN	RC5-3 103300-180100-033-A03 S10300 Homo sapiens cDNA
3460	18528	28426	6.66	3.0E-78	0375559.1	EST - HUMAN	RC5-3 103300-180100-033-A03 S10300 Homo sapiens cDNA
4168	17180	30049	1.14	3.0E-78	0384528.1	EST - HUMAN	RC5-3 103300-180100-033-A03 S10300 Homo sapiens cDNA
5418	18417	38663	2.05	3.0E-78	241314.1	EST - HUMAN	RC5-3 103300-180100-033-A03 S10300 Homo sapiens cDNA
6895	19002	32121	1.04	3.0E-78	0384528.1	EST - HUMAN	KIAA0792 PROTEIN ;
6216	18274	32428	0.6	3.0E-78	AW027705.1	EST - HUMAN	HSC2D042 normalized infant brain cDNA Homo sapiens cDNA clone s-24204 3'
6526	18668	32853	9.03	3.0E-78	AF79568.1	NT	z07307.r1 Stagiagene pancreas (p637208) Homo sapiens cDNA clone IMAGE:502624 5' similar to
6720	21950	35005	1	3.0E-78	AA2077.1	EST - HUMAN	z07307.r1 Stagiagene pancreas (p637208) Homo sapiens cDNA clone IMAGE:502624 5' similar to
10238	23120	35052	3.28	3.0E-78	AA2077.1	EST - HUMAN	z07307.r1 Stagiagene pancreas (p637208) Homo sapiens cDNA clone IMAGE:502624 5' similar to
10261	23151	35059	0.81	3.0E-78	AA2077.1	EST - HUMAN	z07307.r1 Stagiagene pancreas (p637208) Homo sapiens cDNA clone IMAGE:502624 5' similar to
10261	23151	35059	0.81	3.0E-78	AA2077.1	EST - HUMAN	z07307.r1 Stagiagene pancreas (p637208) Homo sapiens cDNA clone IMAGE:502624 5' similar to
12237	20707	31573	2.7	3.0E-78	AA2077.1	EST - HUMAN	z07307.r1 Stagiagene pancreas (p637208) Homo sapiens cDNA clone IMAGE:502624 5' similar to
12237	20707	31573	2.7	3.0E-78	AA2077.1	EST - HUMAN	z07307.r1 Stagiagene pancreas (p637208) Homo sapiens cDNA clone IMAGE:502624 5' similar to
12237	20707	31573	2.7	3.0E-78	AA2077.1	EST - HUMAN	z07307.r1 Stagiagene pancreas (p637208) Homo sapiens cDNA clone IMAGE:502624 5' similar to
3011	13394	28313	1.03	2.0E-78	0384528.1	NT	Human mRNA for possible protein TRPC1, complete cds
362	13449	28300	2.96	2.0E-78	0384528.1	NT	Human mRNA for possible protein TRPC1, complete cds
362	13449	28301	2.96	2.0E-78	0384528.1	NT	Human mRNA for possible protein TRPC1, complete cds
483	13564		1.24	2.0E-78	4507184	NT	Human sapiens immunoglobulin G (cDNA) binding protein 1 (IGBP1) mRNA
611	13578	28578	0.95	2.0E-78	4503944	NT	Human sapiens glucagon (cDNA) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Exon Signal	Most Similar (Top Hit) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
12543	25006	31772	25-24	8.0E-77	R02045.1	EST_HUMAN	y69804.1 Soares fetal liver spleen (NHLS) Homo sapiens cDNA clone IMAGE:22007.3 similar to contains MER 10 repetitive element.
1944	14995	27944	3.21	7.0E-77	AA629765.1	EST_HUMAN	z69701.1 Soares, fetal, NHT Homo sapiens cDNA clone IMAGE:74582.3'
2435	15459	28439	3.76	7.0E-77	450944	NT	Homo sapiens polyomavirus (RNA II) (DNA directed) polyomavirus E (28S) (POLICE) mRNA
2435	15459	28440	3.76	7.0E-77	450944	NT	Homo sapiens polyomavirus (RNA II) (DNA directed) polyomavirus E (28S) (POLICE) mRNA
262	13376	26291	4.07	6.0E-77	450490	NT	Homo sapiens interleukin (delta, beta and omega) receptor 2 (INRA2) mRNA
1165	14210	27148	1.12	6.0E-77	AY997763.1	EST_HUMAN	EST358523 IMAGE: ressequencing, NKCE Homo sapiens cDNA clone IMAGE:74509.3
1955	14568	27568	1.4	6.0E-77	AD04065.1	EST_HUMAN	g470122.1 Soares, fetal, NHT Homo sapiens cDNA clone IMAGE:74509.3
195	13258	26713	3.59	5.0E-77	AF154535.1	NT	Homo sapiens calcium phospholipase A2 (cPLA2) complete cds
195	13258	26714	3.59	5.0E-77	AF154535.1	NT	Homo sapiens calcium phospholipase A2 (cPLA2) complete cds
1264	14258	27244	1.77	6.0E-77	AF041016.1	NT	Homo sapiens glucocorticoid (GC) gene, exon 2
1387	14418	27373	1.18	6.0E-77	AF041016.1	NT	Homo sapiens glucocorticoid (GC) gene, exon 2
2134	15727	28524	0.34	5.0E-77	AF152686	EST_HUMAN	Homo sapiens diacylglycerol and monophosphate domain 10 (ADAM10) mRNA
2134	15727	28524	0.34	5.0E-77	AF152686	EST_HUMAN	Homo sapiens diacylglycerol and monophosphate domain 10 (ADAM10) mRNA
5833	18920	26524	1.68	5.0E-77	8394199	NT	Homo sapiens cyclin 1 (CLN1) mRNA, complete cds
5925	19047	33091	2.39	5.0E-77	AL045953.1	EST_HUMAN	Homo sapiens ubiquitin specific protease 9 (USP9), mRNA
7024	20027	33697	0.87	6.0E-77	M13075.1	NT	U972434G1728.11.344 (synonym: hacc) Homo sapiens cDNA clone DK-22-343G1728.5
7111	20453	33940	0.44	5.0E-77	X88266.1	NT	Homo sapiens protein kinase C beta-II type (PRKC31) mRNA, complete cds
8353	20543	33940	0.44	5.0E-77	X88266.1	NT	Homo sapiens protein kinase C beta-II type (PRKC31) mRNA, complete cds
8640	21870	36228	1.98	6.0E-77	11428349	NT	Homo sapiens mRNA for ubiquitin hydrolase
8640	21870	36228	1.98	6.0E-77	11428349	NT	Homo sapiens mRNA for ubiquitin hydrolase
10098	22647	36335	3.05	6.0E-77	11421928	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
10098	22647	36335	3.05	6.0E-77	11421928	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
10955	23553	37279	0.7	6.0E-77	AB002297.1	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
10955	23553	37280	0.7	6.0E-77	AB002297.1	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
12212	25046	38549	1.83	6.0E-77	AL111168.2	NT	Human mRNA for KIAA269 gene, partial cds
12212	25046	38549	1.83	6.0E-77	AL111168.2	NT	Human mRNA for KIAA269 gene, partial cds
10398	19008	27094	1.5	3.0E-77	AF111168.2	NT	Human mRNA for KIAA269 gene, partial cds
10398	19008	27094	1.5	3.0E-77	AF111168.2	NT	Human mRNA for KIAA269 gene, partial cds
1988	15005	27095	1.5	3.0E-77	6730038	NT	Homo sapiens SET domain and nuclear transport fusion gene (SETMAR) mRNA
1988	15005	27095	1.5	3.0E-77	6730038	NT	Homo sapiens SET domain and nuclear transport fusion gene (SETMAR) mRNA
10780	26606	37064	0.6	3.0E-77	H81697.1	EST_HUMAN	y494901.1 Walzman Olfactory Epithelium Homo sapiens cDNA clone IMAGE:23809.5 similar to SP-S17447 S17447 PHOSPHOLIPASE-LIGAND-BINDING PROTEIN RY256.1
10780	26606	37064	0.6	3.0E-77	H81697.1	EST_HUMAN	y494901.1 Walzman Olfactory Epithelium Homo sapiens cDNA clone IMAGE:23809.5 similar to SP-S17447 S17447 PHOSPHOLIPASE-LIGAND-BINDING PROTEIN RY256.1
11310	26606	37065	0.9	3.0E-77	H81697.1	EST_HUMAN	y494901.1 Walzman Olfactory Epithelium Homo sapiens cDNA clone IMAGE:23809.5 similar to SP-S17447 S17447 PHOSPHOLIPASE-LIGAND-BINDING PROTEIN RY256.1
11310	26606	37065	0.9	3.0E-77	H81697.1	EST_HUMAN	y494901.1 Walzman Olfactory Epithelium Homo sapiens cDNA clone IMAGE:23809.5 similar to SP-S17447 S17447 PHOSPHOLIPASE-LIGAND-BINDING PROTEIN RY256.1
1381	14413	27357	1.2	2.0E-77	AF764674.1	EST_HUMAN	P08-MT007B-00980-005-g03-MT007B Homo sapiens cDNA
1381	14413	27357	1.2	2.0E-77	AF764674.1	EST_HUMAN	AY764674.M05 Homo sapiens cDNA clone M038710.5

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Probe SEQ ID NO.	Exon SEQ ID NO.	CRF SEQ ID NO.	Expression Signal	Most Similar 100 bp BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4643	17769	20614	24.54	1.0E-77	U123041.1	NT	Homo sapiens 359 kb contig between AML1 and CBX1 on chromosome 2 (c22, segment 13)
4644	17796	20629	1.74	1.0E-77	6553222	NT	Homo sapiens breast cancer 1 early onset (BRCA1), transcript variant BRCA1 exonA, mRNA
4688	17697	20844	1.11	1.0E-77	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
6183	19211	32350	1.26	1.0E-77	AF068944.1	NT	Homo sapiens cyclin 1 (CCN1) gene, exons 27 and 28
6183	19211	32351	1.26	1.0E-77	AF068944.1	NT	Homo sapiens cyclin 1 (CCN1) gene, exons 27 and 28
6282	10333	32469	1.64	1.0E-77	U05944.1	NT	Human von Willebrand factor gene, exon 20
6718	16754	32660	1.16	1.0E-77	488582	NT	Homo sapiens diaphanous (Dpochap, homolog) 1 (DAPK1), mRNA
7419	20105	33339	16.46	1.0E-77	5981472	NT	Homo sapiens caslin (caprasin), 2 to 5 exons, Williams-Beuren syndrome (EIN), mRNA
8157	21028	34335	1.47	1.0E-77	11420159	NT	Homo sapiens cyclin 1 (CCN1), mRNA
8232	21137	34469	0.62	1.0E-77	X04571.1	NT	Homo sapiens cyclin 1 (CCN1), mRNA
11004	28998	37321	1.15	1.0E-77	AF025396.1	NT	Homo sapiens cyclin 1 (CCN1), mRNA
11004	28988	37322	1.15	1.0E-77	AF025396.1	NT	Homo sapiens cyclin 1 (CCN1), mRNA
11517	24427	37855	1.59	1.0E-77	U143348	EST_HUMAN	Homo sapiens cyclin 1 (CCN1), mRNA
11028	28912	37354	3.16	9.0E-76	AF178302.1	EST_HUMAN	Homo sapiens cyclin 1 (CCN1), mRNA
6718	19752	32357	2.04	8.0E-76	AF170561.1	EST_HUMAN	Homo sapiens cyclin 1 (CCN1), mRNA
6718	19752	32358	2.04	8.0E-76	AF170561.1	EST_HUMAN	Homo sapiens cyclin 1 (CCN1), mRNA
88	13301	25114	1.70	8.0E-76	AF118789.1	EST_HUMAN	Homo sapiens cyclin 1 (CCN1), mRNA
88	13301	25115	1.70	8.0E-76	AF118789.1	EST_HUMAN	Homo sapiens cyclin 1 (CCN1), mRNA
6841	18073	26115	2.68	6.0E-76	U1143270	NT	Homo sapiens cyclin 1 (CCN1), mRNA
233	13311	26246	1.81	5.0E-76	11423466	NT	Homo sapiens cyclin 1 (CCN1), mRNA
2597	15595	26550	4.66	5.0E-76	AF073424	EST_HUMAN	Homo sapiens cyclin 1 (CCN1), mRNA
2444	18485	26923	4.46	5.0E-76	U05586.1	EST_HUMAN	Homo sapiens cyclin 1 (CCN1), mRNA
5597	19673	31851	2.28	5.0E-76	AF038593.1	NT	Homo sapiens cyclin 1 (CCN1), mRNA
5797	19840	31941	12.03	5.0E-76	11416595	NT	Homo sapiens cyclin 1 (CCN1), mRNA
7515	20454	33740	2.48	5.0E-76	AF053120.1	EST_HUMAN	Homo sapiens cyclin 1 (CCN1), mRNA
9620	22505	33925	7.07	5.0E-76	U06089.1	NT	Homo sapiens cyclin 1 (CCN1), mRNA
9620	22505	33926	3.47	5.0E-76	HE040368.1	EST_HUMAN	Homo sapiens cyclin 1 (CCN1), mRNA
1164	14205	27143	1.57	4.0E-76	AF04314.2	EST_HUMAN	Homo sapiens cyclin 1 (CCN1), mRNA
1539	14503	27629	2	4.0E-76	AF35841.1	NT	Homo sapiens cyclin 1 (CCN1), mRNA
1675	14705	27867	1.06	4.0E-76	AF05804.1	EST_HUMAN	Homo sapiens cyclin 1 (CCN1), mRNA
2339	15347	29351	2.40	4.0E-76	AF107405.1	NT	Homo sapiens cyclin 1 (CCN1), mRNA
4428	17439	30349	2.2	4.0E-76	7866670	NT	Homo sapiens cyclin 1 (CCN1), mRNA

Single Exon Probes Expressed in Adult Liver

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Probe SEQ ID No.	Exon SEQ ID No.	ORF SEQ IDNO:	Exonseq Signal	Maxi Similar BLAST E Value	Top Hit Accession No.	Top HB Deletion Source	Top Hit Descriptor
6076	19041	37163	1.03	4.0E-78	114073263	NT	Homo sapiens SFRRS protein kinase 2 (SFRRK2), mRNA
6078	19042	32836	0.97	4.0E-78	78621003	NT	Homo sapiens KIAA0420 gene product (KIAA0420), mRNA
6414	19422	32937	0.97	4.0E-78	78621003	NT	Homo sapiens KIAA0420 gene product (KIAA0420), mRNA
6415	19423	32937	0.97	4.0E-78	78621003	NT	Homo sapiens KIAA0420 gene product (KIAA0420), mRNA
6455	19887	33101	0.97	4.0E-78	456736	NT	Homo sapiens ribosomal protein S6 kinase, 70SD, polypeptide 1 (RP-SRKB1) mRNA
7017	20835	34139	0.69	4.0E-78	456736	NT	Homo sapiens ribosomal protein S6 kinase, 70MD, polypeptide 1 (RP-SRKB1) mRNA
8412	22340	38704	1.32	4.0E-78	140712872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (PIK230) mRNA, complete cds
8412	22340	38704	1.32	4.0E-78	140712872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (PIK230) mRNA, complete cds
9007	22885	36282	0.71	4.0E-78	11417281	NT	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), mRNA
10325	24810	37228	1.74	4.0E-78	11550159	NT	Homo sapiens hypothetical CSH2 zinc finger protein PUJ22004 (PUJ22004), mRNA
10326	24810	37228	1.74	4.0E-78	11550159	NT	Homo sapiens hypothetical CSH2 zinc finger protein PUJ22004 (PUJ22004), mRNA
11852	24931	38160	2.32	4.0E-78	AF169148.1	NT	Homo sapiens c-Grb1 (CGRB1) mRNA, complete cds
11921	24933	38163	2.65	4.0E-78	X08841.1	NT	Human transforming growth factor-beta precursor gene exons 4-5 (end joined mature peptide)
12839	24942	31778	3.27	4.0E-78	AE011330.1	NT	Homo sapiens gene for AF-2, complete cds
1317	32372	29166	1.45	3.0E-78	AF095801.1	NT	Homo sapiens eRF1 gene, complete cds
1317	32372	29166	1.45	3.0E-78	AF095801.1	NT	Homo sapiens eRF1 gene, complete cds
2323	15331	28334	1.25	3.0E-78	AF095801.1	NT	Homo sapiens apoptosis inhibitor 3 (P33) mRNA
3826	16818		1.25	3.0E-78	AU149004.1	EST_HUMAN	AU149004 PLACE1 Homo sapiens cDNA clone IMAGE300375 5'
3985	16818	20793	0.9	3.0E-78	4507934	EST	Homo sapiens synapsin-like 1 (SNYL1), mRNA
4198	16911	20793	0.71	3.0E-78	4507934	EST	Homo sapiens synapsin-like 1 (SNYL1), mRNA
10776	20654		0.84	3.0E-78	BE144756.1	EST_HUMAN	Q041035.1 Homo sapiens cDNA clone IMAGE304130 5'
11419	24335	37784	1.97	3.0E-78	BE15616.1	EST_HUMAN	Q041035.1 Homo sapiens cDNA clone IMAGE304130 5'
3169	16216		2.84	2.0E-78	U04881.1	EST_HUMAN	U04881.1 Homo sapiens cDNA clone IMAGE304130 5'
4100	17120		1.78	2.0E-78	AS111927.1	EST_HUMAN	EST185853 Homo sapiens cDNA clone IMAGE304130 5'
7850	20400	34110	1.2	2.0E-78	AF042068.1	EST_HUMAN	U14F-BXO-4g-19G-J11 NH_MGC_36 Homo sapiens cDNA clone IMAGE304130 5'
7850	20400	34111	1.2	2.0E-78	AF042068.1	EST_HUMAN	U14F-BXO-4g-19G-J11 NH_MGC_36 Homo sapiens cDNA clone IMAGE304130 5'
8194	21101	34451	0.35	2.0E-78	AF14570.1	EST_HUMAN	AF14570.1 Homo sapiens cDNA clone IMAGE304130 5'
86718	21549	34890	2.48	2.0E-78	AF15769.1	EST_HUMAN	AV271859.1 NH_MGC_49 Homo sapiens cDNA clone IMAGE304130 5'
9020	21549	35304	2.16	2.0E-78	AF15769.1	EST_HUMAN	AV271859.1 Homo sapiens cDNA clone IMAGE304130 5'
9021	21549	35305	2.16	2.0E-78	N857088.1	EST_HUMAN	P2.1_16_B017 tuncm2 Homo sapiens cDNA clone IMAGE304130 5'
11519	24420	37947	3.82	2.0E-78	M197887.1	EST_HUMAN	Q060545 NCI COAP_Bmo35 Homo sapiens cDNA clone IMAGE1559861 3' similar to WF1490.1
11584	24723	37440	2.05	2.0E-78	N66851.1	EST_HUMAN	ZNF827.2.1 SGAPE fetal liver sp1 com NHLFS Homo sapiens cDNA clone IMAGE304130 5'
3140	16146	31444	3.22	4.0E-78	114472804	NT	Homo sapiens GAP-related protein (LOC51135), mRNA

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Probe	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) HI BLAST Value	Top HI Accession No.	Top HI Database Source	Top HI Descriptor
7298	19487	31327	5.48	1.0E-78	AF048999.1	EST_HUMAN	AV148699 GLC Homo sapiens cDNA clone GLO31/001.3
8717	21627		1.97	1.0E-78	U52373.1	NT	Human acetylthioesterase kinase (MIS (mtb) mRNA, complete cds
12480	28224	31858	3.87	1.0E-78	U1439003	NT	Homo sapiens similar to lymphocyte activation-associated protein (H. sapiens) (LOC83140), mRNA
14181	17812	30578	1.59	1.0E-78	U152386.1	NT	Homo sapiens similar to YY (P1Y7), mRNA
3518	18064	31160	14.17	9.0E-79	AF028070.1	NT	Homo sapiens mRNA for activator of S phase Kinase, complete cds
6097	19638	32818	2.33	9.0E-79	U641446	NT	Homo sapiens ubiquitin-like-conjugating enzyme E2E 3 (homoduplex to yeast UBC46) (UBE2E3) mRNA
6095	19638	33152	1.07	9.0E-79	U11430822	NT	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA
7738	28675		1.02	9.0E-79	U142427	NT	Homo sapiens hypothetical protein FLJ10346 (FLJ10346), mRNA
8008	20925	34242	1.07	9.0E-79	U142735	NT	Homo sapiens cAMP response element-binding protein CRE-2p4 (H. GS166.15.1), mRNA
8008	20925	34243	1.07	9.0E-79	U142735	NT	Homo sapiens cAMP response element-binding protein CRE-2p4 (H. GS166.15.1), mRNA
8041	20927	34200	0.61	9.0E-79	D30658.1	NT	Human T-cell mRNA for glycolytic RNA synthetase, complete cds
8020	21850	35204	0.83	9.0E-79	U141760	NT	Homo sapiens thymidylate synthase (TARS), mRNA
8020	21850	35205	0.83	9.0E-79	U141760	NT	Homo sapiens thymidylate synthase (TARS), mRNA
9515	22841	35911	6.45	9.0E-79	D29553.1	NT	Homo sapiens casein kinase II alpha subunit (CK2A), complete cds
9515	22841	35912	6.45	9.0E-79	D29553.1	NT	Homo sapiens casein kinase II alpha subunit (CK2A), complete cds
10881	23781	37160	0.73	9.0E-79	U1438463	NT	Homo sapiens zinc finger protein 219 alpha variant 1 (ZNF219), mRNA, complete cds
10901	23780	37212	1.11	9.0E-79	AF023461.1	NT	Homo sapiens zinc finger protein 219 alpha variant 1 (ZNF219), mRNA, complete cds
10901	23780	37213	1.11	9.0E-79	AF023461.1	NT	Homo sapiens zinc finger protein 219 alpha variant 1 (ZNF219), mRNA, complete cds
11945	24780	35295	3.28	9.0E-79	U1432827	NT	Homo sapiens suppressor of white spotted homology 2 (SWAP2), mRNA
11945	24780	35297	3.28	9.0E-79	U1432827	NT	Homo sapiens suppressor of white spotted homology 2 (SWAP2), mRNA
11945	24780	35297	3.28	9.0E-79	U1432827	NT	Homo sapiens suppressor of white spotted homology 2 (SWAP2), mRNA
13023	25950	31700	2.54	9.0E-79	U141787	NT	Homo sapiens gamma-glutamyltransferrase 1 (GGT1), mRNA
3805	16853	38722	0.9	9.0E-79	AF18270.2	NT	Human mRNA for KIAA0446 gene, complete cds
4659	17017	34748	0.67	9.0E-79	D25478.1	NT	Human mRNA for KIAA0446 gene, complete cds
4659	17017	34748	0.67	9.0E-79	D25478.1	NT	Human mRNA for KIAA0446 gene, complete cds
5261	19248	28248	2.47	9.0E-79	BE110946.1	EST_HUMAN	001472/0611 NIH MG3 68 Homo sapiens cDNA clone IMAGE:3976657.3
5261	19248	28248	2.47	9.0E-79	BE110946.1	EST_HUMAN	001472/0611 NIH MG3 68 Homo sapiens cDNA clone IMAGE:3976657.3
5261	19248	28248	2.47	9.0E-79	BE110946.1	EST_HUMAN	001472/0611 NIH MG3 68 Homo sapiens cDNA clone IMAGE:3976657.3
12259	22570		3.18	9.0E-79	AF098293.1	EST_HUMAN	J9404.21 Sources: fetal liver, spleen, INTLS. 31 Homo sapiens cDNA clone IMAGE:462598.3 similar to
11927	24712	38270	2.77	9.0E-79	AF163262.2	NT	HLA-DQ10 Q15409 NEUTRAL PROTEASE LARGE SUBUNIT
3219	16797		0.65	4.0E-79	89022326	NT	Homo sapiens chromosome 21 segment HS27C046
3333	13423	20539	2.27	3.0E-79	AF114480.1	NT	Homo sapiens chromosome 21 segment HS27C046
1005	14064	20598	3.03	3.0E-79	AF122708.1	NT	Homo sapiens inter-alpha-trypsin inhibitor (ITIN) mRNA, complete cds
1005	14064	20598	3.03	3.0E-79	AF122708.1	NT	Homo sapiens inter-alpha-trypsin inhibitor (ITIN) mRNA, complete cds
1005	14064	20598	3.03	3.0E-79	AF122708.1	NT	Homo sapiens inter-alpha-trypsin inhibitor (ITIN) mRNA, complete cds

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Table 4

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Emission Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3146	101908	29089	1.96	3.0E-70	U06410.1	NT	Human zinc finger protein ZNF-33 mRNA, partial cds
5259	182856	31104	0.7	3.0E-79	AF114498.1	NT	Homo sapiens intercalin short isoform (ITSN) mRNA, complete cds
8390	182856	31105	0.7	3.0E-79	AF114498.1	NT	Homo sapiens intercalin short isoform (ITSN) mRNA, complete cds
5548	186224	31469	6.86	3.0E-79	AF103322.1	NT	Homo sapiens MSTP010 (MST010) mRNA, complete cds
5925	186822	32111	1.81	3.0E-79	AB020999.1	NT	Homo sapiens mRNA for LMO2/2 protein, partial cds
6964	19021	32141	0.94	3.0E-79	BE78470.1	EST_HUMAN	3014821387 NH_MGC_35 Homo sapiens cDNA clone IMAGE:3804554.8
5964	19021	32142	0.94	3.0E-79	BE78470.1	EST_HUMAN	3014821387 NH_MGC_35 Homo sapiens cDNA clone IMAGE:3804554.8
6977	19042	32164	3.79	3.0E-79	11426770.1	NT	Homo sapiens protein 11426770 mRNA
6977	19042	32166	3.79	3.0E-79	11426770.1	NT	Homo sapiens protein 11426770 mRNA
7049	20076	33308	0.83	3.0E-79	BE25893.1	EST_HUMAN	6011120357 NH_MGC_15 Homo sapiens cDNA clone IMAGE:3352845.9
7414	20113	33347	4.55	3.0E-79	AB011426.1	NT	Homo sapiens mRNA for KIAA0520 protein, partial cds
7414	20113	33348	4.55	3.0E-79	AB011426.1	NT	Homo sapiens mRNA for KIAA0520 protein, partial cds
8370	21274	34607	0.54	3.0E-79	AB011426.1	NT	Homo sapiens mRNA for KIAA0520 protein, partial cds
8742	21672	35016	0.71	3.0E-79	AF242973.1	NT	Homo sapiens protein 35016 mRNA
10845	21726	37884	1.9	3.0E-79	AF242973.1	EST_HUMAN	AV1688115 GIC Homo sapiens cDNA clone GICARE11.8
11298	24218	37885	1.9	3.0E-79	AF242973.1	EST_HUMAN	AV1688115 GIC Homo sapiens cDNA clone GICARE11.8
307	13400	26830	0.83	3.0E-79	H0129.1	EST_HUMAN	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
657	13719	26830	2.34	2.0E-79	BE379926.1	EST_HUMAN	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
958	14058	26952	1.45	2.0E-79	U52947.1	EST_HUMAN	Homo sapiens BCL-2-like 2 (BCL2L2) mRNA
1091	14105	26178	1.37	2.0E-79	U52947.1	EST_HUMAN	Homo sapiens BCL-2-like 2 (BCL2L2) mRNA
2102	16174	26178	9.07	2.0E-79	44559593	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2102	16174	26179	9.07	2.0E-79	44559593	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2334	18342	26147	2.37	2.0E-79	A724138.1	NT	Homo sapiens hepatocellular carcinoma-associated antigen 65 (HCA65) mRNA, complete cds
4292	17278	30147	1.41	2.0E-79	AJ27408.1	NT	Homo sapiens mRNA for Fes-associated factor, FAF1 (FAF1) gene
4801	17602	30989	0.80	2.0E-79	AL162056.2	NT	Homo sapiens chromosome 21 segment HS21C069
5968	18939		1.21	2.0E-79	AA312223.1	EST_HUMAN	EST165206-JuVar T-cell VI Homo sapiens cDNA 5' and similar to C. elegans hypothetical protein, cunf1 D0003.15
5028	18945	32114	0.76	2.0E-79	1111756.1	NT	Homo sapiens X transcription protein 3 (XTP3), mRNA
6491	19535	32713	1.05	2.0E-79	AB020597.1	NT	Homo sapiens mRNA for KIAA0530 protein, partial cds
7297	18495	31336	2.11	2.0E-79	AF200613.1	NT	Homo sapiens membrane associated calcium-independent phospholipase A2 gamma mRNA, complete cds
7530	20450	33767	1.72	2.0E-79	7392479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
7530	20459	33768	1.72	2.0E-79	7392479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	OFF-SEQ ID NO:	Expression Signal	Mod Shifter (Top Hit) BLAST E Value	Top Hit Occasion No.	Top Hit Database Source	Top Hit Descriptor
8879	21610	34651	1.06	2.0E-79	409842	NT	Homo sapiens reticulon-like 1 (p107) (REL1) mRNA
9082	22011	33588	2.37	2.0E-79	11427429	NT	Homo sapiens hypothetical protein FL11069 (FL11069), mRNA
9325	22283	33617	0.74	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FL10275 (FL10275), mRNA
9325	22283	33617	0.74	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FL10275 (FL10275), mRNA
9546	22483	35843	0.86	2.0E-79	11432164	NT	Homo sapiens similar to A17684, H4 transporting lysosomal (vacuolar proton pump) membrane sector associated protein M2-9 (H4 sapiens) (LOC38396), mRNA
10584	23400	39807	1.72	2.0E-79	572869.1	NT	HLA-DQB1*03:01-pulsed cytotoxic T lymphocyte antigen 4 (HLA-DQB1*03:01), mRNA, 3811 nt
10584	23400	39808	1.72	2.0E-79	572869.1	NT	HLA-DQB1*03:01-pulsed cytotoxic T lymphocyte antigen 4 (HLA-DQB1*03:01), mRNA, 3811 nt
11470	24383	37850	5.89	2.0E-79	BE064385.1	EST HUMAN	ROB110310-10300-01579 B10310 Homo sapiens cDNA
11470	24383	37851	5.89	2.0E-79	BE064386.1	EST HUMAN	ROB110310-10300-01579 B10310 Homo sapiens cDNA
12294	14432	31354	4.37	2.0E-79	762387	NT	Homo sapiens KIAA0379 protein (KIAA0379), mRNA
12872	28165	31869	4.94	2.0E-79	4920540.1	NT	Homo sapiens cDNA for KIAA0383 protein, partial cds
12878	28279	31869	4.88	2.0E-79	11418322	NT	Homo sapiens cDNA for EGF LAG receptor, G-type receptor 1 (GELSRI), mRNA
6870	23586	31869	2.89	1.0E-79	BF598307.1	EST HUMAN	M67400001-290000-0174510 NN0387 Homo sapiens cDNA
6891	20016	32420	0.51	1.0E-79	AB813480.1	EST HUMAN	M67400001-290000-0174510 NN0387 Homo sapiens cDNA clone IMAGE:2281286.3 similar to TR-Q29623 Q29623
6891	20016	32421	0.51	1.0E-79	AB813480.1	EST HUMAN	M67400001-290000-0174510 NN0387 Homo sapiens cDNA clone IMAGE:2281286.3 similar to TR-Q29623 Q29623
8830	21750	33906	0.92	1.0E-79	EE942411	EST HUMAN	TEKTN C1:
12048	24389	33903	1.84	1.0E-79	BF047405.1	EST HUMAN	TEKTN C1:
31869	18238	29132	2.95	9.0E-80	A4725949.1	EST HUMAN	Q12110505-120000-359-405 H10-50 Homo sapiens cDNA
31869	18238	29133	2.86	9.0E-80	AA725948.1	EST HUMAN	Q12110505-120000-359-405 H10-50 Homo sapiens cDNA
10516	23423	39816	1.18	9.0E-80	BE739603.1	EST HUMAN	Q12110505-120000-359-405 H10-50 Homo sapiens cDNA
11722	24524	39104	6.06	9.0E-80	11433924	NT	Homo sapiens scellin carrier family 7 (cellular amino acid transporter, Y1 system), member 8 (SLC7A8), mRNA
11722	24524	39105	6.06	9.0E-80	11433924	NT	Homo sapiens scellin carrier family 7 (cellular amino acid transporter, Y1 system), member 8 (SLC7A8), mRNA
3064	18048	34276	1.68	8.0E-80	U64387.1	NT	Homo sapiens X chromosome spermatogenesis candidate protein (RBA) pre-mRNA, partial cds
8048	20051	34277	2.7	8.0E-80	11422947	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
8048	20051	34277	2.7	8.0E-80	11422947	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
9063	22843	39821	1.41	8.0E-80	6056921	NT	Homo sapiens type I functional domain (p115F) (p115F), mRNA
9063	22843	39822	1.41	8.0E-80	6056921	NT	Homo sapiens type I functional domain (p115F) (p115F), mRNA
7313	19481	31304	0.86	7.0E-80	AF127882.1	NT	Callitriche foetida diacyl carrier family 7 (cellular amino acid transporter, Y1 system), member 8 (SLC7A8), mRNA

Table 4

Table 4

Single Exon Probes Expressed in Adult Liver

[illegible]

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	Q57 SEQ ID/NO.	Expression Signal	Met Similar (BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top HE Descriptor
8007	20924	34240	2.79	1.0E-80	AB649731.1	EST_HUMAN	wg25036.x1 NC2_OGAP_KcH1 Homo sapiens cDNA clone IMAGE:217286.9
8007	20924	34241	2.79	1.0E-80	AB649731.1	EST_HUMAN	wg25036.x1 NC2_OGAP_KcH1 Homo sapiens cDNA clone IMAGE:217286.9
8009	21759	35088	0.69	1.0E-80	11421231	NT	Homo sapiens protein tyrosine phosphatase, receptor type 4 (PTPNC1), mRNA
8258	22196	35542	0.73	1.0E-80	11421231	NT	Homo sapiens protein tyrosine phosphatase, receptor type 4 (PTPNC1), mRNA
8258	22196	35543	0.73	1.0E-80	11421231	NT	Homo sapiens protein tyrosine phosphatase, receptor type 4 (PTPNC1), mRNA
8625	22731	36112	1.08	1.0E-80	AF242516.1	NT	Homo sapiens protein tyrosine phosphatase, receptor type 4 (PTPNC1), mRNA
8625	22731	36113	1.08	1.0E-80	AF242516.1	NT	Homo sapiens protein tyrosine phosphatase, receptor type 4 (PTPNC1), mRNA
10088	23793	37222	0.85	1.0E-80	U63479.2	NT	Homo sapiens protein tyrosine phosphatase, receptor type 4 (PTPNC1), mRNA
11089	24027	37470	3.28	1.0E-80	11641276	NT	Homo sapiens protein tyrosine phosphatase, receptor type 4 (PTPNC1), mRNA
11089	24027	37471	3.28	1.0E-80	11641276	NT	Homo sapiens protein tyrosine phosphatase, receptor type 4 (PTPNC1), mRNA
12630	28312	31817	1.68	1.0E-80	11770701	NT	Homo sapiens protein tyrosine phosphatase, receptor type 4 (PTPNC1), mRNA
12845	28497	31970	2.03	1.0E-80	AB101393.1	NT	Homo sapiens protein tyrosine phosphatase, receptor type 4 (PTPNC1), mRNA
11594	24493	31970	2.03	1.0E-80	AB101393.1	NT	Homo sapiens protein tyrosine phosphatase, receptor type 4 (PTPNC1), mRNA
7623	20958	33485	2.17	7.0E-81	AB221153.1	EST_HUMAN	289108.05 Sorex, fetal lung, NH1189 Homo sapiens cDNA clone IMAGE:335280.9
7623	20958	33486	2.17	7.0E-81	AB221153.1	EST_HUMAN	289108.05 Sorex, fetal lung, NH1189 Homo sapiens cDNA clone IMAGE:335280.9
4484	17524	30396	3.69	8.0E-81	BE258639.1	EST_HUMAN	601111979.F1 NH1189 Homo sapiens cDNA clone IMAGE:335280.9
4484	17524	30397	3.69	8.0E-81	BE258639.1	EST_HUMAN	601111979.F1 NH1189 Homo sapiens cDNA clone IMAGE:335280.9
4485	18408	31988	3.18	8.0E-81	48015468	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
5465	18549	31987	1.78	8.0E-81	48015468	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
8020	20945	34261	0.48	6.0E-81	AF036930.1	NT	Homo sapiens chromosome 12p5-p24 beta-1.4-palindromic repeat, complete cds
8020	20945	34261	0.48	6.0E-81	AF036930.1	NT	Homo sapiens chromosome 12p5-p24 beta-1.4-palindromic repeat, complete cds
17178	22702	30087	1.53	6.0E-81	AA360017.1	EST_HUMAN	ES1169128 Fetal lung, 11 Homo sapiens cDNA clone IMAGE:420455.1
17178	22702	30087	1.53	6.0E-81	AA360017.1	EST_HUMAN	ES1169128 Fetal lung, 11 Homo sapiens cDNA clone IMAGE:420455.1
17178	22702	30087	1.53	6.0E-81	AA360017.1	EST_HUMAN	ES1169128 Fetal lung, 11 Homo sapiens cDNA clone IMAGE:420455.1
17178	22702	30087	1.53	6.0E-81	AA360017.1	EST_HUMAN	ES1169128 Fetal lung, 11 Homo sapiens cDNA clone IMAGE:420455.1
2331	15241	28249	1.23	5.0E-81	BF760022.1	EST_HUMAN	602193866.F1 NH1189 Homo sapiens cDNA clone IMAGE:335280.9
2331	15241	28249	1.23	5.0E-81	BF760022.1	EST_HUMAN	602193866.F1 NH1189 Homo sapiens cDNA clone IMAGE:335280.9
8683	21913	35269	2.21	5.0E-81	AB007623.1	NT	Homo sapiens mRNA for KIAA0542 protein, partial cds
8683	21913	35270	2.21	5.0E-81	AB007623.1	NT	Homo sapiens mRNA for KIAA0542 protein, partial cds
10174	23055	39482	1.15	5.0E-81	AB007616.1	NT	Homo sapiens transforming growth factor-beta1 (tgf-beta1) mRNA, complete cds
10174	23055	39483	1.15	5.0E-81	AB007616.1	NT	Homo sapiens transforming growth factor-beta1 (tgf-beta1) mRNA, complete cds
12015	24857	39357	2.24	5.0E-81	9506634	NT	Homo sapiens hypothetical protein (F11105), mRNA
2017	13335	28249	3.37	4.0E-81	AF252281.1	NT	Homo sapiens ORF2 binding protein mRNA, partial cds
3213	18261	29160	4.51	4.0E-81	AB037785.1	NT	Homo sapiens ORF2 binding protein mRNA, partial cds
3898	19728	29619	0.71	4.0E-81	AN004988.1	EST_HUMAN	wg9003.x1 NC2_OGAP_KcH1 Homo sapiens cDNA clone IMAGE:2505289.9 similar to IRO43815 O43815 STRAIN1
4257	17273	39140	1.61	4.0E-81	AF203098.1	NT	Homo sapiens rab5 interacting protein variant 2 mRNA, partial cds
4257	17273	39141	1.61	4.0E-81	AF203098.1	NT	Homo sapiens rab5 interacting protein variant 2 mRNA, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7053	20487	33983	0.81	4.0E-81	4757683	NT	Homo sapiens sodium channel, voltage-dependent L type, alpha 2 (delta subunit) (CACNA2) mRNA
7798	20727	34029	0.42	4.0E-81	11420544	NT	Homo sapiens cdc variant gene 1 (CEV1) mRNA
9844	21764	35146	2.83	4.0E-81	X09695.1	NT	Human mRNA for amyloid A1 (A1) protein
9844	21764	35146	2.83	4.0E-81	X09695.1	NT	Human mRNA for amyloid A1 (A1) protein
9109	22037	35391	3.75	4.0E-81	U20197.1	NT	Human cDNA clone for cell cycle-associated protein (p34 ^{cdc2})
9109	22037	35392	3.75	4.0E-81	U20197.1	NT	Human cDNA clone for cell cycle-associated protein (p34 ^{cdc2})
9767	22661	35977	1.82	4.0E-81	A021603.1	NT	Human sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
10022	25488	36977	1.31	4.0E-81	11435325	NT	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
10697	25953	35985	0.77	4.0E-81	11435325	NT	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
10697	25953	35986	0.77	4.0E-81	11435325	NT	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
11030	26359	36005	4.28	4.0E-81	U78039.1	NT	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
11630	24538	35007	4.28	4.0E-81	U78039.1	NT	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
12250	25338	31452	5.69	4.0E-81	11417862	NT	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
12250	25338	31452	5.69	4.0E-81	11417862	NT	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
12783	25430	31702	5.68	4.0E-81	11417871	NT	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
12783	25430	31702	5.68	4.0E-81	11417871	NT	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
13023	26439	31785	5.68	4.0E-81	11417871	NT	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
13023	26439	31785	5.68	4.0E-81	11417871	NT	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
1304	14337	27272	8.65	3.0E-81	Y18000.1	NT	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
1304	14337	27272	8.65	3.0E-81	Y18000.1	NT	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
2305	15400	26404	1.6	3.0E-81	AF07188.1	NT	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
3032	10084	28584	8.1	3.0E-81	4502230	NT	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
3032	10084	28585	8.1	3.0E-81	4502230	NT	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
2800	16035	28639	1.95	2.0E-81	BE784938.1	EST_HUMAN	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
2800	16035	28639	1.95	2.0E-81	BE784938.1	EST_HUMAN	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
3541	10370	29754	0.78	2.0E-81	AW671542.1	EST_HUMAN	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
3541	10370	29754	0.78	2.0E-81	AW671542.1	EST_HUMAN	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
13522	18670	29754	5.38	2.0E-81	AW671542.1	EST_HUMAN	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
13522	18670	29754	5.38	2.0E-81	AW671542.1	EST_HUMAN	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
4095	17942	30005	2.98	1.0E-81	A0400370.1	EST_HUMAN	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
4750	17701	30023	0.98	1.0E-81	BE07696.1	EST_HUMAN	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
5294	18270	31118	1.03	1.0E-81	9608844	NT	Homo sapiens (HSA) DNA, XTP-3 (p34 ^{cdc2}) (LUC5) mRNA
5417	18410	35852	2.95	1.0E-81	U97928.1	NT	Human scintillation hyaluronate (AC02) gene, exon 3

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar EST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5338	18617	31467	3.74	1.0E-81	11423596	NT	Homo sapiens polymerase (DNA directed), gamma (POL3), mRNA
5338	18617	31468	3.74	1.0E-81	11423596	NT	Homo sapiens polymerase (DNA directed), gamma (POL3), mRNA
6092	18705	31689	0.71	1.0E-81	AJ26599.1	EST_HUMAN	ZR50001.1 Scara, NHHM, 5' Homo sapiens cDNA clone IMAGE:682475 5' similar to SW-PR12, HUMAN
6851	18922	32036	2.89	1.0E-81	U22851.1	NT	P-4643 DNA PHMASE 98 KD SUBUNIT 1
6851	18922	32037	2.89	1.0E-81	U22851.1	NT	Homo sapiens anti-repeat protein NRP1/Proteinase
6396	19435	32653	1.68	1.0E-81	B59744.1	EST_HUMAN	Homo sapiens anti-repeat protein NRP1/Proteinase
6928	19681	33072	0.53	1.0E-81	11423596	NT	P-4643 DNA PHMASE 98 KD SUBUNIT 1
6928	19681	33073	0.53	1.0E-81	11423596	NT	Homo sapiens anti-repeat protein NRP1/Proteinase
7042	20068	33202	0.84	1.0E-81	AJ15220.1	NT	Homo sapiens phosphatase (C; casein kinase-dependent) (PDE3C), mRNA
6242	21147	34450	7.73	1.0E-81	AJ15220.1	NT	Homo sapiens phosphatase (DNA directed), gamma (POL3), mRNA
6272	21777	34613	0.68	1.0E-81	AJ26599.1	NT	Homo sapiens S15 gene for GLB protein
10295	23193	36936	1.37	1.0E-81	BE74546.1	EST_HUMAN	80134593.F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:380228 5'
10295	23193	36937	1.37	1.0E-81	BE74546.1	EST_HUMAN	80134593.F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:380228 5'
10476	23353	36777	0.73	1.0E-81	BE564397.1	EST_HUMAN	801343180.F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:388483 5'
10804	23400	36916	1.19	1.0E-81	A4633784.1	EST_HUMAN	ac14004.01 Sphingomyelinase H4, cell 43 87216 Homo sapiens cDNA clone IMAGE:889427 5' similar to
10804	23402	36921	3.6	1.0E-81	BE74546.1	EST_HUMAN	SW-1938, YEAST P38126 HYPOTHETICAL 90.5 KD PROTEIN IN RPS101-RPS13 INTERGENIC
10804	23402	36922	3.6	1.0E-81	BE74546.1	EST_HUMAN	REGION 1
10804	23470	37290	1.36	1.0E-81	AW697150.1	EST_HUMAN	80157339.F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3833260 5'
11378	24285	37741	1.91	1.0E-81	8923696	NT	CM3 NN0009-140000-147-nt12 NN0059 Homo sapiens cDNA
11631	24411	37960	1.86	1.0E-81	AW644969.1	EST_HUMAN	Homo sapiens grp94-like protein (GRP), mRNA
11631	24411	37961	1.86	1.0E-81	AW644969.1	EST_HUMAN	MRQ-CT0000-260699-019 CT0009 Homo sapiens cDNA
11894	24703	38239	1.62	1.0E-81	BF2042363.1	EST_HUMAN	MRQ-CT0000-260699-019 CT0009 Homo sapiens cDNA
12476	26221	31857	3.72	1.0E-81	11418138	NT	80159774.F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110489 5'
13	13128	28014	3.86	8.0E-42	AF161406.1	NT	Homo sapiens photolabile (similar to scd3) protein B mRNA, selfing protein (DJ42519.2), mRNA
110	13126	28014	2.9	8.0E-42	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
283	13377	29282	1.76	6.0E-42	U06888.1	NT	Homo sapiens HSPC288 mRNA, partial cds
839	13894	29851	3.17	6.0E-42	U06888.1	NT	Human CRFB4 gene, partial cds
912	13964	29511	1.72	6.0E-42	U06888.1	NT	Human CRFB4 gene, partial cds
1509	14540	27502	1.36	6.0E-42	A0303748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most similar (100) BLAST E value	Top Hit Accid No.	Top Hit Database Source	Top Hit Description
1684	14714	27676	1.76	8.0E-42	PF16601	NT	Human sapiens glutathione peroxidase 3 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
4342	17556	30221	0.60	8.0E-42	B924342	NT	Human sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA
1460	1490	1490	1.19	7.0E-42	BF034321	EST	Human sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA
2817	15806	28604	2	7.0E-42	AF144060.1	EST	Homo sapiens cDNA clone IMAGE382065 5'
4222	17228	30104	0.72	6.0E-42	AF144060.1	EST	Homo sapiens cDNA clone IMAGE382065 5'
1697	14727	27691	1.421	6.0E-42	AF081484.1	EST	Human sapiens cDNA clone IMAGE382065 5'
6586	17669	31682	0.677	4.0E-42	AF081484.1	EST	Human sapiens cDNA clone IMAGE382065 5'
5585	18766	31683	0.677	4.0E-42	BF185169.1	EST	Human sapiens cDNA clone IMAGE382065 5'
6584	18765	32152	0.683	4.0E-42	BF185169.1	EST	Human sapiens cDNA clone IMAGE382065 5'
11047	23831	31731	0.52	4.0E-42	U28833.1	EST	Human sapiens cDNA clone IMAGE382065 5'
12198	24769	36479	3.37	4.0E-42	AF27900.1	EST	Human sapiens cDNA clone IMAGE382065 5'
12170	23582		3.85	4.0E-42	AF27900.1	EST	Human sapiens cDNA clone IMAGE382065 5'
297	13351	28510	13.28	3.0E-42	AF021661	NT	Human sapiens presenilin-1 gene, exons 1 and 2
726	13461	29756	4.14	3.0E-42	B000303	EST	Human sapiens amyloid beta (A4) precursor protein (protease inhibitor, Alzheimer disease) (APP), mRNA
814	13569	29805	4.14	3.0E-42	BF17400	NT	Human sapiens amyloid beta (A4) precursor protein (protease inhibitor, Alzheimer disease) (APP), mRNA
895	13548	29805	4.08	3.0E-42	AF021661	EST	Human sapiens amyloid beta (A4) precursor protein (protease inhibitor, Alzheimer disease) (APP), mRNA
1038	14141	27370	1.06	3.0E-42	AF157948.1	EST	Human sapiens amyloid beta (A4) precursor protein (protease inhibitor, Alzheimer disease) (APP), mRNA
1333	14415	27370	1.06	3.0E-42	AF157948.1	EST	Human sapiens amyloid beta (A4) precursor protein (protease inhibitor, Alzheimer disease) (APP), mRNA
1486	14516	27417	1.42	3.0E-42	AF157948.1	EST	Human sapiens amyloid beta (A4) precursor protein (protease inhibitor, Alzheimer disease) (APP), mRNA
1719	14540	27417	1.42	3.0E-42	AF157948.1	EST	Human sapiens amyloid beta (A4) precursor protein (protease inhibitor, Alzheimer disease) (APP), mRNA
3316	16303	33003	1.42	3.0E-42	AF157948.1	EST	Human sapiens amyloid beta (A4) precursor protein (protease inhibitor, Alzheimer disease) (APP), mRNA
8721	21691	35007	2.85	3.0E-42	U1425260	NT	Human sapiens amyloid beta (A4) precursor protein (protease inhibitor, Alzheimer disease) (APP), mRNA
9119	22047	35406	1.03	3.0E-42	U1425260	NT	Human sapiens amyloid beta (A4) precursor protein (protease inhibitor, Alzheimer disease) (APP), mRNA
9119	22047	35406	1.03	3.0E-42	U1425260	NT	Human sapiens amyloid beta (A4) precursor protein (protease inhibitor, Alzheimer disease) (APP), mRNA
10339	23228	36614	6.56	0.5E-49	AB029000.1	NT	Human sapiens amyloid beta (A4) precursor protein (protease inhibitor, Alzheimer disease) (APP), mRNA
10339	23228	36614	6.56	0.5E-49	AB029000.1	NT	Human sapiens amyloid beta (A4) precursor protein (protease inhibitor, Alzheimer disease) (APP), mRNA
918	13983	29805	1.90	2.0E-42	AB023216.1	NT	Human sapiens amyloid beta (A4) precursor protein (protease inhibitor, Alzheimer disease) (APP), mRNA
918	13983	29805	1.90	2.0E-42	AB023216.1	NT	Human sapiens amyloid beta (A4) precursor protein (protease inhibitor, Alzheimer disease) (APP), mRNA
1711	14769	27708	0.46	2.0E-42	AF023390.1	EST	Human sapiens amyloid beta (A4) precursor protein (protease inhibitor, Alzheimer disease) (APP), mRNA
3019	16071	29873	1.38	2.0E-42	AF163201.2	EST	Human sapiens amyloid beta (A4) precursor protein (protease inhibitor, Alzheimer disease) (APP), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	CRF SEQ ID NO.	Extension Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
663	19726	26836	1.95	4.0E-43	AF224698.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene and ubiquitin-conjugating enzyme E2D 3 (UBE2D) genes, complete cds
3573	19870	25913	3.47	4.0E-43	BE868076.1	EST_HUMAN	EST115309F1 NIH_MGC_71 Homo sapiens cDNA similar to endogenous telomerase RNA
1020	14074		3.06	3.0E-43	AJ368311.1	EST_HUMAN	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
2827	19918		1.98	3.0E-43	AJ368311.1	EST_HUMAN	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
6900	19922		0.7	3.0E-43	AJ177225.1	EST_HUMAN	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
1822	14845	27030	1.28	2.0E-43	AJ368311.1	EST_HUMAN	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
1822	14846	27025	1.28	2.0E-43	AJ368311.1	EST_HUMAN	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
1940	14851	27939	0.51	2.0E-43	N92051.1	EST_HUMAN	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
2134	12020	28046	1.30	2.0E-43	AB023068.1	NT	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
3313	18360	28046	1.30	2.0E-43	BE868076.1	EST_HUMAN	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
3313	18360		2.22	2.0E-43	11430634	NT	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
3942	18971		0.76	2.0E-43	AL463302.2	NT	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
4462	17458	30515	6.73	2.0E-43	AF220279.1	NT	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
4752	17757	30630	1.84	2.0E-43	AF220279.1	NT	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
4752	17757	30631	1.84	2.0E-43	77035308	NT	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
5435	18534	31076	0.77	2.0E-43	U65979.1	NT	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
5558	18732	31037	0.44	2.0E-43	11024711	NT	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
6059	18722	31636	0.49	2.0E-43	11428031	NT	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
6192	19249	32395	1.15	2.0E-43	BE868076.1	EST_HUMAN	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
7030	20078	33039	0.44	2.0E-43	AF129533.1	NT	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
7539	20797	34070	0.71	2.0E-43	AF129533.1	NT	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
8312	21216	34662	0.47	2.0E-43	BF129597.1	EST_HUMAN	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
8426	21357	34695	0.65	2.0E-43	AB001025.1	NT	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
8426	21357	34695	0.65	2.0E-43	AB001025.1	NT	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
8596	21497	34840	1.73	2.0E-43	U66707.1	NT	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
8859	21819	35170	2.5	2.0E-43	AF011820.1	NT	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
8859	21819	35171	2.5	2.0E-43	AF011820.1	NT	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
10517	29423	36838	2.2	2.0E-43	M22684.1	NT	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA
10517	29423	36839	2.2	2.0E-43	M22684.1	NT	EST176542 Human1 Homo sapiens cDNA similar to similar to endogenous telomerase RNA

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ IDNO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10617	23653	39637	1.35	2.0E-83	AF117699.1	EST_HUMAN	AUT17699/HEM1A1 Homo sapiens cDNA clone HEH6A1001910 3'
10686	23692	37002	1.98	2.0E-83	AF150960.1	EST_HUMAN	UHF-ENO-endo-H-07-QUL11 NIH_MGC 30 Homo sapiens cDNA clone IMAGE:3081852 3'
11284	24205	37955	4.46	2.0E-83	U1149448	NT	Homo sapiens KIA00895 protein (KIA00895), mRNA
11385	24293	37726	1.74	2.0E-83	AL13452.1	EST_HUMAN	UKF-p507/1183_P1 547 (synonym: hbc11) Homo sapiens cDNA clone DKF25657J185 5'
11386	24293	37727	1.74	2.0E-83	AL134492.1	EST_HUMAN	DKF25657J185_P1 547 (synonym: hbc11) Homo sapiens cDNA clone DKF25657J185 5'
12842	25454		5.7	2.0E-83	AB013989.1	NT	Homo sapiens gene for AF-8, complete cds
1435	14466	27421	2.02	1.0E-83	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase-3-like-1/Coenzyme A hydratase (functional protein), best subset (H4D18) mRNA
1435	14466	27422	2.02	1.0E-83	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase-3-like-1/Coenzyme A hydratase (functional protein), best subset (H4D18) mRNA, complete cds
1478	14509	27459	4.08	1.0E-83	AF105067.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
1478	14509	27470	4.08	1.0E-83	AF105067.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
2032	15046	28048	1.48	1.0E-83	4503652	NT	Homo sapiens fatty-acyl-Coenzyme A ligase, very long-chain 1 (FACL1) mRNA
2705	15699	28594	2.18	1.0E-83	BE889690.1	EST_HUMAN	1015073791 NIH_MGC-71 Homo sapiens cDNA clone KIA03683, mRNA
3228	16274	29175	0.77	1.0E-83	762349	NT	Homo sapiens cell recognition molecule 1 (CD133) protein (gp130), partial cds
3537	16995	29517	3.65	1.0E-83	AF053763.1	NT	Rattus norvegicus fish specific cell surface protein gp130 (gp130), partial cds
4343	17357	30222	2.52	1.0E-83	225922.1	NT	11 sapiens gene for melanotransferrin/CD4 melanotransferrin, exon 3
6983	20020	33293	1.7	1.0E-83	AB27914.1	EST_HUMAN	698068.AT Saccus, testis, NHT Homo sapiens cDNA clone IMAGE:364541 3' similar to gb:AB24241.0M
3861	15900	20775	4.16	7.0E-84	BE307209.1	EST_HUMAN	6016760235 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3658653 5'
1321	14354	27290	3.95	6.0E-84	BE338854.1	EST_HUMAN	R23.FN0119-20050-011-q05 FN0119 Homo sapiens cDNA
1321	14354	27300	3.95	6.0E-84	BE338854.1	EST_HUMAN	R23.FN0119-20050-011-q05 FN0119 Homo sapiens cDNA
2420	14244	28425	7.2	6.0E-84	BE170574.1	EST_HUMAN	242033.41 Singapore zebrafish brain S11 Homo sapiens cDNA clone IMAGE:371020 3'
5420	15418		1.83	6.0E-84	AL02683.2	EST_HUMAN	DKF256440322_P1 544 (synonym: hbc3) Homo sapiens cDNA clone DKF256440322 5'
5798	15757	31711	1.68	6.0E-84	AA873389.1	EST_HUMAN	451763.41 Swiss_NEL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1460500 3' similar to gb:AF14338
5687	18928	32045	1.36	6.0E-84	11426718	NT	VITAMIN K-DEPENDENT PROTEIN 3 (PRECURSOR (HUMAN); Homo sapiens acyl LDL receptor, SRE-Coxa/wingtip receptor expressed by endothelial cells (SRECL), mRNA
5687	18928	32045	1.36	6.0E-84	11426718	NT	Homo sapiens acyl LDL receptor, SRE-Coxa/wingtip receptor expressed by endothelial cells (SRECL), mRNA
7903	20819	34125	3.45	8.0E-84	BE810371.1	EST_HUMAN	PM0.L10019-10000-307-F02.L10019 Homo sapiens cDNA
8145	21054	34985	0.81	6.0E-84	BE133891.1	EST_HUMAN	Homo sapiens ure-mRNA splicing factor (PRP19) mRNA, complete cds
8634	21632	34917	2.71	6.0E-84	BE177089.1	EST_HUMAN	PM0.F10054-10050-004-e10.F10054 Homo sapiens cDNA
7707	13795	26720	0.75	6.0E-84	AA382811.1	EST_HUMAN	EST196094.1 testis 1 Homo sapiens cDNA 5' end

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8556	21866	352545	0.56	2.0E-54	AL163204.2	NT	Human sapiens chromosome 21 segment 145713034
9884	27760	36185	1.05	2.0E-54	AU122626.1	EST_HUMAN	AU122626.1 Hs3851 Homo sapiens cDNA clone HELMS1000359 5'
10352	23142	30651	0.64	2.0E-54	U22941.1	EST_HUMAN	U22941.1 Hs3851 Homo sapiens cDNA clone IMAGE:1383 5' similar to SPAPOH RAT
12602	25236	31853	1.86	2.0E-54	BF46900.1	EST_HUMAN	BF46900.1 Hs3851 Homo sapiens cDNA clone IMAGE:490025 3' similar to
12502	25235	31854	1.69	2.0E-54	BF46900.1	EST_HUMAN	BF46900.1 Hs3851 Homo sapiens cDNA clone IMAGE:490025 3' similar to
332	13422	28538	1.58	1.0E-54	AF114488.1	NT	Human sapiens intrachain short isoform (ITSN) mRNA, complete cds
571	13635	29548	6.27	1.0E-54	4507552	NT	Homo sapiens lysine 5-methoxyglutamate lysochitin 5-methoxyglutamate activation protein, zeta polypeptide (YVHAZ) mRNA
743	13901	14562	2.78	1.0E-54	11427831	NT	Homo sapiens complement component 6 (C6), mRNA
1316	14562	27297	2.16	1.0E-54	AA984379.1	EST_HUMAN	AA984379.1 Hs3851 Homo sapiens cDNA clone IMAGE:1829385 3'
2087	15082	28081	2.16	1.0E-54	BE92137.1	EST_HUMAN	BE92137.1 Hs3851 Homo sapiens cDNA clone IMAGE:302657 5'
3814	16844	29730	2.53	1.0E-54	AA122951.1	EST_HUMAN	AA122951.1 Hs3851 Homo sapiens cDNA clone IMAGE:1230102 3'
4324	17333	30395	0.59	1.0E-54	A122951.1	NT	Homo sapiens 596 to 597 contig between AML1 and CBRT on chromosome 21q22 segment 1/3
4812	17813	30679	2.35	1.0E-54	AL043314.2	EST_HUMAN	DKFZ343N0323.1 434 (synonym: hms3) Homo sapiens cDNA clone DKFZ343N0323 5'
4812	17813	30680	2.35	1.0E-54	AL043314.2	EST_HUMAN	DKFZ343N0323.1 434 (synonym: hms3) Homo sapiens cDNA clone DKFZ343N0323 5'
5016	17833	30695	3.24	1.0E-54	A122951.1	NT	Homo sapiens 596 to 597 contig between AML1 and CBRT on chromosome 21q22 segment 1/3
6114	19203	52340	0.59	1.0E-54	11434422	NT	Homo sapiens spectrin-type POZ protein (SPOP), mRNA
6431	19478	32655	1.2	1.0E-54	575482.1	NT	Uterine water channel-29 kDa glycoprotein integral membrane protein homolog (Juman), mRNA, 1340 nt
7207	20207	33452	2.17	1.0E-54	AL049784.1	NT	Novel human gene mapping to chromosome 13
7207	20207	33460	2.17	1.0E-54	AL049784.1	NT	Novel human gene mapping to chromosome 13
7469	20406	33682	2.62	1.0E-54	AL049784.1	NT	Novel human gene mapping to chromosome 13
7887	20813	34119	4.20	1.0E-54	839304	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
7887	20813	34231	0.82	1.0E-54	11430964	NT	Homo sapiens Nucleic acid binding protein 1 (NAB1), mRNA
8044	20915	34231	1.82	1.0E-54	11430964	NT	Homo sapiens Nucleic acid binding protein 1 (NAB1), mRNA
10054	23680	35502	2.59	1.0E-54	503184	NT	Homo sapiens nuclear transport factor 2 (nuclear protein 15), pP15, mRNA
10300	23180	35502	0.54	1.0E-54	AF224911.1	NT	Homo sapiens Cdk2-inhibiting protein Cdk2i3 (Cdk2i3) gene, exon 6 and partial cds
10308	18624	31346	1.78	1.0E-54	4507948	NT	Homo sapiens ubiquitin specific protease 13 (ubiquitinase 13) (USP-13), mRNA
10308	18624	31349	1.78	1.0E-54	4507948	NT	Homo sapiens ubiquitin specific protease 13 (ubiquitinase 13) (USP-13), mRNA
10308	18624	31349	1.78	1.0E-54	11417018	NT	Homo sapiens peroxisomal protein 22 kDa, cytoplasmic (P22C1), mRNA
12654	25235	31850	2.83	1.0E-54	11416183	NT	Homo sapiens acyl-CoA oxidase 2, mitochondrial (ACOX2), mRNA

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Probe Seq ID NC:	Exon Seq ID NC:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
963	14243		1.11	0.0E-95 AL163209.2	NT		Homo sapiens chromosome 21 segment HS21C006
1100	14143	27090	1.81	0.0E-95 U51432.1	NT		Homo sapiens nuclear protein 55kD mRNA, complete cds
1100	14143	27091	1.81	0.0E-95 U51432.1	NT		Homo sapiens nuclear protein 55kD mRNA, complete cds
1800	14631	27590	15.18	0.0E-95 U33282.1	NT		Human plasminogen gene, exon 7
1800	14631	27591	15.18	0.0E-95 U33282.1	NT		Human plasminogen gene, exon 7
1701	14730	27606	2.32	0.0E-95	7657020	NT	Homo sapiens DKF7434P211 protein (DKF7434P211), mRNA
3548	16577	29791	1.2	0.0E-95	7618123	NT	Homo sapiens KIA00125 gene product (KIA00125), mRNA
3595	16595	29776	0.92	0.0E-95	7114118	NT	Homo sapiens nuclear GTPase (HMAJANTG), mRNA
4350	17594	30228	1.17	0.0E-95 AL163200.2	NT		Homo sapiens chromosome 21 segment HS21C080
4985	17618	30842	1.14	0.0E-95	5001979	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
5021	18018	30577	1.53	0.0E-95 AL163208.2	NT		Homo sapiens chromosome 21 segment HS21C086
1163	14204	27142	8.33	7.0E-95 U6254.1	NT		Homo sapiens ribosomal protein L27 mRNA, complete cds
12055	24610		3.45	7.0E-85 AF113710.1	NT		Homo sapiens MSTP030 mRNA, complete cds
11549	24699	38100	3.25	0.0E-95	11488573	NT	Homo sapiens DEADH (Aap-Glu-Ala-Asp-His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
11549	24699	38101	3.25	0.0E-95	11488573	NT	Homo sapiens DEADH (Aap-Glu-Ala-Asp-His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
2355	15362	28365	4.70	5.0E-95 AL163284.2	NT		Homo sapiens chromosome 21 segment HS21C094
4540	17549			5.0E-85 AF21189.1	NT		Homo sapiens T-type calcium channel alpha subunit Alperin-1a isoform (CACNA1I), mRNA, complete cds
6538	18712	31612	1.84	5.0E-95 BF035974.1	EST_HUMAN		607489549F11NF_1002_20 Homo sapiens cDNA clone IMAGE382402 5'
6538	18712	31613	1.84	5.0E-95 BF035974.1	EST_HUMAN		607489549F11NF_1002_20 Homo sapiens cDNA clone IMAGE382402 5'
11559	24498	37693	1.62	5.0E-85 AF24689.1	NT		Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E20 3 (UBP23) genes, complete cds
13530	17549		3.87	5.0E-85 AF21189.1	NT		Homo sapiens T-type calcium channel alpha subunit Alperin-1a isoform (CACNA1I), mRNA, complete cds
6388	18437	32974	0.82	4.0E-95 BF113710.1	EST_HUMAN		603847395F11NF_1002_80 Homo sapiens cDNA clone IMAGE248097 5'
7162	19201	33514	1.45	4.0E-85 BF070283.1	EST_HUMAN		604401141 NC1 CGAP Kc11 Homo sapiens cDNA clone IMAGE238506 3'
11055	20203		0.92	4.0E-95 BF070283.1	EST_HUMAN		Homo sapiens protein phosphatase 2A B15 gamma subunit gene, exon 6
1325	14369	27269	0.9	3.0E-95 U7651.1	EST_HUMAN		ye55p10.1 Saccharomyces cerevisiae 11U1.8 Homo sapiens cDNA clone IMAGE121804 5'
1804	1804	27797	3.64	3.0E-95	11024951	NT	Homo sapiens F-box only protein 24 (FBX024), mRNA
5007	19005	30953	1.11	3.0E-95	11024951	NT	Homo sapiens F-box only protein 24 (FBX024), mRNA
5007	18005	30894	1.11	3.0E-95	11024951	NT	Homo sapiens F-box only protein 24 (FBX024), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6397	21201	34057	0.52	1.0E-49	BE303561.1	EST_HUMAN	IMAGE:10254-221193-002-633-510284 Homo sapiens cDNA
10090	23190	36001	2.85	1.0E-46	BE257917.1	EST_HUMAN	IMAGE:10107-281 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:350854 5'
11391	24779	37721	2.15	1.0E-36	AA177851	EST_HUMAN	IMAGE:35245 3'
11391	24779	37721	2.15	1.0E-36	AA177851	EST_HUMAN	IMAGE:35245 3'
11435	24591	37768	3.41	1.0E-36	BF31455.1	EST_HUMAN	IMAGE:35245 3'
11435	24591	37768	3.41	1.0E-36	BF31455.1	EST_HUMAN	IMAGE:35245 3'
12184	26020	38622	1.47	1.0E-35	AF18454.1	EST_HUMAN	IMAGE:35245 3'
12400	25316	31619	6.29	1.0E-36	AF17962	EST_HUMAN	IMAGE:35245 3'
12537	25316	31619	6.29	1.0E-36	AF17962	EST_HUMAN	IMAGE:35245 3'
1463	19418	32660	0.13	1.0E-40	BE27131.1	EST_HUMAN	IMAGE:35245 3'
1463	19418	32660	0.13	1.0E-40	BE27131.1	EST_HUMAN	IMAGE:35245 3'
12720	26360	38464	1.96	8.0E-46	AB22224	EST_HUMAN	IMAGE:35245 3'
12720	26360	38464	1.96	8.0E-46	AB22224	EST_HUMAN	IMAGE:35245 3'
594	14014	29855	0.26	7.0E-40	AA39061.1	EST_HUMAN	IMAGE:35245 3'
594	14014	29855	0.26	7.0E-40	AA39061.1	EST_HUMAN	IMAGE:35245 3'
8437	19494	33659	0.96	7.0E-46	BC59396	EST_HUMAN	IMAGE:35245 3'
8437	19494	33659	0.96	7.0E-46	BC59396	EST_HUMAN	IMAGE:35245 3'
7317	19495	31309	6.87	7.0E-40	11421737	EST_HUMAN	IMAGE:35245 3'
6003	22231	35661	2.95	7.0E-40	136557.1	EST_HUMAN	IMAGE:35245 3'
10222	23113	35351	1.77	7.0E-46	5453907	EST_HUMAN	IMAGE:35245 3'
10270	23106	35351	1.94	7.0E-46	11633027	EST_HUMAN	IMAGE:35245 3'
11336	24315	37761	1.6	7.0E-40	11417012	EST_HUMAN	IMAGE:35245 3'
11336	24315	37761	1.6	7.0E-40	11417012	EST_HUMAN	IMAGE:35245 3'
1320	14533	27266	1.96	6.0E-40	4505492	EST_HUMAN	IMAGE:35245 3'
225	13323	26241	2.97	4.0E-40	BE54173.1	EST_HUMAN	IMAGE:35245 3'
6258	10319	32433	10.82	4.0E-40	BE23843.1	EST_HUMAN	IMAGE:35245 3'
11657	13323	26241	1.98	4.0E-40	BE54173.1	EST_HUMAN	IMAGE:35245 3'
4395	17402	39271	0.79	3.0E-40	BE657706.1	EST_HUMAN	IMAGE:35245 3'
5790	18662	31970	6.08	3.0E-40	AA340646.1	EST_HUMAN	IMAGE:35245 3'
8536	21766	35114	1.23	3.0E-40	AV72239.1	EST_HUMAN	IMAGE:35245 3'
10716	28602	37029	4.98	3.0E-40	BE669479.1	EST_HUMAN	IMAGE:35245 3'
10716	28602	37029	4.98	3.0E-40	BE669479.1	EST_HUMAN	IMAGE:35245 3'
11896	25648	37404	5.29	3.0E-40	AB66240.1	EST_HUMAN	IMAGE:35245 3'
12374	25719		2.69	3.0E-40	BE410354.1	EST_HUMAN	IMAGE:35245 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
437	13390	26254	1.87	2.0E-66	AA006294.1	EST_HUMAN	EST172522 Unint ² ccds VI Homo sapiens cDNA 5' end
298	13390	26254	2.2	2.0E-66	AL102033.2	NT	Homo sapiens chromosome 21 segment RS210089
1218	14795	27196	2.32	2.0E-66	N39677.1	EST_HUMAN	Yer386.71 Source: multiple, unrelated, 2184808P Homo sapiens cDNA clone IMAGE38178.5
2207	16276	28222	7.73	2.0E-66	N39677.1	EST_HUMAN	Human endogenous factor, complex protein
2287	16276	28223	1.89	2.0E-66	A535103.1	NT	Human cDNA for KIAA1112
3475	16315	29416	1.47	2.0E-66	A535103.1	EST_HUMAN	EST192416 MGC for KIAA1112
3809	16339	29726	3.26	2.0E-66	AF160718.1	NT	Homo sapiens lipopolysaccharide and acyltransferase-like (LPAT) cDNA, complete cds
3809	16339	29726	3.26	2.0E-66	AF160718.1	NT	Homo sapiens lipopolysaccharide and acyltransferase-like (LPAT) cDNA, complete cds
4124	17147	30780	3.67	2.0E-66	A535103.1	EST_HUMAN	cds7938.1 UGI COGIPR_G06 Homo sapiens cDNA clone IMAGE281853.3
4302	18191	32282	3.32	2.0E-66	U455402.1	NT	Homo sapiens cAMP-specific phosphodiesterase 5A (PDE5A) mRNA, partial cds
6397	18191	32282	3.32	2.0E-66	U455402.1	NT	Homo sapiens cAMP-specific phosphodiesterase 5A (PDE5A) mRNA, partial cds
8597	18148	32284	1.42	2.0E-66	U45411.1	NT	Homo sapiens mRNA encoding phospholipase 5
7429	26693	33597	0.83	2.0E-66	11419429	NT	Homo sapiens similar to estradiol-induced lipopolysaccharide/phosphodiesterase 5 (H sapiens) (LOC83241), mRNA
5586	21610	34963	0.65	2.0E-66	U64744.1	NT	Human Chediak-Higashi syndrome protein short isoform (LY81) mRNA, complete cds
9137	22095	35429	3.11	2.0E-66	11437135	NT	Homo sapiens butyrobactin (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobactin hydroxylase) (BBOX), mRNA
9137	22095	35429	3.11	2.0E-66	11437135	NT	Homo sapiens butyrobactin (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobactin hydroxylase) (BBOX), mRNA
9137	22095	35429	3.11	2.0E-66	11437135	NT	Homo sapiens butyrobactin (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobactin hydroxylase) (BBOX), mRNA
9460	22389	35761	1.06	2.0E-66	10963879	NT	Homo sapiens phosphatidyl serine-1 (PLSCR1), mRNA
9859	22773	35160	1.66	2.0E-66	11420944	NT	Homo sapiens chromosome segregation 1 (yeast homolog-like CGE1), mRNA
10028	23813	37241	2.86	2.0E-66	11543849	NT	Homo sapiens bac C-helix-loop-helix-PAS protein (NPAS3), mRNA
10028	23813	37241	2.86	2.0E-66	11543849	NT	Homo sapiens bac C-helix-loop-helix-PAS protein (NPAS3), mRNA
10391	23865	37262	1.95	2.0E-66	AE037832.1	NT	Homo sapiens mRNA for KIAA1111 protein, partial cds
11341	24291	37701	1.09	2.0E-66	4759051	NT	Homo sapiens ribosome protein S6 lineage, 900D, polypeptide 5 (RPS6K5) mRNA
12798	26116	31789	3.57	2.0E-66	11418109	NT	Homo sapiens thyroid autoantigen 70MD (Ku antigen) (GZPT), mRNA
12944	29510		3.21	2.0E-66	AU01938.1	NT	Homo sapiens gene for A1-3, complete cds
1020	14690	27613	1.82	1.0E-66	4808656	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (750D) (NADH-coenzyme Q reductase) (NDUFS1) mRNA
9205	16253	29149	1.58	1.0E-66	5153949	NT	Homo sapiens fibulin 5 (FBLN5) mRNA
3282	16330	25236	2.80	1.0E-66	L20492.1	NT	Human (gamma-glutamyl) transpeptidase mRNA, complete cds
3339	16386	25284	2.25	1.0E-66	AL169203.2	NT	Homo sapiens chromosome 21 segment RS210089
3339	16386	25285	2.25	1.0E-66	AL169203.2	NT	Homo sapiens chromosome 21 segment RS210089
4023	17650	29540	0.83	1.0E-66	7706161	NT	Homo sapiens hypothetical protein [LOC51516], mRNA

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Table 4
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Probe SEQ ID NO.	Exon SEC ID NO.	CRF ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4023	17050	28941	0.93	1.0E-58	7703101	NT	Homo sapiens hypothetical protein (LOC51319), mRNA
4954	17378	30242	0.5	1.0E-58	AL163300.2	NT	Homo sapiens chromosome 21 segment H521C100
4734	17378	30501	0.7	1.0E-58	AF057294	NT	Homo sapiens glycylserine 1 (SVN1), mRNA
5744	19377	31613	1.98	1.0E-58	AL163294.2	NT	Homo sapiens chromosome 21 segment H521C084
5641	18920		1.37	0.0E-87	AI153703.1	EST_HUMAN	BT7203.1 Score: 1641, Ident: 99% Homo sapiens cDNA clone IMAGE:706128 3' similar to
7582	20779	34390	2.36	0.0E-87	AF197721	NT	SW K1C11.MOUSE: P03655 IERAT11, TYPE1 CYTOSKELETAL 10:
7603	19379	34391	2.54	0.0E-87	AF197721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
7603	19379	34391	35.07	8.0E-87	X02245.1	NT	O conserved mRNA for detection factor 1 alpha
2015	18923	28524	2.46	7.0E-87	BF043211.1	EST_HUMAN	765602.21 NC1 CGAP Cor6 Homo sapiens cDNA clone IMAGE:3322779 3'
2015	18923	28525	2.46	7.0E-87	BF043211.1	EST_HUMAN	765602.21 NC1 CGAP Cor6 Homo sapiens cDNA clone IMAGE:3322779 3'
6655	19703	33698	0.81	0.0E-87	AF160336.1	EST_HUMAN	NR0-NT0039-009500-304-411 NT0039 Homo sapiens cDNA
6655	19703	33698	3.23	7.0E-87	BF132781.1	EST_HUMAN	LS-H10702-180600-103-409 HT0702 Homo sapiens cDNA
6655	19703	33698	3.23	7.0E-87	BF132781.1	EST_HUMAN	LS-H10702-180600-103-409 HT0702 Homo sapiens cDNA
9498	21344	34679	0.85	7.0E-87	AF132781.1	EST_HUMAN	DKFZp44N0323.11 434 (synonym: Hnc3) Homo sapiens cDNA clone DKFZp44N0323.5'
10573	23459	36860	4.06	7.0E-87	AL043314.2	EST_HUMAN	DKFZp44N0323.11 434 (synonym: Hnc3) Homo sapiens cDNA clone DKFZp44N0323.5'
10573	23459	36860	4.06	7.0E-87	AL043314.2	EST_HUMAN	DKFZp44N0323.11 434 (synonym: Hnc3) Homo sapiens cDNA clone DKFZp44N0323.5'
10947	22658		0.37	7.0E-87	AB018665.1	EST_HUMAN	0459101.41 Scores: N/A-HIP1.S1 Homo sapiens cDNA clone IMAGE:168367 3'
11328	24247	37884	7.39	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-FLA-SB-1 Intron A
11328	24247	37884	7.39	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-FLA-SB-1 Intron A
3588	19025	29528	0.86	6.0E-87	7697213	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
6898	10724	33924	1.45	6.0E-87	AB074004.1	NT	Homo sapiens mRNA for NDA1081 protein, partial cds
11167	24096		3.56	6.0E-87	11432444	NT	Homo sapiens similar to SET translocation (myeloid leukemia-associated) (H: sapiens) (LOC58102), mRNA
1185	14225	27183	1.73	5.0E-87	AA382811.1	EST_HUMAN	EST166604 Testis Homo sapiens cDNA 5' and
12639	14225	27183	1.85	5.0E-87	AA382811.1	EST_HUMAN	EST166604 Testis Homo sapiens cDNA 5' and
982	14042	29884	1.1	4.0E-87	AL163210.2	NT	Homo sapiens chromosome 21 segment H521C010
1200	14296	27176	10.9	4.0E-87	AB037836.1	NT	Homo sapiens mRNA for NDA10414 protein, partial cds
2043	15000	28001	1.8	4.0E-87	AB007626.1	NT	Homo sapiens mRNA for K040005 protein, partial cds
3528	16594	29168	1.84	4.0E-87	517457.1	NT	Homo sapiens myeloid lymphoid or mixed-lineage leukemia (t(9p21+)) homolog, transcribed to 4
6631	18707	31606	14.18	4.0E-87	U000321	SWISSPROT	(MLT14) mRNA
5957	10024	32144	0.47	4.0E-87	U65459.1	NT	ETS-RELATED PROTEIN 71 (ETS TRANSDUCTION VARIANT 2)
6290	10331	32487	4.48	4.0E-87	BE247284.1	EST_HUMAN	Human transcription factor NPA1.3 mRNA, complete cds
							TCGA-P14601 Fetal testis pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCGA Homo sapiens cDNA clone TCGA-4001

Table 4
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Probe SEQ ID SEQ ID NO.	Exon NO.	CRF SEQ ID NO.	Expression Signal	Most Similar (Top) Ht BLASTE Value	Top Ht Accession No.	Top Ht Database Source	Top Ht Descriptor
7647	20485	33714	0.87	1.0E-37	4503786	NT	Homo sapiens 10 motif containing GTPase activating protein 1 (GIGAP-1) mRNA
7707	20725	34028	1.25	1.0E-37	11431590	NT	Homo sapiens protein kinase C, beta 1 (PKC β 1) mRNA
7955	20897	34198	0.44	1.0E-37	4503786	NT	Homo sapiens 10 motif containing GTPase activating protein 1 (GIGAP-1) mRNA
8201	21106	34501	0.51	1.0E-37	4505528	NT	Homo sapiens soluble carrier family 22 (organic cation transporter), member 1-like (SC22A1L) mRNA
8603	21924	34907	0.95	1.0E-37	AF121462.1	NT	Homo sapiens histone H4-enriched protein (H4EN) gene, complete cds
8406	22354	35755	1.44	1.0E-37	AB022918.1	NT	Homo sapiens mRNA for apolipoprotein A-II (APOA2) gene, complete cds
8406	22354	35756	1.44	1.0E-37	AB022918.1	NT	Homo sapiens mRNA for apolipoprotein A-II (APOA2) gene, complete cds
10139	20050	36470	3.18	1.0E-37	BE81183.1	EST_HUMAN	RG5-BN0276-03700-012-EG3 BN0276 Homo sapiens cDNA
10139	20050	36461	3.18	1.0E-37	BE81183.1	EST_HUMAN	RG5-BN0276-03700-012-EG3 BN0276 Homo sapiens cDNA
10891	20747	37171	0.73	1.0E-37	U10333.1	NT	Human 1 protein mRNA, 5' end
11437	24393	37171	1.03	1.0E-37	D10333.1	NT	Homo sapiens RGH1 gene, retinoid-like domain
12726	26058	31965	1.95	1.0E-37	707932	NT	Homo sapiens sulfotransferase-related protein (SULT3), mRNA
13108	26023	31965	5.49	1.0E-37	AF108558.1	NT	Homo sapiens beta-ureidopropionase (SUP-1) gene, exon 9
13108	26023	31967	5.49	1.0E-37	AF108558.1	NT	Homo sapiens beta-ureidopropionase (SUP-1) gene, exon 9
9417	13948	25941	2.32	9.0E-38	5453807	NT	Homo sapiens protease inhibitor 4 (Lipidase) (PI4) mRNA
1133	14175	27112	0.38	9.0E-38	AF167465.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1378	14410	27364	2.49	9.0E-38	AB037820.1	NT	Homo sapiens mRNA for KIAA1359 protein, partial cds
1378	14410	27365	2.49	9.0E-38	AB037820.1	NT	Homo sapiens mRNA for KIAA1359 protein, partial cds
2194	15147	28148	1.01	9.0E-38	7851701	NT	Homo sapiens DKFZP559P1322 protein (DKFZP559P1322) mRNA
3264	15725	28015	1.04	9.0E-38	AL163200.2	NT	Homo sapiens chromosome 21 segment HS210559
4398	17382	30246	3.43	9.0E-38	X01929.1	NT	H sapiens EGE-1 gene (exon 9)
4398	17382	30247	3.43	9.0E-38	X01929.1	NT	H sapiens EGE-1 gene (exon 9)
5124	18120	30882	0.97	9.0E-38	AB020988.1	NT	Homo sapiens DNA, DLEC1 to ORG1L4 gene region, section 12 (DLEC1, ORG1L3, ORG1L4 genes, complete cds)
9572	22499	31885	3.09	6.0E-38	AF005028.1	NT	Homo sapiens X-linked androgenic endometrial dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1852	14374		0.93	5.0E-38	7891187	NT	Homo sapiens KIAA00083 gene product (KIAA00083), mRNA
2687	15881	26882	3.0	5.0E-38	N85998.1	EST_HUMAN	X0718F Human HGF, Lambda ZIP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
3043	15395	26897	0.95	5.0E-38	AF114485.1	NT	Homo sapiens interchain short isoform (ITSN) mRNA, complete cds
3054	15106	26011	0.68	5.0E-38	AF114485.1	NT	Homo sapiens interchain short isoform (ITSN) mRNA, complete cds
3054	15106	26011	0.68	5.0E-38	AF114485.1	NT	Homo sapiens interchain short isoform (ITSN) mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	QTF SEQ ID NO.	Expression Signal	Most Similar (Top) HI BLAST E Value	Top HI Accession No.	Top HI Database Source	Top HI Descriptor
1092	11108	27043	1.94	2.0E-38	7305166	NT	Homo sapiens Calpainin, preventin-binding protein, EF hand inactivation factor (CSEIN), mRNA
1624	14678	27041	2.21	2.0E-38	AF242876.1	NT	Homo sapiens SNARE protein kinase SNARE, complete cds
1775	14671	27041	3.61	2.0E-38	AF242876.1	NT	Homo sapiens SNARE protein kinase SNARE, complete cds
403	17541	27043	2.13	2.0E-38	AF242876.1	NT	Homo sapiens SNARE protein kinase SNARE, complete cds
6134	42501	32377	4.82	1.0E-48	AY151653.1	EST_HUMAN	UH-BH-ase-3-04-04-01-1 NCI CGAP S303 Homo sapiens cDNA clone IMAGE/2719150 3'
6131	42500	32377	3.92	1.0E-48	AY151653.1	EST_HUMAN	UH-BH-ase-3-04-04-01-1 NCI CGAP S303 Homo sapiens cDNA clone IMAGE/2719150 3'
8637	10986	33187	22.47	1.0E-58	U500787.1	NT	Homo sapiens KIA0447 mRNA, complete cds
8637	10986	33188	22.47	1.0E-58	U500787.1	NT	Homo sapiens KIA0447 mRNA, complete cds
7481	20421	33706	1.36	1.0E-58	A59034.1	EST_HUMAN	act-11.1 NCI CGAP C03 Homo sapiens cDNA clone IMAGE/271668 3'
7548	20495	33715	3.95	1.0E-58	AA46894.1	EST_HUMAN	act-11.1 NCI CGAP C03 Homo sapiens cDNA clone IMAGE/271668 3'
8715	21946	34692	0.95	1.0E-58	AF151183.1	NT	CD00651 ;
8784	22746	35130	1.12	1.0E-48	AA160988.1	EST_HUMAN	Homo sapiens RNAi kinase 2 (RCK2) gene, alternative splice products, complete cds
10108	22969	35350	3.12	1.0E-48	AL04314.2	EST_HUMAN	Homo sapiens RNAi kinase 2 (RCK2) gene, alternative splice products, complete cds
11137	24059	37311	1.8	1.0E-48	AA367511.1	EST_HUMAN	SNAP-1, HUMAN, 2289 bp, 5' to 3' (5' to 3' orientation);
11878	23978	37416	3.31	1.0E-48	AA081475.1	EST_HUMAN	SNAP-1, HUMAN, 2289 bp, 5' to 3' (5' to 3' orientation);
12890	23847	37416	4.5	1.0E-48	AL103246.2	NT	SNAP-1, HUMAN, 2289 bp, 5' to 3' (5' to 3' orientation);
15774	15774	28770	2.05	8.0E-49	BC131557.1	EST_HUMAN	SNAP-1, HUMAN, 2289 bp, 5' to 3' (5' to 3' orientation);
7262	20171	33412	1.18	8.0E-50	11421814.1	NT	SNAP-1, HUMAN, 2289 bp, 5' to 3' (5' to 3' orientation);
456	13528	26160	1.22	7.0E-49	7857213.1	NT	SNAP-1, HUMAN, 2289 bp, 5' to 3' (5' to 3' orientation);
456	13528	26451	1.22	7.0E-49	7857213.1	NT	SNAP-1, HUMAN, 2289 bp, 5' to 3' (5' to 3' orientation);
4563	17952	30046	3.78	7.0E-49	4657260.1	NT	SNAP-1, HUMAN, 2289 bp, 5' to 3' (5' to 3' orientation);
5042	18035	30055	7.08	7.0E-49	AL045748.1	EST_HUMAN	SNAP-1, HUMAN, 2289 bp, 5' to 3' (5' to 3' orientation);
5916	18032	31537	1.17	7.0E-49	U50832.1	NT	SNAP-1, HUMAN, 2289 bp, 5' to 3' (5' to 3' orientation);
5916	18032	31538	1.17	7.0E-49	U50832.1	NT	SNAP-1, HUMAN, 2289 bp, 5' to 3' (5' to 3' orientation);
6900	19541	32822	1.05	7.0E-49	U50832.1	NT	SNAP-1, HUMAN, 2289 bp, 5' to 3' (5' to 3' orientation);
9000	19541	32823	1.05	7.0E-49	U50832.1	NT	SNAP-1, HUMAN, 2289 bp, 5' to 3' (5' to 3' orientation);
7620	20243	34147	1.87	7.0E-49	11420754.1	NT	SNAP-1, HUMAN, 2289 bp, 5' to 3' (5' to 3' orientation);
8459	21300	34730	0.52	7.0E-49	11417119.1	NT	SNAP-1, HUMAN, 2289 bp, 5' to 3' (5' to 3' orientation);
8459	21300	34731	0.52	7.0E-49	11417119.1	NT	SNAP-1, HUMAN, 2289 bp, 5' to 3' (5' to 3' orientation);
11011	23865	37326	1.07	7.0E-49	G25548.1	NT	SNAP-1, HUMAN, 2289 bp, 5' to 3' (5' to 3' orientation);

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Probe ID	Exon ID	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Blast E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4459	17659	30376	0.76	2.0E-89 AL163263.2	NT	NT	Homo sapiens chromosome 21 segment HS21C030
4517	17923	30486	1.23	2.0E-89 AL1607976.1	NT	NT	Human C12orf105
4527	18056	0	0.83	2.0E-89 BS524744.1	EST_HUMAN	EST_HUMAN	687053508F11H1.MGC (10 Homo sapiens cDNA clone IMAGE:5452423 5'
5069	10743	31653	4.81	2.0E-89 AB007624.1	NT	NT	Human C12orf105
5069	10743	32131	1.41	2.0E-89 AL103363.1	NT	NT	Human C12orf105
8454	19499	32973	0.71	2.0E-89 AL163263.2	NT	NT	Homo sapiens chromosome 21 segment HS21C048, partial cds
8120	21031	34358	5.52	2.0E-89 UB1004.1	NT	NT	Human C12A (C12A) mRNA, partial cds
8513	21444	34736	2.59	2.0E-89	11423901	NT	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA
8593	21917	35272	0.98	2.0E-89 AJ245503.1	NT	NT	Homo sapiens protein for PE23 related protein
9795	22759	35145	0.77	2.0E-89 AB037754.1	NT	NT	Homo sapiens mRNA for KIAA1333 protein, partial cds
10320	23215	36527	0.65	2.0E-89 AF170814.1	NT	NT	Homo sapiens CabP5 (CABP5) gene, exon 5
10320	23215	36528	0.6	2.0E-89 AF170814.1	NT	NT	Homo sapiens CabP5 (CABP5) gene, exon 5
11812	24733	38224	2.45	2.0E-89	11434411	NT	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA
12003	24945	38342	4.22	2.0E-89	11433973	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (C-L1), mRNA
12139	24979	39480	1.83	2.0E-89 UT0092.1	NT	NT	Human IMAGE-7 antigen (IMAGE7) pseudogene, complete cds
13109	25524		2.82	2.0E-89 AB012722.2	NT	NT	Homo sapiens mRNA for kinesin-like protein, complete cds
12006	24851	38350	7.24	1.0E-89 BF190092.1	EST_HUMAN	EST_HUMAN	h181069.x1 NC_004971 Homo sapiens cDNA clone IMAGE:313497 3' similar to TR-054778 054778
12006	24851	38351	7.24	1.0E-89 BF190092.1	EST_HUMAN	EST_HUMAN	h181069.x1 NC_004971 Homo sapiens cDNA clone IMAGE:313497 3' similar to TR-054778 054778
8908	21756	35394	1.43	9.0E-89 AL163263.2	NT	NT	SOLUTE CARRIER FAMILY 22 - LIKE 2 PROTEIN
8908	21756	35095	1.49	9.0E-89 AL163263.2	NT	NT	SOLUTE CARRIER FAMILY 22 - LIKE 2 PROTEIN
1000	14134	27070	3.02	8.0E-89 AL163263.2	NT	NT	Homo sapiens chromosome 21 segment HS21C048
1091	14134	27070	2.48	8.0E-89 AL163263.2	NT	NT	Homo sapiens chromosome 21 segment HS21C048
1350	13588	27340	3.75	8.0E-89 BS520591.1	EST_HUMAN	EST_HUMAN	h18080.x1 NC_004971 Homo sapiens cDNA clone IMAGE:3284683 3'
1350	13588	27340	3.75	8.0E-89 BS520591.1	EST_HUMAN	EST_HUMAN	h18080.x1 NC_004971 Homo sapiens cDNA clone IMAGE:3284683 3'
8723	2227	39471	0.63	8.0E-89 SE17830.1	EST_HUMAN	EST_HUMAN	KC-1110258-12040-422-408 117058 Homo sapiens cDNA
11143	24072	37518	1.58	8.0E-89 AJ222086.1	EST_HUMAN	EST_HUMAN	9585084.1 Senses, NFL, L1, LOC_51 Homo sapiens cDNA clone IMAGE:1640222 3' similar to g154131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN) (soluble) Au negative element.

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11143	24072	37516	1.55	8.0E-40	A122205.1	EST_HUMAN	q9r408.x1 Sorensen, N.R.L.T. GBC. S1 Homo sapiens cDNA clone IMAGE:1649022 3' similar to gb:J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element
801	13916		3.4	7.0E-40	AF723391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exon 7-8; end partial cds, alternatively spliced
8894	21023		2.01	7.0E-40	AA782977.1	EST_HUMAN	af303083.1 Sorensen, Isabella N.H.T. Homo sapiens cDNA clone 1375593 3'
6516	22445	35028	2.33	7.0E-40	BE62525.2	EST_HUMAN	601655537.R1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3815524 3'
6516	22445	34950	2.33	7.0E-40	BE64252.2	EST_HUMAN	601655537.R1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3815524 3'
10335	23521	39645	2.02	7.0E-40	H68949.1	EST_HUMAN	Y86904.s1 Sorensen fetal liver spleen 1N16S Homo sapiens cDNA clone IMAGE:212100 3' similar to SP-C1TC_HUMAN P11595 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOSOLIC
10335	23521	39645	2.02	7.0E-40	H68949.1	EST_HUMAN	Y86904.s1 Sorensen fetal liver spleen 1N16S Homo sapiens cDNA clone IMAGE:212100 3' similar to SP-C1TC_HUMAN P11595 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOSOLIC
10334	23519	37245	0.65	7.0E-40	BF526099.1	EST_HUMAN	502071208.F1 NCLOGAP_Brn44 Homo sapiens cDNA clone IMAGE:4714237 5'
3116	15167	25001	1.24	0.0E-40	X91626.1	NT	H. sapiens ECE-1 gene (exon 6)
4326	17340	32025	6.55	0.0E-40	E522368	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4326	17340	32026	6.55	0.0E-40	E522368	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
8214	16289	32421	3.25	0.0E-40	U77700.1	NT	Homo sapiens HGGON1 mRNA, partial cds
8214	16289	32422	3.25	0.0E-40	U77700.1	NT	Homo sapiens HGGON1 mRNA, partial cds
8002	21832	35168	3.54	0.0E-40	4504754	NT	Homo sapiens Incollal 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
8002	21832	35167	3.54	0.0E-40	4504754	NT	Homo sapiens Incollal 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
105	13099		16.05	5.0E-40	A3035344.1	NT	Homo sapiens TOL5 gene, exon 1-10b
1220	14258	27198	6.75	5.0E-40	U80226.1	NT	Homo sapiens gamma-aminobutyric acid transaminase mRNA, partial cds
1543	14595	27847	1.44	5.0E-40	A122205.1	EST_HUMAN	q9r408.x1 Sorensen, N.R.L.T. GBC. S1 Homo sapiens cDNA clone IMAGE:1649022 3' similar to gb:J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element
1543	14595	27846	1.44	5.0E-40	A122205.1	EST_HUMAN	q9r408.x1 Sorensen, N.R.L.T. GBC. S1 Homo sapiens cDNA clone IMAGE:1649022 3' similar to gb:J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element
7520	19594	25620	2.86	5.0E-40	AF114497.1	NT	Homo sapiens long control region (LCSR) mRNA, complete cds
4585	17851	30520	2.27	5.0E-40	AF114497.1	NT	Homo sapiens long control region (LCSR) mRNA, complete cds
5755	18517	31655	2.65	5.0E-40	Z16411.1	NT	H. sapiens mRNA, encoding phospholipase
5803	18576		0.59	5.0E-40	A1208015.1	NT	Homo sapiens EVI5 homolog mRNA, complete cds
5551	18560	32070	1.05	5.0E-40	A3015817.1	NT	Homo sapiens ELAS mRNA, complete cds

Single Exon Probes Expressed in Adult Liver

P1 Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Mean Similar (Top) H BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
5974	18897	31905	2.12	5.0E-50	Z16411.1	NT	H sapiens mRNA encoding phospholipase c
7024	20060	33329	0.57	5.0E-50	5910985	NT	Homo sapiens Cationic arylphosphatase-related protein 19 (LOC56834), mRNA
7024	20060	33329	0.57	5.0E-50	5910986	NT	Homo sapiens Cationic arylphosphatase-related protein 19 (LOC56834), mRNA
7582	20519	33936	1.98	5.0E-50	AF13709.1	NT	Homo sapiens encephalatin 4 (ANCA), mRNA, partial cds
7582	20519	33937	1.98	5.0E-50	AF13709.1	NT	Homo sapiens encephalatin 4 (ANCA), mRNA, partial cds
7959	20714	34230	8.64	4.57295	NT	NT	Homo sapiens adenovirus cryptase 9 (ADCV9), mRNA
8569	20514	34230	8.64	4.57295	NT	NT	Homo sapiens adenovirus cryptase 9 (ADCV9), mRNA
8569	20514	34230	8.64	4.57295	NT	NT	Homo sapiens adenovirus cryptase 9 (ADCV9), mRNA
8569	20514	34230	8.64	4.57295	NT	NT	Homo sapiens adenovirus cryptase 9 (ADCV9), mRNA
10205	23095	36426	1.57	5.0E-50	11494429	NT	Homo sapiens uricase 1, cytosolic, phosphoribosyltransferase 3 (H sapiens) (LOC83274), mRNA
10773	23056	37048	0.92	5.0E-50	AF13393.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10527	23812	37240	13.14	5.0E-50	11463721	NT	Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA
10583	23887	37294	0.59	5.0E-50	7682051	NT	Homo sapiens KIAA0317 gene product (KIA0317), mRNA
10583	23887	37295	0.59	5.0E-50	7682051	NT	Homo sapiens KIAA0317 gene product (KIA0317), mRNA
11593	24271	37713	4.85	5.0E-50	D48307.1	NT	Human mRNA for NADP-dependent isulterine 5,4 12-hydroxylase, partial cds
12227	28061	38559	1.47	5.0E-50	X98411.1	NT	H sapiens mRNA for myosin-II
12262	29520	3716	5.0E-50	A523395.1	EST_HUMAN	at78053.1 Barlsted acute HPLR88 Homo sapiens cDNA clone IMAGE2126761 3'	
12582	29620	3716	5.0E-50	A523395.1	EST_HUMAN	at78053.1 Barlsted acute HPLR88 Homo sapiens cDNA clone IMAGE2126761 3'	
322	13414	28331	3.16	4.0E-50	AF21620.1	NT	Homo sapiens chromosome 21 unknown mRNA
322	13414	28332	1.88	4.0E-50	AF21620.1	NT	Homo sapiens chromosome 21 unknown mRNA
1113	14155	27064	8.1	4.0E-50	4505316	NT	Homo sapiens myosin phosphatase, large subunit 1 (MYPT1), mRNA
1715	14743	27712	6.89	4.0E-50	X99033.1	NT	H sapiens gene encoding discoidin receptor tyrosine kinase, exon 10
3037	16169	28940	0.57	4.0E-50	AF00744.1	NT	Homo sapiens prostate-specific membrane antigen (PSM) gene, complete cds
4787	17772	30659	2.34	4.0E-50	D37075.1	NT	Homo sapiens DNA for myeloid precursor antigen, complete cds
4913	17912	30780	2.12	4.0E-50	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4932	17931	30790	2.22	4.0E-50	AB033087.1	NT	H sapiens proboscis converting enzyme (NEC2) gene, exon 8
8456	21987	34707	0.91	3.0E-50	BF16108.1	EST_HUMAN	UHH-BW1-amy-50-04-DU1.1 NC CGAP 5UG7 Homo sapiens cDNA clone IMAGE 3088539 3'
8456	21987	34708	0.91	3.0E-50	BF16108.1	EST_HUMAN	UHH-BW1-amy-50-04-DU1.1 NC CGAP 5UG7 Homo sapiens cDNA clone IMAGE 3088539 3'
9459	21987	34708	0.91	3.0E-50	BF16108.1	EST_HUMAN	UHH-BW1-amy-50-04-DU1.1 NC CGAP 5UG7 Homo sapiens cDNA clone IMAGE 3088539 3'
12056	24697	38402	1.16	3.0E-50	BE063333.1	EST_HUMAN	901355944F1 NH IMAGE-38 Homo sapiens cDNA clone IMAGE398147 5'
228	13327	26244	3.32	2.0E-50	BE057913.1	EST_HUMAN	901067276F1 NH IMAGE-10 Homo sapiens cDNA clone IMAGE3428354 5'
1201	14240	27180	4.64	2.0E-50	5031748	NT	Homo sapiens high-mobility group (nucleosome chromosomal) protein 17 (HMG17), mRNA
1201	14240	27181	4.64	2.0E-50	5031748	NT	Homo sapiens high-mobility group (nucleosome chromosomal) protein 17 (HMG17), mRNA
8941	16342	28921	2.82	2.0E-50	AF13243.1	EST_HUMAN	q54d02.11 Somax, placenta, blowflies, 2N6P80W Homo sapiens cDNA clone IMAGE1713410 3'
5071	15151	33374	10.91	2.0E-50	9726555	NT	Similar to SW-OLP3_MOUSE P22275 OLFACTORY RECEPTOR OR3 ; Homo sapiens GRB2-related adaptor protein (GRAP) mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe	Exon SEQ ID No.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top BLAST Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5994	16049	32170	0.63	2.0E-60	11529001	NT	Homo sapiens R422 transacting protein 8 (RBP20), mRNA
5994	16049	32174	0.53	2.0E-60	11529801	NT	Homo sapiens R422 transacting protein 8 (RBP20), mRNA
5993	16058	32185	3.94	2.0E-60	AW127598.1	EST_HUMAN	hs496835 NIH_MGC_10 Homo sapiens cDNA, clone IMAGE:289081 5' similar to FR076208 OT6208 HYPOTHETICAL 35.5 CD PROTEIN 1
10308	23198	36607	1.79	2.0E-60	11427320	NT	Homo sapiens similar to laminin receptor 1 (67K), ribosomal protein 5A (H. sapiens) (LOC263454), mRNA
10309	23199	36608	1.79	2.0E-60	11427320	NT	Homo sapiens similar to laminin receptor 1 (67K), ribosomal protein 5A (H. sapiens) (LOC263454), mRNA
10466	23364	36768	0.88	2.0E-60	ALU18995.1	EST_HUMAN	ALU18995 HEMBA1 Homo sapiens cDNA, clone HEMBA104795 5'
10466	23364	36769	0.85	2.0E-60	ALU18995.1	EST_HUMAN	ALU18995 HEMBA1 Homo sapiens cDNA, clone HEMBA104795 5'
11902	24002	37441	3.66	2.0E-60	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
296	13300	28308	3.81	1.0E-60	4902166	NT	Homo sapiens amyloid beta (A4) precursor protein (precursor protein (precursor protein) (APP), mRNA
395	18544	28398	1.35	1.0E-60	AF231620.1	NT	Homo sapiens chromosome 21 unknown mRNA
395	18544	28398	1.37	1.0E-60	AF231620.1	NT	Homo sapiens chromosome 21 unknown mRNA
719	13771	29098	1.78	1.0E-60	AJ237698.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
719	13771	29098	1.76	1.0E-60	AJ237698.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
753	13810	28735	7.36	1.0E-60	AF294750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
753	13810	28737	7.36	1.0E-60	AF294750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
11371	14179		1.86	1.0E-60	4907028	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1332	14368	27315	3.13	1.0E-60	AF08154.1	NT	Homo sapiens protein phosphatase 2A ER gamma subunit gene, exon 3
1332	14368	27315	3.13	1.0E-60	AF08154.1	NT	Homo sapiens protein phosphatase 2A ER gamma subunit gene, exon 3
1694	14724		1.02	1.0E-60	BC376394.1	EST_HUMAN	9071360372 NIH_MGC_10 Homo sapiens cDNA, clone IMAGE:3511118 5'
1920	14941	27618	2.41	1.0E-60	11420514	NT	Homo sapiens similar to SALL1 (sat (Drosophila)) like (LOC37167), mRNA
2869	18550	28650	6.01	1.0E-60	6095720	NT	Homo sapiens chromosome 8 open reading frame 2 (ORF2), mRNA
3818	18848	28828	1.12	1.0E-60	AB020710.1	NT	Homo sapiens mRNA for KIA00603 protein, partial cds
3818	18848	28827	1.12	1.0E-60	AB020710.1	NT	Homo sapiens mRNA for KIA00603 protein, partial cds
4830	17538	38401	1.4	1.0E-60	AF167940.1	NT	Homo sapiens soluble inter-alpha-1 receptor accessory protein (LIIRAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced
8072	18842	33308	2.04	1.0E-60	AB014633.1	NT	Homo sapiens mRNA for KIA00603 protein, partial cds
9230	18172	32241	0.86	1.0E-60	11428916	NT	Homo sapiens KIA00603 gene product (KIA00603), mRNA
9248	18831	33018	0.45	1.0E-60	11419403	NT	Homo sapiens cyclophilin 40, 51 (cyclophilin 40-like domain) (CYP40), mRNA
9248	18831	33018	0.45	1.0E-60	11419403	NT	Human rat-oncogene POU-domain factor 1 mRNA, complete cds
7087	20020	39820	0.85	1.0E-60	6006092	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8124	21034	54393	2.37	1.0E-20	11426759	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporters), member 6 (SLC1A8), mRNA
5560	22016	55666	3.97	1.0E-20	11423068	NT	Homo sapiens brain 14-kilodalton anionic nucleoside-symporter 2 (B1G2), mRNA
9633	22718	35669	0.29	1.0E-20	AF10394.1	NT	Homo sapiens SUGT1 homolog (SUGT1), gene, complete cds, alternatively spliced
9635	22718	35671	1.57	1.0E-20	11423069	NT	Homo sapiens CSH-15 protein (COSH15), mRNA
9636	22718	35668	1.57	1.0E-20	11423069	NT	Homo sapiens CSH-15 protein (COSH15), mRNA
11477	24590	37840	1.46	1.0E-20	U4674.1	NT	Homo braconid chain splicing acid dehydrogenase mRNA, 3' end
4292	17300	30775	7.55	9.0E-31	D1234.1	EST	HUM005381 Liver HepG2 cell line. Homo sapiens cDNA, clone c381 3'
1461	14468	27456	1.24	7.0E-31	AE03708.1	NT	Rattus norvegicus brain specific car actin-binding protein, C8P50 mRNA, partial cds
8981	21811	35164	1.58	7.0E-31	11419324	NT	Homo sapiens melanin, thin finger protein, 1 (MKRF1), mRNA
10760	23072	29476	1.59	5.0E-31	AF02415.1	EST	CMAB 045-000399-076 B1643 Homo sapiens cDNA
3304	19372	39476	1.59	5.0E-31	AA102794.1	EST	HOMO24.31 Source: fetal liver, spleen, INFILS. S1 Homo sapiens cDNA clone IMAGE:41815 3'
4337	17843	39040	1.14	5.0E-31	AU143930.1	EST	AUT143930 Y76A11 Homo sapiens cDNA clone Y76A1102387 5'
4337	17843	39050	1.14	5.0E-31	AU143930.1	EST	AUT143930 Y76A11 Homo sapiens cDNA clone Y76A1102387 5'
4823	17823	30785	0.57	5.0E-31	7110824	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
4823	17823	30786	0.57	5.0E-31	7110824	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
6903	19033	33151	1.02	5.0E-31	M87995.1	EST	su4903.1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2818121 3' similar to SW-ASP6 FLAME 047858 N4-(BETA-N-ACETYL-GLUCOSAMINYL)-L-ASPARTACINASE PRECURSOR ;
8783	21713	35060	1.53	5.0E-31	BF14882.1	EST	0070012/FT NIH MCC. 1B Homo sapiens cDNA clone IMAGE:4130033 5'
9319	22247	35000	1.77	5.0E-31	AV04978.1	EST	AV049787 CLC Homo sapiens cDNA clone GL05YF08 3
9319	22247	35010	1.77	5.0E-31	AV04978.1	EST	AV049787 CLC Homo sapiens cDNA clone GL05YF08 3
3246	10254	29107	1.57	4.0E-31	AF156776.1	NT	Homo sapiens lymphoproliferative acid synthetase-delta (LPX1)-delta mRNA, complete cds
3246	10254	29106	1.57	4.0E-31	AF156776.1	NT	Homo sapiens lymphoproliferative acid synthetase-delta (LPX1)-delta mRNA, complete cds
11958	24286	37731	1.55	4.0E-31	AL16384.2	NT	Homo sapiens chromosome 21 segment HS210364
12442	25197	31846	3.04	4.0E-31	M7794.1	EST	ES101570 Hippocampus, Striatum (cat. #695225) Homo sapiens cDNA clone H10CM06 similar to Reticular-related gene polypeptide
12442	25197	31892	3.04	4.0E-31	M7794.1	EST	Reticular-related gene polypeptide
12442	25197	31834	1.83	3.0E-31	11430703	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1940	14771	27833	1.83	3.0E-31	11430703	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1911	15953	27812	1.31	3.0E-31	AF256655.1	NT	Homo sapiens cDNA-encoding putative BIR-domain enzyme FOLLICULON mRNA, complete cds
2165	15168	28170	1.03	3.0E-31	BE265792.1	EST	BE265792 NIH CC7. 1C Homo sapiens cDNA clone IMAGE:3039663 3' similar to TC026061 026061 2'-DEOXY-5'-UTR-ADENOSINE-5'-PHOSPHATASE, penicillin AU, positive strand.

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe Seq ID No.	Exon Seq ID No.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) HT BLAST E Value	Top HT Accession No.	Top HT Database Source	Top HT Descriptor
2708	15702	28697	2.4	3.0E-91	AF169555.1	NT	Homo sapiens beta-undodecaproteinase (BUP) gene, exon 6
2708	15702	28698	2.4	3.0E-91	AF169555.1	NT	Homo sapiens beta-undodecaproteinase (BUP) gene, exon 6
3388	16331	29238	1.13	3.0E-91	AL183283.2	NT	Homo sapiens HST10385
3388	16331	29239	1.13	3.0E-91	AL183283.2	NT	Homo sapiens HST10385
3523	16591	29494	3.48	3.0E-91	AB203104.1	NT	Homo sapiens mRNA for KIAA1272 protein, partial cds
3523	16591	29495	3.48	3.0E-91	AB203104.1	NT	Homo sapiens mRNA for KIAA1272 protein, partial cds
3853	16942	29707	0.72	3.0E-91	AF044800.1	NT	Homo sapiens cytochrome P450 2D6, complete cds
4703	17708	32571	4.4	3.0E-91	AF044800.1	NT	Homo sapiens cytochrome P450 2D6, complete cds
5101	18060	30945	1.29	3.0E-91	AL183283.2	NT	Homo sapiens chromosome 21 segment HST10385
5101	18060	30946	1.29	3.0E-91	AL183283.2	NT	Homo sapiens chromosome 21 segment HST10385
5884	18593	32098	1.52	3.0E-91	11434094.1	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6059	19001		3.02	3.0E-91	4802740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
9555	19587	33112	3.37	3.0E-91	11407611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
9555	19587	33113	3.37	3.0E-91	11407611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
8087	20099	34320	3.76	3.0E-91	UB9259.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 10 and 11
8087	20099	34321	3.76	3.0E-91	UB9259.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 10 and 11
8625	21465	34736	0.55	3.0E-91	U001589	NT	Human mRNA for very low density lipoprotein receptor, complete cds
9530	22268	35602	2.74	3.0E-91	D18494.1	NT	Human mRNA for very low density lipoprotein receptor, complete cds
9628	22734	36116	0.94	3.0E-91	AB011185.1	NT	Homo sapiens mRNA for KIAA0694 protein, complete cds
11226	24245	37693	1.56	3.0E-91	AB052179.2	NT	Homo sapiens ERM2 mRNA, complete cds
12072	25038	31823	1.61	3.0E-91	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12086	15702	28697	9.82	3.0E-91	AF169555.1	NT	Homo sapiens beta-undodecaproteinase (BUP) gene, exon 6
12086	15702	28698	9.82	3.0E-91	AF169555.1	NT	Homo sapiens beta-undodecaproteinase (BUP) gene, exon 6
51	13158	29035	2.07	3.0E-91	AF183283.2	NT	Homo sapiens HST10385
1273	14307	27258	4.77	1.0E-91	AF044746.1	EST HUMAN	UHHB-ale-01-Q11 NCL CGAP. Subst Homo sapiens cDNA clone IMAGE:2763260 3'
5588	16574	31552	0.86	1.0E-91	11434092	EST HUMAN	802020881 NCL CGAP. Brnrf Homo sapiens cDNA clone IMAGE:4197804 5'
7158	20257	33522	1.71	1.0E-91	BF348162.1	EST HUMAN	802020881 NCL CGAP. Brnrf Homo sapiens cDNA clone IMAGE:4197804 5'
7158	20257	33523	1.71	1.0E-91	BF348162.1	EST HUMAN	802020881 NCL CGAP. Brnrf Homo sapiens cDNA clone IMAGE:4197804 5'
9388	21802	34553	0.46	1.0E-91	AF001058.1	NT	Homo sapiens NKG2D gene, exon 10
1273	14307	27258	4.77	1.0E-91	AF044746.1	EST HUMAN	Homo sapiens NKG2D gene, exon 10
1280	14304	27252	7.34	3.0E-91	AF001058.1	NT	Homo sapiens NKG2D gene, exon 10
5837	18343	31187	1.21	3.0E-91	AB020466.1	NT	Homo sapiens mRNA for KIAA0655 protein, partial cds

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Table 4

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Probe Seq ID No.	Exon Seq ID No.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Ht BLAST E Value	Top Ht Accession No.	Top Ht Disease Source	Top Ht Descriptor
5949	18728	31429	3.62	0.05-92/03007.1	NT	Human Ncr K(A) Virus alpha subunit mRNA, partial cds	
5769	18671	31979	2.82	0.05-92/11427146	NT	Homo sapiens cytoplasmic protein FL22030 (FL22030) mRNA	
8724	19760	32907	4.13	0.05-92/AF310105.1	NT	Homo sapiens cytoplasmic protein FL22030 (FL22030) mRNA	
8548	21076	35236	1.2	0.05-92/AB040945.1	NT	Homo sapiens mRNA for KIAA1312 protein, partial cds	
8648	21076	35237	1.2	0.05-92/AB040945.1	NT	Homo sapiens mRNA for KIAA1312 protein, partial cds	
8614	22720	35103	2.3	0.05-92/11422068	NT	Homo sapiens protein 2 protein, partial cds	
86	13268	28120	6.86	0.05-92/W26367.1	EST HUMAN	283 Human melanocyte-specific protein, partial cds	
305	13369	20316	2.69	0.05-92/BC36653.1	EST HUMAN	50127513F1 NIH, clone 20 Homo sapiens cDNA, clone IMAGE3514037.5	
5577	18665	31532	0.76	0.05-92/AB046820.1	NT	Homo sapiens mRNA for KIAA1000 protein, partial cds	
5688	18761	31685	0.63	0.05-92/AF264717.1	NT	Homo sapiens FIVE domain-containing dual specificity protein phosphatase FIVE-DSP2 mRNA, complete cds	
6826	18660	33071	1.03	0.05-92/AJ000779.1	NT	Homo sapiens M3P-4 gene	
6930	18693	33078	0.97	0.05-92/AF170128.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit variant 1 (REV3L) mRNA, complete cds	
8241	21146	34478	7.75	0.05-92/X99538.1	NT	H sapiens gene for liver alpha-trypan inhibitor heavy chain H1, exon 7-8	
8241	21146	34479	7.75	0.05-92/X99538.1	NT	H sapiens gene for liver alpha-trypan inhibitor heavy chain H1, exon 7-8	
8670	21011	34278	0.67	0.05-92/11415961	NT	Homo sapiens AAK-1 protein (LOC81151), mRNA	
8695	21024	35278	4.05	0.05-92/LO4180.1	NT	Human lens membrane protein (lmp19) gene, exon 11	
8695	21024	35279	4.05	0.05-92/LO4180.1	NT	Human lens membrane protein (lmp19) gene, exon 11	
9083	22017	35373	0.9	0.05-92/11428560	NT	Homo sapiens transcription termination factor, RNA polymerase II (TTF2), mRNA	
9914	22540	35910	3.04	0.05-92/AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds	
10329	23415	38029	1.11	0.05-92/Y13029.1	NT	Homo sapiens mRNA for MBNL protein	
11243	24168	37615	3.46	0.05-92/AF074983.1	NT	Homo sapiens nuclear ribonuclease and stress-activated protein kinase-1 (MSK1) mRNA, complete cds	
11759	24721	38214	1.36	0.05-92/4903540	NT	Homo sapiens dihydropyrimidine 5-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DUST) mRNA	
201	13142	28029	0.81	7.0E-92/AB01007.1	NT	Homo sapiens DNA, MHC class I region, 7.1, encodes a haplo type	
256	18670	25267	1.11	7.0E-92/AB019301.1	NT	Homo sapiens mRNA for KIAA0788 protein, partial cds	
256	18670	25268	1.11	7.0E-92/AB019301.1	NT	Homo sapiens cytoplasmic Segress truncated isoform mRNA, complete cds	
0121	13071	27287	1.34	7.0E-92/AF007627.1	NT	Homo sapiens 5' cell G11 lymphoma T8 (GCLT8) mRNA	
13083	14338	27287	0.8	7.0E-92/490284	NT	Homo sapiens 5' cell G11 lymphoma T8 (GCLT8) mRNA	
2202	18213	28215	1.33	7.0E-92/531570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACR2), mRNA	
2562	18213	28215	1.33	7.0E-92/531570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACR2), mRNA	
2562	18213	28215	1.33	7.0E-92/AF167008.1	NT	Homo sapiens cytoplasmic actin-related protein 352 precursor, mRNA, complete cds	
2772	18704	38788	1.03	7.0E-92/3300738	NT	Homo sapiens NDKS-related gene (D1512E), mRNA	

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe Seq ID NO:	Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) HE BLAST E Value	Top HE Accession No.	Top HE Source	Top HE Description
2801	15790	28789	0.72	7.0E-32	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
3394	18401	29336	0.72	7.0E-32	495760/NT	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TJMT) mRNA
3394	18401	29340	0.72	7.0E-32	495760/NT	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TJMT) mRNA
4701	17700	30689	1.07	7.0E-32	571824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OES2-R, mRNA, 2550 nt]
5378	18893		0.58	4.0E-32	BE070721.1	EST HUMAN	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
2811	15875	28603	2.34	3.0E-32	BE070721.1	EST HUMAN	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
4346	17355		0.94	3.0E-32	AA482068.1	EST HUMAN	z660121.1 Soares, Italia, NHT Homo sapiens alpha clone IMAGE3505013.6
6391	19152	32288	7.87	3.0E-32	MI0976.1	EST HUMAN	BT12307321 NIH MGC 17 Homo sapiens alpha clone IMAGE3505013.6
11263	24128	31578	1.92	3.0E-32	AA482068.1	EST HUMAN	BT12307321 NIH MGC 17 Homo sapiens alpha clone IMAGE3505013.6
11263	24128	31577	1.92	3.0E-32	AA482068.1	EST HUMAN	BT12307321 NIH MGC 17 Homo sapiens alpha clone IMAGE3505013.6
150	13320	26370	24.85	2.0E-32	AF154830.1	EST HUMAN	Homo sapiens alpha 1 receptor, type IIe (ACVR2B) mRNA
190	13260	26202	23.81	2.0E-32	AF154830.1	EST HUMAN	Homo sapiens alpha 1 receptor, type IIe (ACVR2B) mRNA
190	13260	26203	23.81	2.0E-32	AF154830.1	EST HUMAN	Homo sapiens alpha 1 receptor, type IIe (ACVR2B) mRNA
190	13260	26203	23.81	2.0E-32	AF154830.1	EST HUMAN	Homo sapiens alpha 1 receptor, type IIe (ACVR2B) mRNA
773	18830	26792	16.21	2.0E-32	BE294190.1	EST HUMAN	BT11833731 NIH MGC 17 Homo sapiens alpha clone IMAGE3505013.6
773	18830	26793	16.21	2.0E-32	BE294190.1	EST HUMAN	BT11833731 NIH MGC 17 Homo sapiens alpha clone IMAGE3505013.6
1743	14770		1.65	2.0E-32	Z76653.1	EST	BT11833731 NIH MGC 17 Homo sapiens alpha clone IMAGE3505013.6
1951	14871	27592	1.3	2.0E-32	AB181919.1	EST HUMAN	w427407.4 NCL CGAP Probes Homo sapiens alpha clone IMAGE3505013.6
1951	14871	27593	1.3	2.0E-32	AB181919.1	EST HUMAN	w427407.4 NCL CGAP Probes Homo sapiens alpha clone IMAGE3505013.6
1978	14850	27650	0.95	2.0E-32	4507462/NT	EST HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN: 1
1978	14850	27651	0.95	2.0E-32	4507462/NT	EST HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN: 1
2052	15078	28078	5.02	2.0E-32	4506860/NT	EST HUMAN	Homo sapiens transforming growth factor, beta 3 (TGFB3) mRNA
2707	15078	28096	34.53	2.0E-32	6912457/NT	EST HUMAN	Homo sapiens transforming growth factor, beta 3 (TGFB3) mRNA
3677	16710	29000	0.91	2.0E-32	AF201910.1	EST HUMAN	Homo sapiens cadherin binding protein 1 (RGA03303) mRNA
3677	16710	29001	0.91	2.0E-32	AF201910.1	EST HUMAN	Homo sapiens cadherin binding protein 1 (RGA03303) mRNA
3677	16710	29001	0.91	2.0E-32	AF201910.1	EST HUMAN	Homo sapiens chromosome 21 unknown mRNA
3677	16710	29001	0.91	2.0E-32	AF201910.1	EST HUMAN	Homo sapiens chromosome 21 unknown mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe Seq ID No.	Exon Seq ID No.	ORF SEQ ID No.	Expression Signal	Mol Similar (Top Hit BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3752	10794	29673	7.66	2.0E-92	5903180	NT	Homo sapiens stress-induced phosphoprotein 1 (Hsp70Hsp26-organizing protein) (STIP1), mRNA
4396	17601	30293	1.33	2.0E-92	AF10276.1	NT	Homo sapiens estrogen receptor DNA (5.1), complete cds
4858	17683	30732	0.67	2.0E-92	AF10623.1	NT	Homo sapiens histone H4, all isoforms (H4), complete cds
5116	18113	31711	5.28	2.0E-92	AL004937.1	EST_HUMAN	ORF243420414.11.434 (unverified), Homo sapiens cDNA, clone DKFZ43420414.5
5269	18351		0.97	2.0E-92	4769160	NT	Homo sapiens distal regulatory element binding transcription factor 2 (SREBF2) mRNA
5267	19334	32135	0.73	2.0E-92	AF106355.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
6556	19593		2.77	2.0E-92	4504766	NT	Homo sapiens Interferon- γ (IFN- γ) (w/IFN- γ), lymphocyte function-associated antigen 1, alpha polypeptide (ITGAL) mRNA
6500	19630	33147	2.48	2.0E-92	AB028991.1	NT	Homo sapiens mRNA for KIAA1068 protein, partial cds
7876	20803		0.59	2.0E-92	U67180.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
7909	20803		0.59	2.0E-92	U67180.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
9414	22342	35707	1.41	2.0E-92	AW34074.1	EST_HUMAN	h02902.x1 Scores_NEL_T_GSC_S1 Homo sapiens cDNA clone IMAGE:2008371 5' similar to TR-002711
11159	24125	37571	6.13	2.0E-92	11434900	NT	002711 PRO-POUTPASE POLYPROTEIN ;
11446	24352	37810	1.5	2.0E-92	11434759	NT	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA
11465	24358	37848	1.47	2.0E-92	6633103	NT	Homo sapiens zinc finger protein 198 (ZNF198), mRNA
11584	24453	37961	1.57	2.0E-92	AN 630260.1	EST_HUMAN	Homo sapiens male-specific lethal-3 (MSL3), mRNA
11584	24453	37962	1.57	2.0E-92	AN 630260.1	EST_HUMAN	OM4L10026-161258-032-g05 T10029 Homo sapiens cDNA
12770	25569	31810	4.57	2.0E-92	AB02016.1	NT	OM4L10026-161258-032-g05 T10029 Homo sapiens cDNA
13009	15701	28698	66.73	2.0E-92	6912457	NT	Homo sapiens calcitonin binding protein 1 (CABP1), partial cds
1874	14694	27878	1.20	1.0E-92	R78078.1	EST_HUMAN	Homo sapiens calcitonin binding protein 1 (CABP1), partial cds
1974	14694	27879	1.20	1.0E-92	R78078.1	EST_HUMAN	h00608.1 Scores placenta h0249P Homo sapiens cDNA clone IMAGE:145574 5'
2087	15101	28101	27.05	1.0E-92	4509958	NT	h00608.1 Scores placenta h0249P Homo sapiens cDNA clone IMAGE:145574 5'
8522	21752	35088	0.63	1.0E-92	BE459025.1	EST_HUMAN	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA
8707	22532	38011	3.01	1.0E-92	AB06356.1	EST_HUMAN	h01902.x1 NG2_GCAP_GLI1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW-PTNF_HUMAN
8707	22532	38012	3.01	1.0E-92	AB06356.1	EST_HUMAN	Q18625 PROTEIN-TYROSIENE PHOSPHATASE D1 ; contains AU repetitive element/contains element
2092	19086	28060	2.7	9.0E-93	AF106181	EST_HUMAN	Q18625 PROTEIN-TYROSIENE PHOSPHATASE D1 ; contains AU repetitive element/contains element
2096	19073		8.46	9.0E-93	AF106181	EST_HUMAN	Q18625 PROTEIN-TYROSIENE PHOSPHATASE D1 ; contains AU repetitive element/contains element

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2655	15689		2.12	9.0E-03	AF23391.1	NT	Human sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-46, and partial cds, alternatively spliced
3679	16712	26603	1.1	9.0E-03	BE39671.1	EST_HUMAN	907281.66711 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:3703832 5'
12074	24618		8.72	9.0E-03	11418326	NT	Homo sapiens fibronectin protein Uta (FBN1A) mRNA
6712	19748	32651	0.42	8.0E-03	AW01042.1	EST_HUMAN	U91810.66711 NIH_MGC_41 NCI CGAP_Sut1 Homo sapiens cDNA clone IMAGE:2706371 3'
6712	19748	32652	0.42	8.0E-03	AW01042.1	EST_HUMAN	U91810.66711 NIH_MGC_41 NCI CGAP_Sut1 Homo sapiens cDNA clone IMAGE:2706371 3'
6879	19907	33122	3.08	3.0E-03	AF03634.1	EST_HUMAN	9014603211 NIH_MGC_08 Homo sapiens cDNA clone IMAGE:3836308 5'
265	13360	26275	6.07	7.0E-03	AF23191.1	NT	Homo sapiens chromosome 21 unknown mRNA
5213	10268	32419	0.44	6.0E-03	11480204	NT	Homo sapiens hypothetical protein FLJ10857 (FLJ10857) mRNA
5213	10268	32420	0.44	6.0E-03	11480204	NT	Homo sapiens hypothetical protein FLJ10857 (FLJ10857) mRNA
5977	20014	33236	1.12	6.0E-03	AF030393.1	NT	Homo sapiens PTH-responsive osteocalcin B1 protein (B1) mRNA, complete cds
7245	20154	33394	1.24	6.0E-03	AF056771.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
1403	14439	27363	1.26	5.0E-03	AB014811.1	NT	Homo sapiens mRNA for KIAA6711 protein, partial cds
1432	14463	27416	2.49	5.0E-03	AF074184.1	EST_HUMAN	wc0608.41 NCI CGAP_P28 Homo sapiens cDNA clone IMAGE:2314670 3'
1432	14463	27417	2.49	5.0E-03	AF074184.1	EST_HUMAN	wc0608.41 NCI CGAP_P28 Homo sapiens cDNA clone IMAGE:2314670 3'
1463	14624		0.57	5.0E-03	AL03201.2	NT	Human skeletal osteonin 21 segment HS21001
3260	16328	29233	2.06	5.0E-03	X0201.1	NT	Human skeletal osteonin 21 segment HS21001
3979	17006	26894	1.01	5.0E-03	892209	NT	Homo sapiens hypothetical protein FLJ2029 (FLJ2029) mRNA
6010	18073	32199	1.01	5.0E-03	M2878.1	NT	Human somatic cytochrome c (HCT) processed pseudogene, complete cds
6347	10397		1.39	5.0E-03	AF046655.1	NT	Homo sapiens vhsor1 (VBSOR1) and vhsor5 (VBSOR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
8774	21081	34411	3.39	5.0E-03	AF097108.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product
8795	22604	35462	0.79	5.0E-03	4657929	NT	Homo sapiens ates, large (Desophila) homolog 2 (cncp-110) (LOC2) mRNA
9765	22641	35463	0.79	5.0E-03	4657929	NT	Homo sapiens ates, large (Desophila) homolog 2 (cncp-110) (LOC2) mRNA
10149	23640	36439	2.26	5.0E-03	AF274983.1	NT	Homo sapiens secondary pathway component Sac3/B-1 mRNA, alternatively spliced, complete cds
10225	23722	36524	1.09	5.0E-03	802163	NT	Homo sapiens TUBB (TUBB) mRNA, complete cds
10225	23722	36525	1.09	5.0E-03	AF09813.2	NT	Homo sapiens WST1 protein (WST1) mRNA, complete cds
13131	24455	32650	1.31	5.0E-03	AF09813.2	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
1324	24455	32651	0.97	5.0E-03	AF09813.2	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
12676	26921	31724	2.04	5.0E-03	1141787	NT	Homo sapiens gamma-aminobutyrate 1 (GABT) mRNA
90	13303		0.04	4.0E-03	AA459033.1	EST_HUMAN	25509.1 Swiss-Prot, hMT Homo sapiens cDNA clone IMAGE:79698 3' similar to SW CLP4_RAT
407	13338	23640	1.62	4.0E-03	4657979	NT	P27897 CALPONIN, ACIDIC ISOFORM
							Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
467	13536	26461	1.62	4.0E-63	4597975	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
759	13853	29758	1.44	4.0E-63	7657454	NT	Homo sapiens perlecan (perlecan) homolog 1, containing EGF domain (PES1) mRNA
766	13853	29758	1.44	4.0E-63	7657454	NT	Homo sapiens perlecan (perlecan) homolog 1, containing EGF domain (PES1) mRNA
1211	14745	27160	1.44	4.0E-63	8623585	NT	Homo sapiens hypoxanthine phosphoribosyl transferase (HGPRT) mRNA
1820	15011	29001	3.05	3.0E-55	4504767.1	NT	Homo sapiens TGF-beta2 (TGF-beta2) mRNA
2850	15545	28545	2.16	3.0E-53	765927	NT	Homo sapiens tumor necrosis factor receptor 1 (TNFR1) mRNA
3025	16523	28562	0.83	1.0E-53	765927	NT	Homo sapiens tumor necrosis factor receptor 1 (TNFR1) mRNA
4132	17154	30031	2	3.0E-53	450464	NT	Homo sapiens interleukin 15 receptor 1 (IL15R1) mRNA
5130	16223	28402	0.59	4.0E-55	7703695	NT	Homo sapiens tumor antigen SLP-3p (SLP-3p) mRNA
5940	16811	32037	4.31	4.0E-53	1469641	EST_HUMAN	Y64612.1 Striatum liver (463724) Homo sapiens cDNA clone IMAGE78538 5' similar to similar to SP-A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN .
11073	24422	37950	0.62	4.0E-55	AV62051	EST_HUMAN	AV62051 GKC Homo sapiens cDNA clone QICORF07 5'
3720	16752	28530	2.98	3.0E-53	BF60030.1	EST_HUMAN	G02246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE-4832038 5'
3720	16752	28540	2.98	3.0E-53	BF60030.1	EST_HUMAN	G02246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE-4832038 5'
4333	17348		1.6	3.0E-53	AF22386.1	NT	Homo sapiens keratin mRNA, complete cds
6944	19076	33091	1.21	3.0E-53	11428182	NT	Homo sapiens GON5 (general control of amino-acid synthesis, yeast, homolog-like 2 (GON5L2), mRNA
11240	24462	37612	3.7	3.0E-53	AB54623.1	EST_HUMAN	w602d95.2 NC1 CGAP_G05 Homo sapiens cDNA clone IMAGE230488 3'
203	13302	26217	7.85	2.0E-53	AB516810.1	NT	Chlorococcus sulfatus mRNA, for ribosomal protein S1A, complete cds
203	13302	26217	7.85	2.0E-53	AB516810.1	NT	Chlorococcus sulfatus mRNA, for ribosomal protein S1A, complete cds
343	13433	26548	6.56	2.0E-53	AL162285.2	NT	Homo sapiens chromosome 21 segment HS210385
344	13433	26548	7.2	2.0E-53	AL162285.2	NT	Homo sapiens chromosome 21 segment HS210385
1038	14866	27632	2.36	2.0E-53	AF22656.1	NT	Homo sapiens keratin mRNA, complete cds
2144	15167	28150	1.07	2.0E-53	AF2765.1	NT	Human Ck-associated RS cyclophilin GNR5-Cyp mRNA, complete cds
2000	15510	28513	1.06	2.0E-53	HE252942.1	EST_HUMAN	G0117559F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE-3386220 5'
5902	18674	31156	5.33	2.0E-53	AW043385.1	EST_HUMAN	EST1370453 MAGE_resequences, MAGE Homo sapiens cDNA
5913	18686	31184	0.6	2.0E-53	AF2765.1	NT	Human Ck-associated RS cyclophilin GNR5-Cyp mRNA, complete cds
5733	18686	31184	0.75	2.0E-53	BF551459.1	EST_HUMAN	GVA-H110613-200300-126-RN1 H110613 Homo sapiens cDNA
5833	18604	32019	1.95	2.0E-53	11430039	NT	Homo sapiens hydrophobic protein (LOC31316), mRNA
5845	18619	32033	0.58	2.0E-53	U76313.1	EST_HUMAN	HSU74513 Human chromosome 14 Homo sapiens cDNA clones 1456
6860	20007	19193	1.3	2.0E-53	AW50002.1	EST_HUMAN	UHRF-BNC-46-5-45-0-0-171 NIH_MGC_30 Homo sapiens cDNA clone IMAGE-3076329 5'
12955	25528		2.39	2.0E-53	U41825.1	NT	Homo sapiens CYP11 genes, 5' end
12900	25488		5.72	2.0E-53	BF405327.1	EST_HUMAN	G0145851F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE-3892386 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO;	Exon SEQ ID NO;	ORF SEQ ID NO;	Expression Signal	Mean Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9098	2146	34681	1.21	1.0E-93	F091305.1	NT	Homo sapiens Tiro toxin mRNA, complete cds
10116	23007	39401	4.95	1.0E-93	G33747.1	NT	Human PDK4 gene for 735-amino acid kinase (A) amplified protein precursor (cont 9)
10116	23007	39402	4.98	1.0E-93	G33747.1	NT	Human PDK4 gene for 735-amino acid kinase (A) amplified protein precursor (cont 9)
10249	23137	39542	0.74	1.0E-93	AJ048801.1	NT	Novel human gene mapping to chromosome 17, similar to rat Tbc2d3P
10249	23137	39562	0.67	1.0E-93	U143946	NT	Homo sapiens GGT repeat region 2 (GTG) cDNA
12266	25719	31996	1.85	1.0E-94	AJ26522.1	EST HUMAN	hG91421 NC_004307.1 Homo sapiens cDNA, clone IMAGE:180758 3' similar to YP71084.4 (CEG142)
12572	25734		2.33	1.0E-93	AJ230733.1	NT	Homo sapiens GGT1 gene, exon 1
12575	25455		3.54	1.0E-93	U117936	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
33248	26541		2.21	1.0E-93	AJ240796.1	NT	Homo sapiens chromosome 21 segment 18521C009
10294	32149	29929	1.93	0.0E-94	AJ163203.2	NT	Homo sapiens transcription enhancer factor 6 mRNA, complete cds
4045	37072	31928	3.94	0.0E-94	AJ142453.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
5562	19830	31500	3.94	0.0E-94	AB014812.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
5562	19830	31500	3.94	0.0E-94	AB014812.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
6283	19334	32800	18.24	0.0E-94	AJ172284.1	EST HUMAN	3537g6.5.1 Soares, test, heart, N82H19W Homo sapiens cDNA clone IMAGE:408654 3'
7554	20530	33017	1.39	0.0E-94	AJ075580.1	EST HUMAN	083205.1 Soares, test, testis, N82H19W Homo sapiens cDNA clone IMAGE:1623359 3'
9183	21720	35482	0.68	0.0E-94	BF629115.1	EST HUMAN	802942163F1 NC_004307.1 Homo sapiens cDNA clone IMAGE:4180029 5'
11410	24326	31776	1.93	0.0E-94	U1142962	NT	Homo sapiens adenylyl kinase 2 (AK2), mRNA
11410	24326	31776	1.93	0.0E-94	U1142962	NT	Homo sapiens adenylyl kinase 2 (AK2), mRNA
12555	25946	31975	3.02	0.0E-94	U180098.1	EST HUMAN	yc18014.1 Soares fetal liver spleen TNELS Homo sapiens cDNA clone IMAGE:110230 3'
1305	25865		1.5	0.0E-94	D52321.2	NT	Homo sapiens mRNA for KIAA0627 protein, partial cds
1867	14985		6.75	4.0E-94	J05094.1	NT	ye8912.x1 Soares, NEL ⁺ G9C, S1 Homo sapiens cDNA clone IMAGE:2701679 3'
3729	16771	20857	1.11	4.0E-94	AW197851.1	EST HUMAN	ye8912.x1 Soares, NEL ⁺ G9C, S1 Homo sapiens cDNA clone IMAGE:2701679 3'
3729	16771	20858	1.11	4.0E-94	AW197851.1	EST HUMAN	ye8912.x1 NC_004307.1 Homo sapiens cDNA clone IMAGE:2285403 3' similar to TRQ18266 Q18266 PROTEIN TYROSINE PHOSPHATASE ;
4391	17832	30702	3.28	4.0E-94	AB91312.1	EST HUMAN	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1), mRNA
6741	19775	32897	1.54	4.0E-94	U1140570	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1), mRNA
6741	19775	32898	1.64	4.0E-94	U1140470	NT	Homo sapiens huntingtin (HD) gene, exon 37
7240	20416		1.04	4.0E-94	U7306.1	NT	Homo sapiens gene for Sma1 5, exon 8
11945	24457	37620	1.46	4.0E-94	AB04020.1	NT	Homo sapiens hypodermal protein PL2455 (PLI2455), mRNA
11897	23897	37725	1.41	4.0E-94	U1154762	NT	Homo sapiens hypodermal protein PL2455 (PLI2455), mRNA

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Table 4

Single Exon Probes Expressed in Adult Liver

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Exposure

Single Exon Probes Expressed in Adult Liver

Protein ID NO.	Enon ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11702	24603	38148	2.42	1.0E-04/AJ27244.1	EST_HUMAN	EST_HUMAN	9022602.1 Schiller diploidendone Homo sapiens cDNA clone IMAGE:089122.3 similar to TRQ92646
12936	13269	26177	1.57	1.0E-04/BE26671.1	EST_HUMAN	EST_HUMAN	Q63846 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR. 1
12322	12322	26177	2.02	1.0E-04/BE26671.1	EST_HUMAN	EST_HUMAN	NC01175/GENE1 NIH MGSC T7 Homo sapiens cDNA clone IMAGE:351038.5
14626	14626	27488	1.86	6.0E-05/AJ02702.1	EST_HUMAN	EST_HUMAN	001170/GENE1 NIH MGSC T7 Homo sapiens cDNA clone IMAGE:351038.5
3199	10247	29142	1.25	9.0E-05	7963207	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC30), complete cds
3199	10247	29145	1.25	9.0E-05	7963207	NT	Homo sapiens KUA00255 gene product (KUA00255), mRNA
6550	18606	31544	1.25	6.0E-05/X32556.1	EST_HUMAN	EST_HUMAN	Homo sapiens KUA00255 gene product (KUA00255), mRNA
9590	18606	31544	1.22	6.0E-05/X32556.1	EST_HUMAN	EST_HUMAN	Homo sapiens KUA00255 gene product (KUA00255), mRNA
8827	21757	35101	1.71	9.0E-05/AJ274763.1	EST_HUMAN	EST_HUMAN	M.musculus gylt1 gene (exons 1 to end 2)
154	13924	29172	12.12	8.0E-05/AF154930.1	EST_HUMAN	EST_HUMAN	M.musculus gylt1 gene (exons 1 to end 2)
7280	20243	33489	6.0	8.0E-05	11418379	NT	Homo sapiens progressive amyloid-like protein (ANK) mRNA, complete cds
7611	20548	33938	1.02	8.0E-05	11428529	NT	Homo sapiens catalytic phosphatase synthetase 1 mRNA, complete cds
7611	20548	33939	1.02	8.0E-05	11428529	NT	Homo sapiens catalytic phosphatase synthetase 1 mRNA, complete cds
8776	21755	35050	2.05	8.0E-05/AJ023897.1	EST_HUMAN	EST_HUMAN	Homo sapiens KUA00168 gene product (KUA00168), mRNA
9004	22662	36277	2.23	8.0E-05	11429044	NT	Homo sapiens KUA00255 gene product (KUA00255), mRNA
9004	22662	36278	2.22	8.0E-05	11429044	NT	Homo sapiens KUA00255 gene product (KUA00255), mRNA
10302	22651	36971	3.15	8.0E-05	6170448	NT	Homo sapiens mRNA for KUA1361 protein, 14416 cds
10391	22651	36971	3.15	8.0E-05	6170448	NT	Homo sapiens mRNA for KUA1361 protein, 14416 cds
10730	20618	37043	0.78	9.0E-05/AJ087916.1	EST_HUMAN	EST_HUMAN	Homo sapiens alpha1-galactosidase 2 (GAL2) mRNA, complete cds
11196	24608	37632	1.98	9.0E-05/AJ112512.1	EST_HUMAN	EST_HUMAN	Homo sapiens alpha1-galactosidase 2 (GAL2) mRNA, complete cds
11915	25492	36259	1.42	8.0E-05	10384263	NT	Homo sapiens alpha1-galactosidase 2 (GAL2) mRNA, complete cds
12963	24589	26186	2.86	9.0E-05/AJ03956.1	EST_HUMAN	EST_HUMAN	0024001.1 Scaevola_NHT Homo sapiens cDNA clone IMAGE:341469.3 similar to contains L11 L11
285	13368	23308	6.41	9.0E-05/AJ03956.1	EST_HUMAN	EST_HUMAN	0024001.1 Scaevola_NHT Homo sapiens cDNA clone IMAGE:341469.3 similar to contains L11 L11
295	13368	23307	6.41	9.0E-05/AJ03956.1	EST_HUMAN	EST_HUMAN	0024001.1 Scaevola_NHT Homo sapiens cDNA clone IMAGE:341469.3 similar to contains L11 L11
304	13368	23307	6.41	9.0E-05/AJ03956.1	EST_HUMAN	EST_HUMAN	0024001.1 Scaevola_NHT Homo sapiens cDNA clone IMAGE:341469.3 similar to contains L11 L11
452	17530	31020	0.83	7.0E-05/AJ163248.2	EST_HUMAN	EST_HUMAN	0024001.1 Scaevola_NHT Homo sapiens cDNA clone IMAGE:341469.3 similar to contains L11 L11
5163	10175	31020	1.02	7.0E-05/AJ03956.1	EST_HUMAN	EST_HUMAN	0024001.1 Scaevola_NHT Homo sapiens cDNA clone IMAGE:341469.3 similar to contains L11 L11
67199	18726	35058	0.53	4.0E-05/BE26671.1	EST_HUMAN	EST_HUMAN	0024001.1 Scaevola_NHT Homo sapiens cDNA clone IMAGE:341469.3 similar to contains L11 L11
223	13322	26238	18.69	3.0E-05/AF520641.1	EST_HUMAN	EST_HUMAN	0024001.1 Scaevola_NHT Homo sapiens cDNA clone IMAGE:341469.3 similar to contains L11 L11
6526	18703	31603	1.89	3.0E-05/AF520641.1	EST_HUMAN	EST_HUMAN	0024001.1 Scaevola_NHT Homo sapiens cDNA clone IMAGE:341469.3 similar to contains L11 L11
9571	24604	32057	0.7	3.0E-05	4503354	EST_HUMAN	0024001.1 Scaevola_NHT Homo sapiens cDNA clone IMAGE:341469.3 similar to contains L11 L11
7598	20407	38755	1.72	3.0E-05/AJ412321.1	EST_HUMAN	EST_HUMAN	0024001.1 Scaevola_NHT Homo sapiens cDNA clone IMAGE:341469.3 similar to contains L11 L11

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Table 4

Single Exon Probes Expressed in Adult Liver

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Table 4

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Description
587	13620	28888	3.73	5.0E-98	U03269.1	Homo sapiens mRNA for KIAA1172 protein, partial cds
2883	13666	33280	1.8	5.0E-98	11416707	Homo sapiens phosphatidylchase 9A, cytosolic, partial cds
3073	19126	29622	0.93	5.0E-98	891235	Homo sapiens transient receptor potential channel 5 (TRP5), mRNA
4019	17048	24895	1.19	5.0E-98	4786507	Homo sapiens transient receptor potential channel 5 (TRP5), mRNA
5072	18010	24895	1.13	5.0E-98	891235	Homo sapiens transient receptor potential channel 5 (TRP5), mRNA
6842	19971	33104	0.99	5.0E-98	AF169783.1	Homo sapiens NOD1 protein (NOD1) gene, exon 1, 2, and 3
7009	20038	33280	0.5	5.0E-98	U27557.1	Homo sapiens dNT-3 gene for mitochondrial 8191-deoxyribonucleoside kinase (dNT-3 gene), exons 1-5
7030	20038	33280	4.1	5.0E-98	11426369	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
7030	20038	33280	4.1	5.0E-98	11426369	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
7030	20038	33280	1.01	5.0E-98	U03269.1	Homo sapiens mRNA for KIAA0500 protein, partial cds
7030	20038	33280	1.46	5.0E-98	AB024334.1	Homo sapiens mRNA for 14-3-3gamma, complete cds
7030	20038	33280	1.46	5.0E-98	U03269.1	Homo sapiens mRNA for 14-3-3gamma, complete cds
8884	21415	34897	2.03	5.0E-98	U03269.1	Homo sapiens IV collagenase (COL4A3) gene, exon 5
8884	21415	34898	2.03	5.0E-98	U03269.1	Homo sapiens IV collagenase (COL4A3) gene, exon 5
12217	26051	38840	1.69	5.0E-98	U03269.1	Human mRNA for KIAA0161 gene, partial cds
4297	17901	33061	5.4	3.0E-98	U03269.1	Human mRNA for KIAA0161 gene, partial cds
4297	17901	33061	2.7	2.0E-98	4503396	EST_HUMAN
771	13828	23759	2.03	2.0E-98	AL183248.2	Homo sapiens chromosome 21 segment HS21Q348
7868	20765	34067	0.62	2.0E-98	BF350731.1	EST_HUMAN
7868	20765	34068	0.62	2.0E-98	BF350731.1	EST_HUMAN
8532	22160	34068	0.62	2.0E-98	AF098040.1	EST_HUMAN
12364	25151	25151	2.4	2.0E-98	AW24946.1	EST_HUMAN
845	13706	20612	0.7	1.0E-98	4825963	EST_HUMAN
845	13706	20613	0.7	1.0E-98	4825963	EST_HUMAN
894	13754	26071	2.14	1.0E-98	U16904.1	EST_HUMAN
1805	14831	27769	1.86	1.0E-98	AW95064.1	EST_HUMAN
2242	15292	28297	1	1.0E-98	U76507.1	EST_HUMAN
2242	15292	28298	1	1.0E-98	U76507.1	EST_HUMAN
2242	15292	28299	1	1.0E-98	U51472.2	EST_HUMAN
2242	15292	28300	1.19	1.0E-98	U51472.2	EST_HUMAN
5306	13800	33822	3.82	1.0E-98	54650913	EST_HUMAN
7303	18472	31263	1.08	1.0E-98	6912735	EST_HUMAN
7402	20101	33336	0.67	1.0E-98	6912459	EST_HUMAN
8751	21721	35068	1.04	1.0E-98	7981803	EST_HUMAN

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Signal Emission	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9779	22107	354505	0.85	4.EE-97	11423323	NT	Homo sapiens cytochrome P450, subfamily IVB, polypeptide 1 (CYP4B1), mRNA
9790	22764	36136	1.22	4.EE-97	AB011168.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
9790	22764	36137	1.22	4.EE-97	AB011168.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
11604	24573	37891	1.84	4.EE-97	11853122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11604	24573	37892	1.84	4.EE-97	11853122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11867	20920	371403	1.69	4.EE-97	AB042357.1	NT	Homo sapiens mRNA, similar to rat myomagnin, complete cds
12524	20548	371403	7.05	4.EE-97	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
262	13358	28273	1.3*	3.EE-97	AB032598.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
899	13952	28890	7.56	3.EE-97	4802106	NT	Homo sapiens amyloid beta1 (A1) precursor protein (prodesmosin-II; Alzheimer disease) (APP), mRNA
899	13952	28900	7.56	3.EE-97	4802106	NT	Homo sapiens amyloid beta1 (A1) precursor protein (prodesmosin-II; Alzheimer disease) (APP), mRNA
1490	16501	271453	1.43	3.EE-97	4757913	NT	Homo sapiens H-myo (and STAT) activator (NMU), mRNA
2462	16556	284493	2.06	3.EE-97	U03255.1	NT	Human beta-prime-actin (BACT2) gene, exon 7
3212	16590	29156	14.55	3.EE-97	X02212.1	NT	Human alpha-1-fetoprotein (A1) gene, exon 7
3305	16583	29255	1.17	3.EE-97	8714478	NT	Homo sapiens perlecan (PCL1), mRNA
3305	16583	29255	1.17	3.EE-97	8714478	NT	Homo sapiens perlecan (PCL1), mRNA
3584	16532	32799	0.82	3.EE-97	AF18623.1	NT	Homo sapiens late salt export pump (SEEP), mRNA, complete cds
4852	17851	30797	4.95	1.EE-97	4834370	NT	Homo sapiens YAC123, a human cationic oligopeptide repeat (YAC123), cDNA
6658	18751	32031	2.44	1.EE-97	BE066483.1	EST, HUMAN	Human sapiens YAC123, a human cationic oligopeptide repeat (YAC123), cDNA
7727	20139	33376	6.55	1.EE-97	5463681	EST, HUMAN	Human sapiens YAC123, a human cationic oligopeptide repeat (YAC123), cDNA
9077	21355	34920	0.60	1.EE-97	AK134978.1	EST, HUMAN	Human sapiens YAC123, a human cationic oligopeptide repeat (YAC123), cDNA
9077	21355	34920	0.60	1.EE-97	AK134978.1	EST, HUMAN	Human sapiens YAC123, a human cationic oligopeptide repeat (YAC123), cDNA
10234	21373	34856	1.39	1.EE-97	U18087.1	EST, HUMAN	Human sapiens YAC123, a human cationic oligopeptide repeat (YAC123), cDNA
11148	24077	37928	8.3	1.EE-97	U18087.1	EST, HUMAN	Human sapiens YAC123, a human cationic oligopeptide repeat (YAC123), cDNA
11465	24077	37928	8.3	1.EE-97	U18087.1	EST, HUMAN	Human sapiens YAC123, a human cationic oligopeptide repeat (YAC123), cDNA
11505	24063	37438	1.73	1.EE-97	AA053761.1	EST, HUMAN	Human sapiens YAC123, a human cationic oligopeptide repeat (YAC123), cDNA
11505	24063	37438	1.73	1.EE-97	AA053761.1	EST, HUMAN	Human sapiens YAC123, a human cationic oligopeptide repeat (YAC123), cDNA
11920	24060	37439	6.95	1.EE-97	11423272	NT	Homo sapiens thymosin protein S16 (RPS16), mRNA
11920	24060	37439	6.95	1.EE-97	11423272	NT	Homo sapiens thymosin protein S16 (RPS16), mRNA
850	1787	28824	3.7	9.0E-98	BE000078.1	EST, HUMAN	Human sapiens thymosin protein S16 (RPS16), mRNA
850	1787	28824	3.7	9.0E-98	BE000078.1	EST, HUMAN	Human sapiens thymosin protein S16 (RPS16), mRNA
4784	1789	28824	0.92	9.0E-98	8490716	NT	Human sapiens thymosin protein S16 (RPS16), mRNA
6557	19503	33001	0.72	9.0E-98	AB014360.1	NT	Human sapiens thymosin protein S16 (RPS16), mRNA
7069	20603	33901	0.54	9.0E-98	2691871	NT	Human sapiens thymosin protein S16 (RPS16), mRNA
7184	20713	34015	0.52	9.0E-98	11410408	NT	Human sapiens thymosin protein S16 (RPS16), mRNA
9503	21534	34715	7.2	9.0E-98	4758119	NT	Human sapiens thymosin protein S16 (RPS16), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	OPF SEQ ID NO.	Expression Signal	Mean Single (Top) HI BLAST Value	Top HI Accession No.	Top HI Database Source	Top HI Description
8503	21434	34776	7.2	0.05-98	4759119	NT	Homo sapiens death-associated protein (DAP), mRNA
6090	22596	35957	4.34	0.05-98	X06959	NT	Human mRNA for amyloid A (A1) protein
9765	22990	36074	5.67	0.05-98	11321890	NT	Homo sapiens succinyl-CoA ligase, GTP-forming, alpha subunit (SUCCLA), mRNA
6832	22738	36120	1.83	0.05-98	AB057793.1	NT	Homo sapiens mRNA for KIAA1350 protein, partial cds
9078	22793		1.16	0.05-98	AF597726.1	NT	Homo sapiens 11S ribonucleoprotein A2 (RNP11S), mRNA
6006	22894	36290	1.13	0.05-98	4537070	NT	Homo sapiens 11S ribonucleoprotein A2 (RNP11S), mRNA
9006	22894	36291	1.19	0.05-98	4537070	NT	Homo sapiens 11S ribonucleoprotein A2 (RNP11S), mRNA
10751	22839	37072	0.81	0.05-98	AF415255.1	NT	Homo sapiens nuclear polyphosphate 1-phosphatase (NPP1), gene, complete cds
10552	22831	37101	0.81	0.05-98	AF415255.1	NT	Homo sapiens nuclear polyphosphate 1-phosphatase (NPP1), gene, complete cds
11421	24355	37602	2.22	0.05-98	BE292222.1	NT	Homo sapiens mRNA for KIAA1036 protein, partial cds
11422	24355	37602	2.32	0.05-98	AB033222.1	NT	Homo sapiens mRNA for KIAA1036 protein, partial cds
11423	24355	37602	2.32	0.05-98	AB033222.1	NT	Homo sapiens mRNA for KIAA1036 protein, partial cds
12535	17578	26624	6.11	0.05-98	BE590073.1	EST_HUMAN	PM4-B10724-01040-008-412.610724 Homo sapiens cDNA
26	19141		0.77	0.05-98	AJ251193.1	NT	Homo sapiens partial MICB, gene for MHC class I chain-related protein B, exons 2-3 and joined CDS
1691	14611	27673	1.69	0.05-98	5031910	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1691	14611	27674	1.69	0.05-98	5031910	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1691	14611	27674	1.69	0.05-98	5031910	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1769	14783	27753	4.42	0.05-98	AJ017007.1	NT	Homo sapiens PMS2, 16 mRNA, partial cds
1769	14783	27754	4.42	0.05-98	AJ017007.1	NT	Homo sapiens PMS2, 16 mRNA, partial cds
3054	10360	29555	1.27	0.05-98	AJ250411.1	NT	Homo sapiens 559 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1.3
3054	10360	29555	1.27	0.05-98	AJ250411.1	NT	Homo sapiens 559 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1.3
3054	10360	29555	1.27	0.05-98	AJ250411.1	NT	Homo sapiens 559 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1.3
3054	10360	29555	1.27	0.05-98	AJ250411.1	NT	Homo sapiens 559 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1.3
6319	16369	29774	11.61	0.05-98	AJ44659.1	NT	Human mitochondrial epsilon kinase (COM1) gene, complete cds
6319	16369	29774	11.61	0.05-98	AJ44659.1	NT	Human mitochondrial epsilon kinase (COM1) gene, complete cds
5409	18397	32538	1.62	0.05-98	BE598873.1	EST_HUMAN	PM4-B10724-01040-008-412.610724 Homo sapiens cDNA
5409	18397	32538	1.62	0.05-98	BE598873.1	EST_HUMAN	PM4-B10724-01040-008-412.610724 Homo sapiens cDNA
2191	16202	29207	1.1	0.05-98	AJ403194.1	EST_HUMAN	PM4-B10724-01040-008-412.610724 Homo sapiens cDNA
2191	16202	29207	1.1	0.05-98	AJ403194.1	EST_HUMAN	PM4-B10724-01040-008-412.610724 Homo sapiens cDNA
2561	16040	29049	2.92	0.05-98	AB014607.1	NT	Homo sapiens 12 open reading frame 4 (C12ORF4), mRNA
2768	15787		4.29	0.05-98	AA077468.1	EST_HUMAN	PM4-B10724-01040-008-412.610724 Homo sapiens cDNA
7279	20226	33476	0.41	0.05-98	11419210	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
7279	20226	33476	0.41	0.05-98	11419210	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
7279	20226	33476	0.41	0.05-98	11419210	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
7279	20226	33476	0.41	0.05-98	11419210	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
7279	20226	33476	0.41	0.05-98	11419210	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
9311	22739	39000	4.21	0.05-98	HA0068.1	EST_HUMAN	PM4-B10724-01040-008-412.610724 Homo sapiens cDNA
9311	22739	39000	4.21	0.05-98	HA0068.1	EST_HUMAN	PM4-B10724-01040-008-412.610724 Homo sapiens cDNA
9837	22742	38123	0.74	0.05-98	BE220951	NT	Homo sapiens uncharacterized bone marrow protein BM039 (BM039), mRNA
10395	23284	39704	1.47	0.05-98	AJ403124.1	EST_HUMAN	PM4-B10724-01040-008-412.610724 Homo sapiens cDNA

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9560	29477	35586	0.72	1.0E-96 AF41946.1	NT	EST_HUMAN	Homo sapiens beta-tubulin mRNA, complete cds
9560	19622	32219	0.69	1.0E-96 AF03004.1	EST_HUMAN	EST_HUMAN	QV47673.0P339.013 E1073 Homo sapiens cDNA
9560	19622	32220	0.69	9.0E-96 AF03004.1	EST_HUMAN	EST_HUMAN	QV47673.0P339.013 E1073 Homo sapiens cDNA
8778	18326	32483	4.39	9.0E-96 AY059538.1	EST_HUMAN	EST_HUMAN	EST390717 MAGC gene, MAGC Homo sapiens cDNA
11862	24471	37937	2.91	8.0E-96 AF79820.1	EST_HUMAN	EST_HUMAN	EST390717 NCL CGAP Brd4 Homo sapiens cDNA, clone IMAGE2103421 3' similar to SW-BID_HUMAN
11862	24471	37937	2.91	8.0E-96 AF79820.1	EST_HUMAN	EST_HUMAN	EST390717 NCL CGAP Brd4 Homo sapiens cDNA, clone IMAGE2103421 3' similar to SW-BID_HUMAN
11862	24471	37938	2.91	9.0E-96 AF79820.1	EST_HUMAN	EST_HUMAN	EST390717 NCL CGAP Brd4 Homo sapiens cDNA, clone IMAGE2103421 3' similar to SW-BID_HUMAN
8296	22214	35572	0.50	8.0E-96 AF033094.1	NT	EST_HUMAN	Human endonuclease telomerase, complete genome
8947	19105	32250	0.01	7.0E-96 AF033094.1	NT	EST_HUMAN	Homo sapiens coxIII (hL) gene, exon 3
12037	24759	38366	2.76	7.0E-96 AF011966.1	NT	EST_HUMAN	Homo sapiens Nlr-receptor (NLR-2) gene, liver region exon
464	13861	28483	0.76	6.0E-96 U19361.1	NT	EST_HUMAN	Human G2 protein mRNA, partial cds
3568	18686	25872	1.76	6.0E-96 AW57684.1	EST_HUMAN	EST_HUMAN	EST388478 MAGC resequences, MAGC Homo sapiens cDNA
4802	17804	30726	1	6.0E-96	4920300	NT	Homo sapiens CD34 antigen (CD34) mRNA
6804	18914	33130	0.74	6.0E-96	7706132	NT	Homo sapiens GAP-like protein (LOC31306) mRNA
6974	20001	33232	0.59	6.0E-96 AF3810.1	NT	EST_HUMAN	Homo sapiens polycystic kidney disease (PKD) gene, exon 27-30
6974	20001	33233	0.69	6.0E-96 AF3810.1	NT	EST_HUMAN	Homo sapiens polycystic kidney disease (PKD) gene, exon 27-30
8983	21674	34966	1.32	6.0E-96 NG9101.1	NT	EST_HUMAN	H. sapiens mRNA for est-ogen receptor
8700	21431	84978	0.72	6.0E-96	5801869	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
9324	22362	35501	2.66	6.0E-96 AB06426.1	NT	EST_HUMAN	Homo sapiens NDS1A mRNA for N-deucylase/N-sulfotransferase 4, complete cds
9422	22366	35715	4.44	6.0E-96 AF09235.1	NT	EST_HUMAN	Homo sapiens beta-actin protein mRNA, complete cds
9422	22366	35715	4.44	6.0E-96 AF09235.1	NT	EST_HUMAN	Homo sapiens beta-actin protein mRNA, complete cds
9478	22407	35767	0.67	6.0E-96	11431904	NT	Homo sapiens beta-actin protein mRNA, complete cds
9478	22407	35768	0.67	6.0E-96	11431904	NT	Homo sapiens beta-actin protein mRNA, complete cds
11162	24060	37938	3.79	6.0E-96	11520399	NT	Homo sapiens beta-actin protein mRNA, complete cds
11868	23966	37426	1.65	6.0E-96	9910279	NT	Homo sapiens beta-actin protein mRNA, complete cds
11868	23966	37427	1.65	6.0E-96	9910279	NT	Homo sapiens beta-actin protein mRNA, complete cds
845	13860	26637	3.34	6.0E-96 U34604.1	NT	EST_HUMAN	Homo sapiens beta-actin protein mRNA, complete cds
845	13860	26638	3.34	6.0E-96 U34604.1	NT	EST_HUMAN	Homo sapiens beta-actin protein mRNA, complete cds
1900	14990	27993	1.42	6.0E-96 AF00960.1	NT	EST_HUMAN	Homo sapiens beta-actin protein mRNA, complete cds
4079	17584	30932	1.67	6.0E-96 AF00960.1	NT	EST_HUMAN	Homo sapiens beta-actin protein mRNA, complete cds
12951	25268		1.86	6.0E-96 AF00960.1	NT	EST_HUMAN	Homo sapiens beta-actin protein mRNA, complete cds
8986	21926		5.76	3.0E-96 MB5586.1	NT	EST_HUMAN	Human ZNF141, human protein (ZNF141) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exp SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1287	14802		10.54	2.0E-99	AW27492.1	EST_HUMAN	pcQ606.x1 NCI COAP HND Homo sapiens cDNA clone IMAGE:27386/4 3' similar to gp.M31212 MYOSIN LIGHT CHAIN ALKALI NONMUSCLE ISOFORM (HUMAN);
3343	10350	29254	1.26	2.0E-99	U03693.1	NT	Human K1 (P70580) subunit mRNA, complete cds
4659	17964	36532	1.03	2.0E-99	AF060573.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADI18C) gene, nuclear gene encoding mitochondrial protein, complete cds
8127	21037	34399	0.55	2.0E-99	F535737.1	NT	Homo sapiens cytosolic fatty acylating protein transcription factor, alpha subunit (GAL4) mRNA
8295	22193	35551	10.25	2.0E-99	Z29607.1	EST_HUMAN	2B-6006.x1 Soares, fetal lung, NHE-19W Homo sapiens cDNA clone IMAGE:300839 5' similar to
8665	22620	39098	0.6	2.0E-99	AF162933.1	NT	4B-1006.11 Beta-GALACTOSIDASE PRECURSOR (HUMAN);
11549	24459	37921	3.92	2.0E-99	AF27457.2	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
12104	26709	38530	3.81	2.0E-99	U064930.1	NT	Homo sapiens potassium channel, subfamily X, member 10 (KCNK10), mRNA
338	13426	29341	1.54	1.0E-99	AF114487.1	NT	Homo sapiens intercalin B1 isoform (ITSN) mRNA, complete cds
400	13462	29402	0.94	1.0E-99	U1520169	NT	Homo sapiens ubiquitin protein transcription factor, alpha subunit (GAL4) mRNA
1443	14474	27432	1.48	1.0E-99	U060938.1	NT	Human K1 (P70580) subunit mRNA, complete cds
1578	14668	27598	1.51	1.0E-99	AF162933.1	NT	Homo sapiens uncoupled Nucleolar P23 CS protein (NUP33) mRNA, complete cds
1576	14668	27598	1.51	1.0E-99	AF162933.1	NT	Homo sapiens uncoupled Nucleolar P23 CS protein (NUP33) mRNA, complete cds
1942	14983	27941	1.34	1.0E-99	U050728.1	NT	Homo sapiens 19S ribosomal protein P0 (RPS19) mRNA, complete cds
1942	14983	27942	1.34	1.0E-99	U050728.1	NT	Homo sapiens 19S ribosomal protein P0 (RPS19) mRNA, complete cds
3134	16184	28077	1.52	1.0E-99	U3171.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4487	17498	33358	0.76	1.0E-99	AF030916.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4487	17498	33358	0.76	1.0E-99	AF030916.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
5946	18010	32195	1.42	1.0E-99	U064930.1	NT	Homo sapiens cell recognition molecular cluster 2 (KIA0050), mRNA
7115	20319	33554	1.42	1.0E-99	U142007.1	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
7489	22569	33554	0.83	1.0E-99	U142007.1	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
8741	22569	33720	1.12	1.0E-99	U060221.1	NT	Homo sapiens EGF gene exon 2
					U1410722.1	NT	Homo sapiens ALEX1 protein (LOC31350), mRNA
10050	22969	39395	1.71	1.0E-99	AW340141.1	EST_HUMAN	HO271192.x1 Soares, NFL-1, GBO-33 Homo sapiens cDNA clone IMAGE:260037.3 3' similar to TPOC27211
11937	24468	37654	1.42	1.0E-99	7427614.NT	NT	HO271192.x1 Soares, NFL-1, GBO-33 Homo sapiens cDNA clone IMAGE:260037.3 3' similar to TPOC27211
11517	24185	37955	1.42	1.0E-99	7427614.NT	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
11631	24937	38008	1.59	1.0E-99	5601979.NT	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
11816	24737	38228	3.29	1.0E-99	AB023122.1	NT	Homo sapiens liver shock transcription factor 2 binding protein (HS12BP), mRNA
					AB023122.1	NT	Homo sapiens liver shock transcription factor 2 binding protein (HS12BP), mRNA
					AB023122.1	NT	Homo sapiens liver shock transcription factor 2 binding protein (HS12BP), mRNA
12395	25131		5.38	1.0E-99	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

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Table 4

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Protein SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Definition Source	Top Hit Description
1	13118	26004	1.26	1.0E-100	AI103247.2	NT
	13119	26004	1.46	1.0E-100	AI103247.2	NT
	13118	26004	1.46	1.0E-100	AI103247.2	NT
	13119	26004	1.46	1.0E-100	AI103247.2	NT
	13118	26004	1.3	1.0E-100	114182303	NT
	13119	26004	1.3	1.0E-100	114182303	NT
	13126	26004	1.3	1.0E-100	114182303	NT
	13126	26004	1.3	1.0E-100	114182303	NT
	13262	26116	1.3	1.0E-100	AJW27331.1	EST - HUMAN
	13262	26116	1.3	1.0E-100	AJW27331.1	EST - HUMAN
	13279	26164	1.06	1.0E-100	AI103268.2	NT
	13279	26164	1.06	1.0E-100	AI103268.2	NT
	13279	26164	1.06	1.0E-100	AI103268.2	NT
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13279	26164	1.06	1.0E-100	AI103268.2	NT	
13279	26164	1.06	1.0E-100	AI103268.2		

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9464	19452	32624	1.05	1.0E-100	4557668	NT	Homo sapiens ER to nucleus signaling 1 (ERN1) mRNA
6773	1987	33018	5.1	1.0E-100	AU46741.1	EST_HUMAN	AU46741 PLACE2 Homo sapiens cDNA clone IMAGE:2009137.5
6653	19865	33079	0.71	1.0E-100	AU13690.1	EST_HUMAN	AU13690 PLACE1 Homo sapiens cDNA clone IMAGE:103580.5
6652	20739	33740	1.33	1.0E-100	U01081.1	EST_HUMAN	M35003.1 Somatostatin-like peptide (SIFL) Homo sapiens cDNA clone IMAGE:12914.9
7075	20261	33537	0.85	1.0E-100	735279	NT	Human ribonuclease H1 (RNH1) mRNA
7180	20266	33520	1.07	1.0E-100	M46594.1	EST_HUMAN	G467416 ACTIN FLAMIN-TASSOCIA TED PROTEIN ;
7185	20266	33520	1.07	1.0E-100	M46594.1	EST_HUMAN	G467416 ACTIN FLAMIN-TASSOCIA TED PROTEIN ;
7213	20313	33450	1.17	1.0E-100	B575678.1	EST_HUMAN	MR1-TN0024-000600-004-505 TN0048 Homo sapiens cDNA
7213	20313	33450	1.17	1.0E-100	B575678.1	EST_HUMAN	MR1-TN0024-000600-004-505 TN0048 Homo sapiens cDNA
7221	20220	33468	2.49	1.0E-100	B43571.1	NT	Human mRNA for kidney epithelial growth factor (EGF) precursor
8094	22325	33531	5.23	1.0E-100	BF103653.1	EST_HUMAN	60194735/F1 NH1_MGO_61 Homo sapiens cDNA clone IMAGE:3691310.5
8131	22359	33531	1.74	1.0E-100	AL193203.2	NT	Homo sapiens chromosome 21 segment HS21C003
9566	23623	33645	0.61	1.0E-100	AU116391.1	EST_HUMAN	AU116391 HEMBA1 Homo sapiens cDNA clone HEMBA10003.43
9566	23623	33646	0.61	1.0E-100	AU116391.1	EST_HUMAN	AU116391 HEMBA1 Homo sapiens cDNA clone HEMBA10003.43
9774	22659	33634	3.54	1.0E-100	AB54018.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
9820	22849		1.72	1.0E-100	AB72383.1	EST_HUMAN	MR22 negative element ;
9967	21225	34053	2.43	1.0E-100	AW66951.1	EST_HUMAN	PMA-BN0085-100900-001-006 BN0085 Homo sapiens cDNA
10019	22916		0.59	1.0E-100	AU12720.1	EST_HUMAN	AU12720 NT2P2 Homo sapiens cDNA clone NT2P2007918.5
10112	23023	36599	2.4	1.0E-100	AB504646.1	NT	Homo sapiens mRNA for KIAA1626 protein, partial cds
10112	23023	36400	2.4	1.0E-100	AB504646.1	NT	Homo sapiens mRNA for KIAA1626 protein, partial cds
10358	23247	36966	1.61	1.0E-100	AW930467.1	EST_HUMAN	hH89-11.1 Y1 NCL CGAP_GJ1 Homo sapiens cDNA clone IMAGE:2596939.5
10358	23247	36967	1.61	1.0E-100	AW930467.1	EST_HUMAN	hH89-11.1 Y1 NCL CGAP_GJ1 Homo sapiens cDNA clone IMAGE:2596939.5
10949	23853	37260	0.7	1.0E-100	BF47919.1	EST_HUMAN	602030554/F1 NCL CGAP_Binf7 Homo sapiens cDNA clone IMAGE:416166.5
11035	23916		2.16	1.0E-100	Y10391.1	NT	Human endonuclease retrovirus HERV-K, pol gene
11160	24124	37670	7.02	1.0E-100	BF32782.1	EST_HUMAN	MRO-BN0070-270300-006-BT1 BN0070 Homo sapiens cDNA
11782	2474	38254	4.74	1.0E-100	AF11170.3	NT	Homo sapiens 14q32 Jigsaw2 gene, complete cds; and unknown gene
11792	24714	38205	4.74	1.0E-100	AF11170.3	NT	Homo sapiens 14q32 Jigsaw2 gene, complete cds; and unknown gene
12095	24000		1.59	1.0E-100	AW87646.1	EST_HUMAN	GYZP1-107123-015000-070-004 T10072 Homo sapiens cDNA
12106	24677		1.82	1.0E-100	AF255595.1	NT	Homo sapiens gadin-like protein (GLP) gene, complete cds
12165	25004	36006	1.8	1.0E-100	AAT19005.1	EST_HUMAN	265045.11 Source: Jigant1/Jigant1/Jigant1 Homo sapiens cDNA clone IMAGE:48954.5
12165	25004	35507	1.8	1.0E-100	AAT19005.1	EST_HUMAN	265045.21 Source: Jigant1/Jigant1/Jigant1 Homo sapiens cDNA clone IMAGE:48954.5

Table 4

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Medal Similar (Top) HR BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7165	18457	31938	1.9	1.0E-103	5032262	NT	Homo sapiens electrophin (nuclear envelope, Duchenne and Becker types), includes DXS142, DXS164, DXS165, DXS230, DXS268, DXS269, DXS270, DXS272 (CMD), transcript variant D-9427m, mRNA
7166	18457	31939	1.9	1.0E-103	5032262	NT	Homo sapiens electrophin (nuclear envelope, Duchenne and Becker types), includes DXS142, DXS164, DXS230, DXS268, DXS269, DXS270, DXS272 (CMD), transcript variant D-9427m, mRNA
7208	18476	31298	1.93	1.0E-103	5032262	NT	Homo sapiens electrophin (nuclear envelope, Duchenne and Becker types), includes DXS142, DXS164, DXS230, DXS268, DXS269, DXS270, DXS272 (CMD), transcript variant D-9427m, mRNA
7209	18476	31298	1.93	1.0E-103	5032262	NT	Homo sapiens electrophin (nuclear envelope, Duchenne and Becker types), includes DXS142, DXS164, DXS230, DXS268, DXS269, DXS270, DXS272 (CMD), transcript variant D-9427m, mRNA
7209	20827	33846	1.06	1.0E-103	AI26890.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZ1FL1 gene
7264	20822	33823	1.37	1.0E-103	AI95776.1	EST_HUMAN	ES137849 IMAGE rescreen, VAGI Homo sapiens cDNA
7264	20822	33823	1.37	1.0E-103	AI95776.1	EST_HUMAN	ES137849 IMAGE rescreen, VAGI Homo sapiens cDNA
7719	20851	33945	3.71	1.0E-103	BE14818.1	EST_HUMAN	tr15905.x1 NCI COAP, Brn25 Homo sapiens cDNA clone IMAGE2102289.9 similar to TR-Q13769
8244	21149	34482	4.10	1.0E-103	AI50071.1	EST_HUMAN	tr15905.x1 NCI COAP, Brn25 Homo sapiens cDNA clone IMAGE2102289.9 similar to TR-Q13769
8244	21149	34482	4.10	1.0E-103	AI50071.1	EST_HUMAN	tr15905.x1 NCI COAP, Brn25 Homo sapiens cDNA clone IMAGE2102289.9 similar to TR-Q13769
9181	22100	35447	1.07	1.0E-103	AU40344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE200374.5
9181	22100	35448	1.07	1.0E-103	AU40344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE200374.5
9281	22189	35546	1.26	1.0E-103	BF10244.1	EST_HUMAN	78605.x1 Score1_NSF_F8_JW_OT_PA_F_S1 Homo sapiens cDNA clone IMAGE3525664.3 similar to SW-PTNF_HUMAN Q1626 PROTEIN-TYROSINE PHOSPHATASE D1;
9882	22578	35949	3.52	1.0E-103	600921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9882	22578	35949	3.52	1.0E-103	600921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9891	22817	36042	0.6	1.0E-103	AA61880.1	EST_HUMAN	tr15905.x1 NCI COAP, Brn25 Homo sapiens cDNA clone IMAGE300162.9 similar to gb102426.268
9891	22817	36042	0.6	1.0E-103	AA61880.1	EST_HUMAN	tr15905.x1 NCI COAP, Brn25 Homo sapiens cDNA clone IMAGE300162.9 similar to gb102426.268
9751	22860	36059	3.26	1.0E-103	AA77680.1	EST_HUMAN	tr15905.x1 NCI COAP, Brn25 Homo sapiens cDNA clone IMAGE300162.9 similar to gb102426.268
10060	23446	36088	1.79	1.0E-103	AZ71076.1	NT	tr15905.x1 NCI COAP, Brn25 Homo sapiens cDNA clone IMAGE300162.9 similar to gb102426.268
10081	23467	36016	2.33	1.0E-103	AA76367.1	EST_HUMAN	tr15905.x1 NCI COAP, Brn25 Homo sapiens cDNA clone IMAGE300162.9 similar to gb102426.268
10081	23467	36016	2.33	1.0E-103	AA76367.1	EST_HUMAN	tr15905.x1 NCI COAP, Brn25 Homo sapiens cDNA clone IMAGE300162.9 similar to gb102426.268
10732	23618	37048	11.24	1.0E-103	AI77806.1	EST_HUMAN	tr15905.x1 NCI COAP, Brn25 Homo sapiens cDNA clone IMAGE300162.9 similar to gb102426.268
11174	24017	37547	4.8	1.0E-103	AI79260.1	EST_HUMAN	tr15905.x1 NCI COAP, Brn25 Homo sapiens cDNA clone IMAGE300162.9 similar to gb102426.268
11273	24063	37547	1.70	1.0E-103	1142403	NT	tr15905.x1 NCI COAP, Brn25 Homo sapiens cDNA clone IMAGE300162.9 similar to gb102426.268
11273	24063	37547	1.70	1.0E-103	1142403	NT	tr15905.x1 NCI COAP, Brn25 Homo sapiens cDNA clone IMAGE300162.9 similar to gb102426.268
11813	24734	38225	9.63	1.0E-103	AU156383.1	EST_HUMAN	tr15905.x1 NCI COAP, Brn25 Homo sapiens cDNA clone IMAGE300162.9 similar to gb102426.268
11813	24734	38225	9.63	1.0E-103	AU156383.1	EST_HUMAN	tr15905.x1 NCI COAP, Brn25 Homo sapiens cDNA clone IMAGE300162.9 similar to gb102426.268
11970	23970	37417	3.52	1.0E-103	LA5161.1	NT	Homo sapiens polyoma kidney disease (PKD) gene, clone 21-30

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mean Swirl (Top) HT BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12006	24037		1.43	1.0E-103	AB247499.1	NT	Homo sapiens "SAS355 gene, exon 16 748301.01 Source: NIST_JWT_O1_PJA_51 Homo sapiens cDNA clone IMAGE:5287810.3 similar to contains MEF2B 3' MER235 repetitive element 1, Homo sapiens mammosiderin, beta A, neuronal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D) gene, cytoskeletal protein F.123454 (F.123454), mRNA
12167	25003	38536	2.26	1.0E-103	BE44811.1	EST_HUMAN	
12264	26982		2.32	1.0E-103	AF246099.1	NT	
12264	25005		1.59	1.0E-103	11632291	NT	
12473	25719	31655	2.52	1.0E-103	U01158.1	EST_HUMAN	Homo sapiens gene for AFA, complete cds
252	13350	26303	4.51	1.0E-104	AF031493.1	EST_HUMAN	DKF2654H107.11 B4 (synonym: HBC2) Homo sapiens cDNA clone DKF2654H107.2 5'
252	13350	26304	4.51	1.0E-104	AL037493.3	EST_HUMAN	DKF2654H107.11 B4 (synonym: HBC2) Homo sapiens cDNA clone DKF2654H107.2 5'
1663	14925	27806	1.72	1.0E-104	4652428	NT	Homo sapiens AHP2 (adip-related protein 2) [BVP8] mRNA
2205	13220	28223	3.87	1.0E-104	AA193975.1	EST_HUMAN	302205.11 Streptococcus (6837204) Homo sapiens cDNA clone IMAGE:587628.3 similar to gp:214116, ms1 CD39 G100PROTEIN PRECURSOR (HUMAN): 601677460F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3826438.5
2210	13228	28335	2.03	1.0E-104	BE744638.1	EST_HUMAN	
2262	13367	28400	1.58	1.0E-104	BF34321.1	EST_HUMAN	RG1-C10246-110902-214142 OT0246 Homo sapiens cDNA
2262	13367	28401	1.58	1.0E-104	BF34321.1	EST_HUMAN	RG1-C10246-110902-214142 OT0246 Homo sapiens cDNA
2460	18464	28441	1.69	1.0E-104	5031570.1	NT	Homo sapiens AHP2 (adip-related protein 2, yeast) homolog (ACIR2), mRNA
2527	15528	28529	1.11	1.0E-104	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2574	15677	28589	1.11	1.0E-104	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2595	18011		2.91	1.0E-104	U01158.1	NT	Human lymphocyte antigen CD55/CD55 mRNA, complete cds
3308	18366	20257	1.31	1.0E-104	U11151.1	EST_HUMAN	H. sapiens gene encoding phenylpyruvate decarboxase II
3450	19491		2.35	1.0E-104	AJ133926.1	EST_HUMAN	AU135828 OVACRT Homo sapiens cDNA clone OVAC100935.5
3603	10907	20803	0.65	1.0E-104	AB033102.1	EST_HUMAN	ES121658 Adrenal gland tumor Homo sapiens cDNA, 5' end
4020	17047	20845	0.65	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
4228	17242	30110	0.75	1.0E-104	AB033386.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
4484	17465	32355	8.95	1.0E-104	U02787.1	EST_HUMAN	HSC1A071 normalized infant brain cDNA Homo sapiens cDNA clone c-31407
4719	17724	32086	0.93	1.0E-104	AF231020.1	NT	Human mRNA for Ilacreselin (FN precursor)
4719	17724	32087	0.93	1.0E-104	AF231020.1	NT	Homo sapiens chromosome 21 unincorporated mRNA
6295	18280	31190	1.26	1.0E-104	4802152	NT	Homo sapiens chromosome 21 unincorporated mRNA
6339	18322	31171	1.06	1.0E-104	7807038	NT	Homo sapiens apolipoprotein B (including A2) antigen (APOB) mRNA
9165	19222	32354	0.92	1.0E-104	U43379.1	NT	Homo sapiens death receptor 9 (DR9), mRNA
9165	19222	32355	0.92	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6217	19372	32426	1.03	1.0E-104	AB017932.1	NT	Homo sapiens ald mRNA for Atrial natriuretic factor (ANF) related protein 3, complete cds

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Probe Seq ID NO:	Exon NO:	ORF Seq ID NO:	Expression Signal	Mean Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1766	14731		2.14	1.0E-105	AB020681.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
1764	14731	27731	1.26	1.0E-105	AI103247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1844	14897	27849	2.78	1.0E-105	AL103280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1941	14622	27940	0.41	1.0E-105	U03078.1	NT	Homo sapiens mRNA for KIAA0138, partial cds
2258	15216	28220	1.01	1.0E-105	U03078.1	EST_HUMAN	EST170030 Shcct1 Homo sapiens cDNA 5' end similar to subunit alpha of p70S60 subunit
2264	18700		1.01	1.0E-105	U15849.8.1	EST_HUMAN	EST170030 Shcct1 Homo sapiens cDNA 5' end similar to subunit alpha of p70S60 subunit
3291	18702		3.87	1.0E-105	U15849.8.1	EST_HUMAN	Homo sapiens 95 kb contig between AML1 and CBT1 on chromosome 21q22; segment 1/3
3293	18702		3.87	1.0E-105	U15849.8.1	EST_HUMAN	Homo sapiens 95 kb contig between AML1 and CBT1 on chromosome 21q22; segment 1/3
3294	18702		1.07	1.0E-105	U15849.8.1	EST_HUMAN	Homo sapiens 95 kb contig between AML1 and CBT1 on chromosome 21q22; segment 1/3
3295	18702		1.07	1.0E-105	U15849.8.1	EST_HUMAN	Homo sapiens 95 kb contig between AML1 and CBT1 on chromosome 21q22; segment 1/3
3296	18702		1.07	1.0E-105	U15849.8.1	EST_HUMAN	Homo sapiens 95 kb contig between AML1 and CBT1 on chromosome 21q22; segment 1/3
3297	18702		1.07	1.0E-105	U15849.8.1	EST_HUMAN	Homo sapiens 95 kb contig between AML1 and CBT1 on chromosome 21q22; segment 1/3
3298	18702		1.07	1.0E-105	U15849.8.1	EST_HUMAN	Homo sapiens 95 kb contig between AML1 and CBT1 on chromosome 21q22; segment 1/3
3299	18702		1.07	1.0E-105	U15849.8.1	EST_HUMAN	Homo sapiens 95 kb contig between AML1 and CBT1 on chromosome 21q22; segment 1/3
3300	18702		1.07	1.0E-105	U15849.8.1	EST_HUMAN	Homo sapiens 95 kb contig between AML1 and CBT1 on chromosome 21q22; segment 1/3
3301	18702		1.07	1.0E-105	U15849.8.1	EST_HUMAN	Homo sapiens 95 kb contig between AML1 and CBT1 on chromosome 21q22; segment 1/3
3302	18702		1.07	1.0E-105	U15849.8.1	EST_HUMAN	Homo sapiens 95 kb contig between AML1 and CBT1 on chromosome 21q22; segment 1/3
3303	18702		1.07	1.0E-105	U15849.8.1	EST_HUMAN	Homo sapiens 95 kb contig between AML1 and CBT1 on chromosome 21q22; segment 1/3
3304	18702		1.07	1.0E-105	U15849.8.1	EST_HUMAN	Homo sapiens 95 kb contig between AML1 and CBT1 on chromosome 21q22; segment 1/3
3305	18702		1.07	1.0E-105	U15849.8.1	EST_HUMAN	Homo sapiens 95 kb contig between AML1 and CBT1 on chromosome 21q22; segment 1/3
3306	18702		1.07	1.0E-105	U15849.8.1	EST_HUMAN	Homo sapiens 95 kb contig between AML1 and CBT1 on chromosome 21q22; segment 1/3
3307	18702		1.07	1.0E-105	U15849.8.1	EST_HUMAN	Homo sapiens 95 kb contig between AML1 and CBT1 on chromosome 21q22; segment 1/3
3308	18702		1.07	1.0E-105	U15849.8.1	EST_HUMAN	Homo sapiens 95 kb contig between AML1 and CBT1 on chromosome 21q22; segment 1/3
3309	18702		1.07	1.0E-105	U15849.8.1	EST_HUMAN	Homo sapiens 95 kb contig between AML1 and CBT1 on chromosome 21q22; segment 1/3
3310	18702		1.07	1.0E-105	U15849.8.1	EST_HUMAN	Homo sapiens 95 kb contig between AML1 and CBT1 on chromosome 21q22; segment 1/3
3311	18702		1.07	1.0E-105	U15849.8.1	EST_HUMAN	Homo sapiens 95 kb contig between AML1 and CBT1 on chromosome 21q22; segment 1/3
3312	18744		1.0E-105	11420583.1		EST_HUMAN	Homo sapiens demagogin (DPT), mRNA
4168	17208	30074	2.19	1.0E-105	AI091688.1	EST_HUMAN	EST173761 MAGS, muscivora, MAGS Homo sapiens cDNA
4687	17659	30723	0.8	1.0E-105	BE060891.1	EST_HUMAN	661145023F1 NH1, MGC 65 Homo sapiens cDNA clone IMAGE380166 5'
4687	17659	30724	0.8	1.0E-105	BE060891.1	EST_HUMAN	661145023F1 NH1, MGC 65 Homo sapiens cDNA clone IMAGE380166 5'
4873	17672	30738	0.86	1.0E-105	AA098355.1	EST_HUMAN	ZNF402.31 Squares, fetal, liver, spleen, NFE2L3, S1 Homo sapiens cDNA clone IMAGE439382 3'
5051	18048		6.19	1.0E-105	AI103280.2	NT	Homo sapiens chromosome 21 segment HS21C038
5248	18235	31085	1.09	1.0E-105	AI074839.1	NT	Homo sapiens mRNA for KIAA0769 protein, partial cds
6332	18316	31184	1.35	1.0E-105	AF018394.1	NT	Homo sapiens mRNA for KIAA0769 protein, partial cds
5513	18592	31440	1.14	1.0E-105	AF018394.1	NT	Homo sapiens mRNA for KIAA0769 protein, partial cds
5582	18599		1	1.0E-105	AI070704.1	NT	Homo sapiens E3AP ubiquitin-protein ligase (UBES3A) gene, exon 2
7233	20742	33380	1.26	1.0E-105	BF074302.1	EST_HUMAN	Homo sapiens RefSeq-derived POU-domain factor-1 (RPF-1), mRNA
7233	20742	33381	1.26	1.0E-105	BF074302.1	EST_HUMAN	661101026F1 NH1, MGC 19 Homo sapiens cDNA clone IMAGE410334 5'
7322	18490	31262	3.68	1.0E-105	U1419196.1	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7322	18490	31263	3.68	1.0E-105	U1419196.1	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7373	20397	33036	0.62	1.0E-105	AW051034.1	EST_HUMAN	EST136366 MAGS, muscivora, MAGS Homo sapiens cDNA
7683	20597	33696	0.84	1.0E-105	BE060891.1	EST_HUMAN	661101026F1 NH1, MGC 19 Homo sapiens cDNA clone IMAGE410334 5'
8416	21317	34649	0.43	1.0E-105	U07027.1	NT	Homo sapiens protein tyrosine phosphatase mRNA, complete cds
8441	21373		1.14	1.0E-105	X12656.1	NT	Human mRNA for del proto-oncogene
8505	21537	34879	7.42	1.0E-105	U00087.1	EST_HUMAN	EST102975 Fetal brain, Strategic (catalase) Homo sapiens cDNA, clone H919R22
8693	21868	35284	1.10	1.0E-105	AW070141.1	EST_HUMAN	W6800.1 NCI CGAP Brn2b Homo sapiens cDNA clone IMAGE360063 3' similar to
9493	22411	35972	0.77	1.0E-105	AW069817.1	EST_HUMAN	SW-620, PENH1-26833 ACETYL-COENZYME A SYNTHASE 1
9603	22529	35988	3.18	1.0E-105	AW016879.1	EST_HUMAN	U141-BIP-2435-124U1.5 NCI CGAP 5302 Homo sapiens cDNA clone IMAGE2711782 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	QRF SEQ ID NO:	Expression Signal	Mean Similar TopHit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9745	22699	35051	1.05	1.0E-105	AW62972.1	EST_HUMAN	QV2-010062:14030-683-469 O10062 Homo sapiens cDNA
9745	22699	35052	1.05	1.0E-105	AW62972.1	EST_HUMAN	QV2-010062:14030-683-469 O10062 Homo sapiens cDNA
10066	22946	35333	0.88	1.0E-105	BE6967793.1	EST_HUMAN	35744375071 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:35073854.6
10066	22946	35334	0.88	1.0E-105	BE6967793.1	EST_HUMAN	35744375071 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:35073854.5
11370	24293	37752	5.44	1.0E-105	AF248222.1	NT	Homo sapiens RNU6-1 ribosomal RNA (RNU6-1) gene, testis cds, alternatively spliced
11679	24693	35950	1.83	1.0E-105	Q03546.1	NT	Homo sapiens COX10B gene for adult (COX10B) cDNA
11727	24629	38106	1.36	1.0E-105	7755938	NT	Homo sapiens Ret binding protein 11 (LOC51193), mRNA
12015	24890	38390	2.69	1.0E-105	AN027554.1	EST_HUMAN	35744375071 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:35073854.5
12221	25134	35953	1.45	1.0E-105	BE143293.1	EST_HUMAN	UHFE-BNU-466-07-DJL17 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:35073854.5
011	13222	26224	1.66	1.0E-105	AF103206.1	EST_HUMAN	35744375071 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:35073854.5
018	13141	26544	2.1	1.0E-105	AF103206.1	EST_HUMAN	35744375071 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:35073854.5
859	13361	26536	0.94	1.0E-105	AF035935.1	EST_HUMAN	EST377623 IMAGE resources, MAC3 Homo sapiens cDNA
859	13361	26536	1.7	1.0E-105	AF035935.1	NT	Human dihydrolipoyl succinyltransferase (psd-1)
859	13361	26536	1.7	1.0E-105	AF035935.1	NT	Homo sapiens soluble neuramin-1 mRNA, complete cds
1547	14971	27538	3.05	1.0E-105	AF145712.1	NT	Homo sapiens spinal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
1728	14755	27725	5.20	1.0E-105	U48724.1	NT	Homo sapiens type IV collagen alpha 3 chain (COL4A3) gene, exon 41
1748	14775	27744	2.28	1.0E-105	U04510.1	NT	np41065.1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:357382.3 similar to contains element
1825	14848	27624	4.19	1.0E-105	AA527448.1	EST_HUMAN	LTR3 repetitive element
1825	14848	27625	4.19	1.0E-105	AA527448.1	EST_HUMAN	np41065.1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:357382.3 similar to contains element
2135	15149	29130	2.12	1.0E-105	BE114293.1	EST_HUMAN	LTR3 repetitive element
2339	15345	29330	4.26	1.0E-105	4504184	NT	NTF0-HT0185-140200-010 HT0185 Homo sapiens cDNA
2529	15530	29532	3.15	1.0E-105	AF093508.1	NT	Homo sapiens X-linked embryonic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2543	16039	29838	1.67	1.0E-105	U61676.2	NT	Homo sapiens sperm membrane protein BS-33 mRNA, complete cds
2645	15041	29840	2.08	1.0E-105	BE290201.1	EST_HUMAN	9317407931 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3502401.6
2657	15709	29706	5.88	1.0E-105	AF210509.1	EST_HUMAN	Q1709410.1 Soares_NIH-MF01_51 Homo sapiens cDNA clone IMAGE:178507.3
2873	14483	27443	3.38	1.0E-105	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2873	14483	27444	3.38	1.0E-105	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2983	16034	29838	7.13	1.0E-105	AB037747.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
2983	16034	29837	7.13	1.0E-105	AB037747.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
3223	16271	28170	2.57	1.0E-105	6622665	NT	Homo sapiens hypodermal protein FLJ11273 (FLJ11273), mRNA

Table 4

Table 4

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Table 4
Single Exon Probes Expressed in Adult Liver

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Table 4

Single Exon Probe Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	OSF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11147	24076	37524	3.36	1.0E-107	AB2680.1	EST_HUMAN	g10466.x1 NCL CGAP_GUT Homo sapiens cDNA clone IMAGE 2708363 3' similar to SW 440CT_D10C1
11366	24632	37749	1.76	1.0E-107	U49411.1	NT	Protein ALP-ALPHA-ACTIN 3, NON-MUSCULAR
11367	24513	37789	1.96	1.0E-107	BF063511.1	EST_HUMAN	Homo sapiens heart muscle-specific protein (HSP) gene, exon 4
11766	24697	38153	7.76	1.0E-107	BE40563.1	EST_HUMAN	g021230181 NCL_MOC_10 Homo sapiens cDNA clone IMAGE 2481039 5'
11831	23960	37401	6.24	1.0E-107	U119701	NT	g01030381 NCL_MOC_10 Homo sapiens cDNA clone IMAGE 342829 5'
11831	23960	37402	6.28	1.0E-107	U119701	NT	Homo sapiens HSP-296 protein (HSP296) mRNA
12103	24544	38447	6.21	1.0E-107	AF172693	EST_HUMAN	Homo sapiens HSP-296 protein (HSP296) mRNA
12152	24591	38491	6.86	1.0E-107	4607823	NT	AU772698 DCA Homo sapiens cDNA clone DCANV021 5'
12181	25052	38551	3.36	1.0E-107	4507620	NT	Homo sapiens UDP-glucose 6-phosphate 2 family, polypeptide B11 (UGT2B11) mRNA
12216	25052	38552	3.36	1.0E-107	4507620	NT	Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 1 (SLC10A1) mRNA
12365	25863		7.71	1.0E-107	AA001415.1	EST_HUMAN	Homo sapiens soluble carrier family 10 (sodium/bile acid cotransporter family), member 1 (SLC10A1) mRNA
1681	13287		2.60	1.0E-108	AA341824.1	EST_HUMAN	ES172963 Fetal muscle Homo sapiens cDNA 5' end
581	14032	20975	2.26	1.0E-108	BE26042.1	EST_HUMAN	ES01177818 F1 NCL_MOC_17 Homo sapiens cDNA clone IMAGE 3532348 5'
12322	14325	27270	3.1	1.0E-108	V18000.1	NT	Homo sapiens NF2 gene
2352	15390	28332	3.13	1.0E-108	AB89040.1	EST_HUMAN	g011610.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE 2246533 3' similar to g01M14219 BONE
2352	15390	28332	3.13	1.0E-108	AB89040.1	EST_HUMAN	PROTEOGLYCAN II PRECURSOR (HUMAN);
2352	15390	28332	3.13	1.0E-108	AB89040.1	EST_HUMAN	PROTEOGLYCAN II PRECURSOR (HUMAN);
2452	16450	28433	13.94	1.0E-108	BE20694.1	EST_HUMAN	g022610.x1 NCL_MOC_14 Homo sapiens cDNA clone IMAGE 2963890 3' similar to g01X3771 60S
3001	16053	28947	0.74	1.0E-108	0303979	NT	RIBOSOMAL PROTEIN L25 (HUMAN); g0105277 Mouse hsc/thyroid mRNA, complete cds (NCBI);
3398	16440	29044	0.76	1.0E-108	AF028997.1	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3398	16440	29045	0.75	1.0E-108	AF028997.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
3483	10912	29781	1.16	1.0E-108	5493656	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4264	17279	30138	1.19	1.0E-108	AW694438.1	EST_HUMAN	h12411.x1 NCL CGAP_GUT Homo sapiens cDNA clone IMAGE 2972606 3' similar to SW 35P1_MOUSE
4916	17918	30783	2.78	1.0E-108	7681079	NT	P05041 S15-DINING PROTEIN S3P-1;
5020	18025	30684	0.74	1.0E-108	AW04799.1	EST_HUMAN	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5064	18061	30912	2.22	1.0E-108	AJ09005.1	NT	UHPH-BND-4nc-0404U1 NCL_MOC_30 Homo sapiens cDNA clone IMAGE 3380166 5'
						NT	Homo sapiens PSN1 gene, alternative transcript

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID/NO	Expression Signal	Mean Std Dev BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5331	18315	31103	1.19	1.0E-108	840716	NT	Homo sapiens retinol (R6), mRNA
5394	18346	31169	0.95	1.0E-108	AF1233.1	EST_HUMAN	Ym254r1.1 Source: Ym254r1.1 NIH: Homo sapiens cDNA, clone IMAGE:50889.5
5567	18147	31650	1.71	1.0E-108	AF34064.1	EST_HUMAN	RC4110372241.159-53 110372 Homo sapiens cDNA, clone IMAGE:384690.5
5717	18750	31722	2.45	1.0E-108	BE5907.6.1	EST_HUMAN	501444222.1 NIH: MGC_39 Homo sapiens cDNA, clone IMAGE:384690.5
5717	18750	31723	2.45	1.0E-108	BE5907.6.1	EST_HUMAN	501444222.1 NIH: MGC_39 Homo sapiens cDNA, clone IMAGE:384690.5
6191	19210		0.85	1.0E-108	AF120252.1	NT	Human cDNA, clone IMAGE:384690.5
6224	18265	32447	0.74	1.0E-108	BF34651.1	EST_HUMAN	PM1010403-240703-03-1410 CT0403 Homo sapiens cDNA, complete cds
6279	19426	32595	5.92	1.0E-108	AF294717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6376	19426	32596	5.92	1.0E-108	AF294717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6413	19597	32736	1.27	1.0E-108	AJ183769.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D75522, genes CAV2 (exons 1, 2a, and 2b), CAV7 (exons 1 and 2)
6515	19268	32447	1.08	1.0E-108	BF34651.1	EST_HUMAN	PM1010403-240703-001-110 CT0403 Homo sapiens cDNA
6598	19369	33163	0.74	1.0E-108	AF016706.1	NT	Homo sapiens E3AP ubiquitin-protein ligase (UBE3A) gene, exon 4
6605	19369	33164	0.74	1.0E-108	AF016706.1	NT	Homo sapiens E3AP ubiquitin-protein ligase (UBE3A) gene, exon 4
7519	20468	33744	4.57	1.0E-108	11431657	NT	Homo sapiens G protein-coupled receptor, family C, group 5, member 5 (GPCR5B), mRNA
7543	20770	34073	4.09	1.0E-108	BE52907.1	EST_HUMAN	Homo sapiens delta-5 fatty acid desaturase (FADS5) mRNA
7897	20623	34126	1.95	1.0E-108	BE52907.1	EST_HUMAN	6011134771 NIH: MGC_16 Homo sapiens cDNA, clone IMAGE:3354054.5
7928	20653	34150	1.05	1.0E-108	BF26912.1	EST_HUMAN	602043364F1 NIH: OGAP_Bmg7 Homo sapiens cDNA, clone IMAGE:4161037.5
7928	20653	34157	1.05	1.0E-108	BF26912.1	EST_HUMAN	602043364F1 NIH: OGAP_Bmg7 Homo sapiens cDNA, clone IMAGE:4161037.5
8382	21260	34617	0.46	1.0E-108	11422165	NT	Homo sapiens cyclic fibrillar transmembrane conductance regulator, A TP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8941	21972		1.74	1.0E-108	AF083300.1	EST_HUMAN	UIHF-RMO-ads-e-12-0-U1.1 NIH: MGC_38 Homo sapiens cDNA, clone IMAGE:3052876.5
8941	21972		1.74	1.0E-108	AF083300.1	EST_HUMAN	UIHF-RMO-ads-e-12-0-U1.1 NIH: MGC_38 Homo sapiens cDNA, clone IMAGE:3052876.5
8952	21023	34060	0.65	1.0E-108	AF00994.1	EST_HUMAN	UIHF-RMO-ads-e-12-0-U1.1 NIH: MGC_38 Homo sapiens cDNA, clone IMAGE:3052876.5
9300	22926	34891	0.65	1.0E-108	AF00994.1	EST_HUMAN	Homo sapiens ETS-family transcription factor EHF (EHF) mRNA, complete cds
11111	21217	34853	1.94	1.0E-108	BE530227.1	EST_HUMAN	921087667F1 NIH: MGC_10 Homo sapiens cDNA, clone IMAGE:3443891.5
11207	18454	31350	2.15	1.0E-108	Y12400.1	NT	Homo sapiens mRNA for CagA-associated microtubule-binding protein (CAGAB-210)
11303	24113	37606	1.95	1.0E-108	AF23391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7, 4b, and partial cds, alternatively spliced
11716	24020	38066	4.03	1.0E-108	AF06765.1	EST_HUMAN	ES1 376258 IMAGE:38066, MAGI Homo sapiens cDNA
11707	24060	38154	1.47	1.0E-108	AF06765.1	EST_HUMAN	AV105940 ADC-Homo sapiens cDNA, clone ADCAC63.9
11707	24060	38155	1.47	1.0E-108	AF06765.1	EST_HUMAN	AV105940 ADC-Homo sapiens cDNA, clone ADCAC63.9

Table 4

Single Exon Probes Expressed in Adult Liver

Probe NO.	Even SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) HI BLAST E Value	Top HI Accession No.	Top HI Database Source	Top HI Descriptor
11659	24720		1.62	1.0E-108	U1441635	NT	Human sapiens G protein-coupled receptor 48 (GPR48), mRNA
11860	24720	38243	2.17	1.0E-108	U53301	NT	Human sapiens COX-4A gene for α(IV) collagen, exon 23
12050	25059		4.23	1.0E-108	AQ024447.1	NT	Human sapiens mRNA for FJ-00037 protein, partial cds
12610	25059		3.837	7.79	1.0E-108	AF040356.1	002011857.1F11 CGAP_Bme57 Homo sapiens cDNA clone IMAGE:414297.2
45	13451	20032	0.83	1.0E-108	BF003118.1	EST_HUMAN	U3JUN00717.26A040-079.D087 Homo sapiens cDNA
68	13451	25031	1.47	1.0E-108	D60974.1	NT	Human mRNA for KIA0220 gene, partial cds
234	13352	25049	1.47	1.0E-108	U1142498	NT	Human sapiens hypothetical protein FLJ1316 (FLJ1316), mRNA
245	13432	28244	2.7	1.0E-109	U1438351	NT	Human sapiens calcitriol-11, EF-hand calcium binding domain (RCN1), mRNA
4589	13580	28476	3.8	1.0E-109	45071712	NT	Human sapiens leucine-rich repeat domain 2 (LRR2), mRNA
619	13684	29587	14.29	1.0E-109	AB023216.1	NT	Human sapiens mRNA for KIA0069 protein, partial cds
818	13684	29688	14.29	1.0E-109	AB023216.1	NT	Human sapiens mRNA for KIA0069 protein, partial cds
1230	14287	27210	6.33	1.0E-109	U29699.1	NT	Human sapiens nuclear phosphoprotein B23 (NPB1) mRNA, complete cds
1231	14287	27210	5.93	1.0E-109	U29699.1	NT	Human sapiens nuclear phosphoprotein B23 (NPB1) mRNA, complete cds
1697	14918	27877	5.83	1.0E-109	D15843.2	NT	Human sapiens mRNA for KIA00718 protein, partial cds
2250	15258	28274	5.22	1.0E-109	AL163284.2	NT	Human sapiens chromosome 21 segment HSR1C084
2250	15276	28282	1.81	1.0E-109	Y17123.1	NT	Human sapiens SNAF1 gene, exon 6
2689	16554	28864	3.56	1.0E-109	A0022328.1	EST_HUMAN	006001 at SNAF1, full length, sequence, rFLN3, 3' Homo sapiens cDNA clone IMAGE:164558.3 similar to
2886	15664	28865	3.56	1.0E-109	A0022328.1	EST_HUMAN	TRC02167 at SNAF1, full length, sequence, rFLN3, 3' Homo sapiens cDNA clone IMAGE:1654530.3 similar to
2887	16565	28868	3.18	1.0E-109	4504206	NT	TRC02167 at SNAF1, full length, sequence, rFLN3, 3' Homo sapiens cDNA clone IMAGE:1654530.3 similar to
3106	16157	29002	1.1	1.0E-109	N85190.1	EST_HUMAN	224106 Homo sapiens full length cDNA, clone 2A (clnta) (GUC51A), mRNA
3147	16158	29355	1.32	1.0E-109	N85190.1	EST_HUMAN	224106 Homo sapiens full length cDNA, clone 2A (clnta) (GUC51A), mRNA
3460	16463	29811	1.35	1.0E-109	AF243819.1	EST_HUMAN	FINGER STRONG ZNF 63 Homo sapiens cDNA
3461	16463	29811	1.35	1.0E-109	AF243819.1	EST_HUMAN	FINGER STRONG ZNF 63 Homo sapiens cDNA
3462	16463	29811	1.35	1.0E-109	AF243819.1	EST_HUMAN	FINGER STRONG ZNF 63 Homo sapiens cDNA
3463	16463	29811	1.35	1.0E-109	AF243819.1	EST_HUMAN	FINGER STRONG ZNF 63 Homo sapiens cDNA
3464	16463	29811	1.35	1.0E-109	AF243819.1	EST_HUMAN	FINGER STRONG ZNF 63 Homo sapiens cDNA
3465	16463	29811	1.35	1.0E-109	AF243819.1	EST_HUMAN	FINGER STRONG ZNF 63 Homo sapiens cDNA
3466	16463	29811	1.35	1.0E-109	AF243819.1	EST_HUMAN	FINGER STRONG ZNF 63 Homo sapiens cDNA
3467	16463	29811	1.35	1.0E-109	AF243819.1	EST_HUMAN	FINGER STRONG ZNF 63 Homo sapiens cDNA
3468	16463	29811	1.35	1.0E-109	AF243819.1	EST_HUMAN	FINGER STRONG ZNF 63 Homo sapiens cDNA
3469	16463	29811	1.35	1.0E-109	AF243819.1	EST_HUMAN	FINGER STRONG ZNF 63 Homo sapiens cDNA
3470	16463	29811	1.35	1.0E-109	AF243819.1	EST_HUMAN	FINGER STRONG ZNF 63 Homo sapiens cDNA
3471	16463	29811	1.35	1.0E-109	AF243819.1	EST_HUMAN	FINGER STRONG ZNF 63 Homo sapiens cDNA
3472	16463	29811	1.35	1.0E-109	AF243819.1	EST_HUMAN	FINGER STRONG ZNF 63 Homo sapiens cDNA
3473	16463	29811	1.35	1.0E-109	AF243819.1	EST_HUMAN	FINGER STRONG ZNF 63 Homo sapiens cDNA
3474	16463	29811	1.35	1.0E-109	AF243819.1	EST_HUMAN	FINGER STRONG ZNF 63 Homo sapiens cDNA
3475	16463	29811	1.35	1.0E-109	AF243819.1	EST_HUMAN	FINGER STRONG ZNF 63 Homo sapiens cDNA
3476	16463	29811	1.35	1.0E-109	AF243819.1	EST_HUMAN	FINGER STRONG ZNF 63 Homo sapiens cDNA
3477	16463	29811	1.35	1.0E-109	AF243819.1	EST_HUMAN	FINGER STRONG ZNF 63 Homo sapiens cDNA
3478	16463	29811	1.35				

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Table 4
Single Exon Probes Expressed in Adult Liver

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
11843	24694	38184	4.7	1.0E-100/W10510.1	EST	HUMAN	z603812.1 Soares, fetal_lung_NHEK19W Homo sapiens cDNA clone IMAGE307439 5' similar to	
12110	24691	38184	1.48	1.0E-109	1141801818	NT	PHS-S43890 5'ORF05 p51-beta stress-activated protein kinase, rat	
124589	127879	29282	2.1	1.0E-108/W17123.1	NT	HUMAN	Homo sapiens single-minded (Drosophila) homolog T (SIMT), mRNA	
125566	16276	28282	-8.1	1.0E-100/W17123.1	NT	HUMAN	Homo sapiens SNF5/IN11 gene, exon 8	
12774	25403	31811	8.38	1.0E-100/AB011930.1	NT	HUMAN	Homo sapiens gene for AP-8, complete cds	
3	13119	28005	1	1.0E-110	75688040	NT	Homo sapiens dectinase, bcl2/lympho, type II (DIO2), transcript variant 1, mRNA	
39	13185	28048	4.44	1.0E-110	59030073	NT	Homo sapiens luciferase-appeal-like transcriptional regulator, rat	
39	13185	28048	4.44	1.0E-110	59030073	NT	Homo sapiens luciferase-appeal-like transcriptional regulator, rat	
113	13119	28005	1.07	1.0E-110	75688040	NT	Homo sapiens dectinase, bcl2/lympho, type II (DIO2), transcript variant 2, mRNA	
134	13405	28524	1.73	1.0E-110/D87261.1	NT	HUMAN	Homo sapiens mRNA for inward rectifier potassium channel, complete cds	
550	12697	28527	0.78	1.0E-110/J84560.1	NT	HUMAN	Human dysembryon (DTN) gene, exon 20	
6286	12479	27818	0.88	1.0E-110	50510201	NT	Homo sapiens calcitriol receptor-like (CALCRL) mRNA	
1208	14338	27288	0.9	1.0E-110/AB023933.1	NT	HUMAN	Homo sapiens BCL2 mRNA for bcl2-associated protein 1, clone IMAGE3148, complete cds	
1305	14338	27288	0.9	1.0E-110/AB023933.1	NT	HUMAN	0120745871 NHEK19W Homo sapiens cDNA clone IMAGE30593 5'	
1808	14367	27813	1.14	1.0E-110/BE579117.1	EST	HUMAN	U14621:5047 NHEK19W Homo sapiens cDNA clone IMAGE3045734.3'	
2071	15089		1.31	1.0E-110/BE579117.1	EST	HUMAN	U14621:5047 NHEK19W Homo sapiens cDNA clone IMAGE3045734.3'	
2595	18840		0.84	1.0E-110	6230368	NT	Homo sapiens single-minded (Drosophila) homolog T (SIMT), mRNA	
3077	14333	27288	0.77	1.0E-110/AB023933.1	NT	HUMAN	Homo sapiens BCL2 mRNA for bcl2-associated protein 1, clone IMAGE3148, complete cds	
3138	16108		2.18	1.0E-110/U90273.1	NT	HUMAN	Homo sapiens Bcl-2 protein kinase (BTK), alpha-D-galactosidase A (GLA), L44-like fibronectin protein (L44), and FTS3 (FTPS) genes, complete cds	
3238	12385	25186	1.01	1.0E-110	11458041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA	
3258	12385	25186	1.81	1.0E-110	11458041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA	
4138	20036	30036	0.95	1.0E-110	BC018566.1	EST	HUMAN	KIA0560.1 NHEK19W: 10 Homo sapiens cDNA clone IMAGE3048448 5' similar to T9_O00312 O60312
4747	17782	30610	2	1.0E-110/A017243.1	EST	HUMAN	5628310.1 Soares,NEL1, GGC S1 Homo sapiens cDNA clone IMAGE, 1627693 5' similar to	
4764	17069	30584	2.84	1.0E-110/AU117812.1	EST	HUMAN	SW38-10 AT P82691 NHEK19W ENVELOPE PORE MEMBRANE PROTEIN POM 121 ;	
5004	19091		2.94	1.0E-110	7682441	NT	AL1178187 HEMK17 Homo sapiens cDNA clone HEMK102241 5'	
5004	19091		2.94	1.0E-110	7682441	NT	Homo sapiens KIA1002 protein (KIA1002), mRNA	
5833	18317	31105	3.47	1.0E-110/J83430.1	NT	HUMAN	Human transducin beta-1 subunit mFVLA, 3' end	
5401	18333	31223	2.95	1.0E-110/J83430.1	NT	HUMAN	Homo sapiens sex hormone-binding globulin (SHBG) gene, complete cds	
5477	18559	31400	2.2	1.0E-110/BE200406.1	EST	HUMAN	0311187 GFP NH1 MGC, 17 Homo sapiens cDNA clone IMAGE302858 5'	
5927	18294	32113	0.72	1.0E-110/BE021063.1	EST	HUMAN	0314967 GFP NH1 MGC, 70 Homo sapiens cDNA clone IMAGE306785 5'	
5947	18014	32192	0.72	1.0E-110	114190233	NT	Homo sapiens hypodermal protein FL103000 cDNA clone IMAGE306785 5'	
5947	18014	32194	8.27	1.0E-110	114190233	NT	Homo sapiens hypodermal protein FL103000 (FL103000), mRNA	

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Table 4

Single Exon Probes Expressed in Adult Liver

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Table 4
Single Exon Probe Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Next Smaller (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5954	19738	31647	0.7	1.0E-111	AA15167.1	EST_HUMAN	247607.1 Sares, pregnant, uterine, NM200 Homo sapiens cDNA clone IMAGE:59545 5' similar to
5957	19698	33072	0.73	1.0E-111	BE97899.1	EST_HUMAN	963053 PROGNANT SPECIFIC BETA 1 GYFOROTING PRECURSOR (HUMAN);
5960	19017	32137	0.44	1.0E-111	U19559.1	NT	96714250071 NPL1 NC2059 Homo sapiens cDNA clone IMAGE:3647655 5'
6255	13316	32491	1.77	1.0E-111	AB44769.1	EST_HUMAN	Human liver NCL CGAP 50 Homo sapiens cDNA clone IMAGE:3647655 5'
6915	20333	32328	1.07	1.0E-111	AL040783.1	EST_HUMAN	RELATED PROTEIN RAL-A (HUMAN);
7171	23350	32358	1.49	1.0E-111	AW24464.1	EST_HUMAN	DXF2452C1815.1 1.64 (sporadic, base) Homo sapiens cDNA clone DK75232C1815.5
7172	23350	32359	1.49	1.0E-111	AW24464.1	EST_HUMAN	U1H-BW00-01-1454-JU1.1 NCL CGAP SL68 Homo sapiens cDNA clone IMAGE:2726525 3'
7651	20776	34079	2.75	1.0E-111	BF29223.1	EST_HUMAN	RC2-BN0038-10200-018-105 BN0038 Homo sapiens cDNA
7963	23276	34186	0.94	1.0E-111	0951253	NT	L24710161-2607003-114-E03 NT0101 Homo sapiens cDNA
7961	23983	34184	12.86	1.0E-111	AT071228.1	EST_HUMAN	Homo sapiens A1P-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant A, mRNA
8059	20972	34288	0.8	1.0E-111	U60017.1	NT	w88401.x1 NCL CGAP X612 Homo sapiens cDNA clone IMAGE:2384657 3' similar to gp-04813
8260	21165	34500	0.46	1.0E-111	AA103914.1	EST_HUMAN	CYTCHROME P-450 11A5 (HUMAN);
8673	21604	34945	0.9	1.0E-111	AA276988.1	EST_HUMAN	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
8673	21604	34946	0.8	1.0E-111	AA276988.1	EST_HUMAN	znc6212.1 Stratiogene muscle 837208 Homo sapiens cDNA clone IMAGE:592774 5' similar to gp-X03740
8817	21747	35095	3.60	1.0E-111	U69533.1	NT	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
9237	22165	35518	0.89	1.0E-111	11420516	NT	G1296410 11-ZINC-FINGER TRANSCRIPTION FACTOR 1;
9335	22293	35927	0.84	1.0E-111	AK020463.1	NT	G1296410 11-ZINC-FINGER TRANSCRIPTION FACTOR 1;
9366	22294		0.93	1.0E-111	AF177687.1	EST_HUMAN	Human beta4-kelogen (ITGB4) gene, exon 13
9367	22294		12.87	1.0E-111	BF24602.1	EST_HUMAN	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
9441	22259	35731	16.48	1.0E-111	X17003.1	NT	Homo sapiens mRNA for FL00045 protein, partial cds
9441	22258	35732	16.48	1.0E-111	X17003.1	NT	Homo sapiens core sodium-calcium potassium exchanger splice variant (NCKX) mRNA, complete cds
9533	22569	35628	3.42	1.0E-111	AF073363.1	EST_HUMAN	Human mRNA for nrip2, adult 2, adult
9557	22772	36196	0.68	1.0E-111	F533210.1	EST_HUMAN	Human mRNA for nrip2, complete cds
10649	25835	36628	2.74	1.0E-111	AA504160.1	EST_HUMAN	C127317017-27200-398-026 B1061 Homo sapiens cDNA
							349623.1 NCL CGAP GCB1 Homo sapiens cDNA clone IMAGE:525770 3' similar to gp-08226
							VACUOLAR ATP-SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOLIS (HUMAN);

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	OSF SEQ ID NO:	Expression Signal	Mean Similar (Top) HR BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6571	16012	32797	0.76	1.0E-113	603602	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
6571	16012	32798	0.76	1.0E-113	603602	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7705	20037	39354	0.95	1.0E-113	BE262161.1	EST_HUMAN	3011020781 NH1_MGC_19 Homo sapiens cDNA clone IMAGE368302 5'
7705	20037	39355	0.95	1.0E-113	BE262161.1	EST_HUMAN	3011020781 NH1_MGC_19 Homo sapiens cDNA clone IMAGE368302 5'
8126	21036	34365	0.93	1.0E-113	AW65803.1	EST_HUMAN	8511020781 NH1_MGC_19 Homo sapiens cDNA clone IMAGE368302 5'
8448	22171	35740	0.93	1.0E-113	BE28219	EST_HUMAN	3011020781 NH1_MGC_19 Homo sapiens cDNA clone IMAGE368302 5'
8448	22595	35335	3.14	1.0E-113	BE53245.1	EST_HUMAN	3011020781 NH1_MGC_19 Homo sapiens cDNA clone IMAGE368302 5'
8448	22595	35336	3.14	1.0E-113	BE53245.1	EST_HUMAN	3011020781 NH1_MGC_19 Homo sapiens cDNA clone IMAGE368302 5'
8507	22842	36538	0.91	1.0E-113	BE77267.1	EST_HUMAN	3011020781 NH1_MGC_19 Homo sapiens cDNA clone IMAGE368302 5'
10340	23231	39739	0.25	1.0E-113	U12153.1	EST_HUMAN	3011020781 NH1_MGC_19 Homo sapiens cDNA clone IMAGE368302 5'
10340	23239	39747	0.25	1.0E-113	U12153.1	EST_HUMAN	3011020781 NH1_MGC_19 Homo sapiens cDNA clone IMAGE368302 5'
10551	23430	39555	0.97	1.0E-113	5432697	NT	Homo sapiens RAN binding protein 7 (RANBP7) mRNA
10551	23430	39556	0.97	1.0E-113	5432697	NT	Homo sapiens RAN binding protein 7 (RANBP7) mRNA
11883	24472	37956	1.56	1.0E-113	AW60519.1	EST_HUMAN	UHFF-600-44B-12-2X.U1 NH1_MGC_50 Homo sapiens cDNA clone IMAGE368302 5'
11871	24480	37946	1.57	1.0E-113	AW60291.1	EST_HUMAN	UHFF-600-44B-12-2X.U1 NH1_MGC_50 Homo sapiens cDNA clone IMAGE368302 5'
11571	24480	37947	1.57	1.0E-113	AW60291.1	EST_HUMAN	UHFF-600-44B-12-2X.U1 NH1_MGC_50 Homo sapiens cDNA clone IMAGE368302 5'
11697	16012	32797	2.94	1.0E-113	603602	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
11697	16012	32798	2.94	1.0E-113	603602	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
11708	24910	39037	3.18	1.0E-113	BE202683.1	EST_HUMAN	5011050391 NH1_MGC_19 Homo sapiens cDNA clone IMAGE268330 5'
61	13177	29079	6.19	1.0E-114	V17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
61	13177	29080	6.19	1.0E-114	V17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
61	13177	29081	6.19	1.0E-114	V17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
688	13730	29042	10.22	1.0E-114	V70951.1	EST_HUMAN	g9-A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN) contains Alu repetitive element
1098	14141	27078	1.63	1.0E-114	5523087	NT	Homo sapiens hypothetical protein FL20050 (FL20050). mRNA
1380	14072	27324	3.08	1.0E-114	7657639	NT	Homo sapiens histone H4 nucleosome region protein 1 (H4N1). mRNA
11981	14699	27695	1.17	1.0E-114	0531094-NT	EST_HUMAN	Homo sapiens histone H4 nucleosome region protein 1 (H4N1). mRNA
1098	14723	27692	2.16	1.0E-114	05719073	NT	Homo sapiens histone H4 nucleosome region protein 1 (H4N1). mRNA
2272	15262	28269	1.13	1.0E-114	AB023474.1	NT	Human mRNA for KIAA0730 protein, partial cds
2851	13163	29055	1.03	1.0E-114	AB033102.1	NT	Human mRNA for KIAA1270 protein, partial cds
2851	13163	29056	1.03	1.0E-114	AB033102.1	NT	Human mRNA for KIAA1270 protein, partial cds

Express

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Single Exon Probes Expressed in Adult Liver

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Single Exon Probes Expressed in Adult Liver

Probe Seq ID NC:	Exon Seq ID NC:	ORF SEQ ID NC:	Expression Signal	Most Similar (Top Hit) BLAST E Val. is	Top Hit Accession	Top Hit Source	Top Hit Descriptor
664	13661	26594	1.3	1.0E-116	U627596.2	EST_HUMAN	6012147F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2058875 5'
827	13662	26519	1.28	1.0E-116	4507334	NT	Homo sapiens synapogamin 1 (SYNU1), mRNA
884	13667		0.88	1.0E-116	4507334	NT	Homo sapiens synapogamin 1 (SYNU1), mRNA
2013	15031	26024	1.83	1.0E-116	5174478	NT	Homo sapiens perlecanin 1 (PCH1), mRNA
2030	15030	26026	0.85	1.0E-116	U133066.1	EST_HUMAN	U133066 NT 5824 Homo sapiens cDNA clone NT262401228 5'
2106	15015	26125	0.85	1.0E-116	U133066.1	NT	Homo apolipoprotein B-100 (apoB) gene, exons 17 and 18
2109	15015	26126	0.85	1.0E-116	U133066.1	NT	Homo apolipoprotein B-100 (apoB) gene, exons 17 and 18
2238	15035	26340	1.78	1.0E-116	5463941	NT	Homo sapiens protein phosphatase, EEF hand calcium-binding domain 1 (PPEF1) mRNA
2364	16370		3.68	1.0E-116	U75908.1	NT	Human olfactory receptor subunit 17-01-1 (OR17-01-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor subunit olfr17-01 (OR17-01) pseudogene, complete cds
2490	16432	28403	2.87	1.0E-116	U601833.1	NT	Homo sapiens mRNA for KIAA0760 protein, partial cds
2703	16403	28776	1.50	1.0E-116	BE588266.1	EST_HUMAN	601613337F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3514800 5'
3217	16265	29193	5.91	1.0E-116	17570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
3217	16265	29194	5.91	1.0E-116	17570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
4485	17460	30035	2.46	1.0E-116	6031064	EST_HUMAN	Homo sapiens sodium phosphate transporter 3 (NPT3), mRNA
4695	17633	30621	1.32	1.0E-116	U107096.1	EST_HUMAN	FM4-B1135-0704060-016 BT135 Homo sapiens cDNA
5461	18542		0.83	1.0E-116	A1302662.1	EST_HUMAN	q118043.41 NCL_COAP_Lu6 Homo sapiens cDNA clone IMAGE:1689865 3' similar to contains element MER25 repetitive element ;
6207	16262	32412	4	1.0E-116	W12822.1	EST_HUMAN	zc2407.r1 Saccharomyces cerevisiae, NMD4F Homo sapiens cDNA clone IMAGE:332345 5' similar to SW MDH1A_MOUSE Pos240 MYOAT DEHYDROGENASE, MITOCHONDRIAL PRECURSOR ;
6455	16201	32674	1.79	1.0E-116	A1304866.1	EST_HUMAN	Homo sapiens mRNA for KIAA1639 protein, partial cds
6456	16201	32675	1.79	1.0E-116	A1304866.1	NT	Homo sapiens mRNA for KIAA1639 protein, partial cds
6629	16073	32755	0.99	1.0E-116	BE408097.1	EST_HUMAN	60160228F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3030754 5'
6690	16084	32945	9.55	1.0E-116	U570719.0	EST_HUMAN	603087750F1 NIH_MGC_33 Homo sapiens cDNA clone IMAGE:4249687 5'
6777	16811	33021	0.67	1.0E-116	5725967	NT	Homo sapiens heat domain and RLD 2 (HERC2), mRNA
6777	16811	33022	0.67	1.0E-116	5725967	NT	Homo sapiens heat domain and RLD 2 (HERC2), mRNA
6792	16826		2.52	1.0E-116	BE168133.1	EST_HUMAN	MRP2H110395-01005-102-004 HT059F Homo sapiens cDNA
7274	20227	33476	1.66	1.0E-116	U02944.1	EST_HUMAN	C02944 Homo heart cDNA1 (Tylosaurin) Homo sapiens cDNA clone 3NKC0667
7669	20605	33793	19.36	1.0E-116	A1716314	EST_HUMAN	A1716314 DCC Homo sapiens cDNA clone DCCB006 5'
8641	21671	35290	2.27	1.0E-116	A1345456.1	EST_HUMAN	EST162655 Jural1 T-cells Y Homo sapiens cDNA 5' end similar to human 1
8641	21671	35291	2.27	1.0E-116	A1345456.1	EST_HUMAN	EST162655 Jural1 T-cells Y Homo sapiens cDNA 5' end similar to human 1
9049	21679	35304	0.96	1.0E-116	A1604151.1	EST_HUMAN	Q161145-06255-075 U1340 Homo sapiens cDNA

Table 4

Single Evon Probes Expressed in Adult Liver

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Expn SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Match Similar (Top) Hit SEQ ID Value	Top Hit Accession No.	Top Hit Databases Source	Top Hit Descriptor
10946	24331	37257	0.05	1.0E-118	AW271289.1	EST_HUMAN	perlecan, NCI, CGAP, Hurlr1 Homo sapiens cDNA clone IMAGE:2772693.3 similar to SW_BOOCH, Homo OY6906 GAMA-BUTYRORETINANE, 2-OXOGLUTARATE DIOXYGENASE ;
11013	23827	37352	1.05	1.0E-118	AW259571.1	EST_HUMAN	IFHFWB-ab-07-Q1-71 rat NCI, CGAP, SubH Homo sapiens cDNA clone IMAGE:2729772.3
11715	24617	39003	1.43	1.0E-118	11035966	NT	Homo sapiens protein with polyketamine repeat, calcium (ca2+) homeostasis endoplasmic reticulum protein (ERPROT215.2), mRNA
11723	24625	39100	1.83	1.0E-118	JA1315007.1	EST_HUMAN	EST178843 HCC cell line (metastasis to liver in mouse) T1 Homo sapiens cDNA 5' end similar to clynnh, light chain 1, Oxyechinus
11894	24358	39334	1.56	1.0E-118	EF093487.1	EST_HUMAN	OYO-IMD091-120900-395-b12 UN10091 Homo sapiens cDNA
11894	24358	39335	1.56	1.0E-118	EF093487.1	EST_HUMAN	OYO-IMD091-120900-395-b12 UN10091 Homo sapiens cDNA
782	19339	29773	1.82	1.0E-119	AF170492.1	NT	Homo sapiens orthotic channel CLC4 (CLC4) mRNA, complete cds
782	19339	29773	1.82	1.0E-119	AF170492.1	NT	Homo sapiens OGH-103 channel (LOC51011), mRNA
10293	19351	27044	2.19	1.0E-119	7705807	NT	Homo sapiens mRNA for KIA00350 protein, partial cds
18445	18445	27948	2.47	1.0E-119	AB223147.1	NT	Homo sapiens hypothetical protein FL1106527 (FL170052), mRNA
31449	18158	29041	1.15	1.0E-119	8922205	NT	on10055.1 NCI, CGAP, Lute Homo sapiens cDNA clone IMAGE:169524.9 similar to WP4646.2 CE12714
3288	18333		1.14	1.0E-119	AA16760.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4034	17951	29920	1.07	1.0E-119	4504116	NT	AUT33359 NT26P4 Homo sapiens cDNA clone NT26P4/01991.5
5321	18001	31149	3.02	1.0E-119	AL133369.1	EST_HUMAN	Homo neurofascin (NF1) gene, complete cds
5534	18173	31462	1.77	1.0E-119	BE093141	NT	Homo HUNTER25500-010-119 UN073 Homo sapiens cDNA
5536	18678	31469	2.86	1.0E-119	BE093121.1	EST_HUMAN	U969257 GAC Homo sapiens cDNA clone GACD150.5
56718	18659	31551	0.75	1.0E-119	AL134003.1	EST_HUMAN	DK-20-1007010 J1 T82 (synonym: tmsd2) Homo sapiens cDNA clone DKF57604.010.5
5764	18656	31693	1.19	1.0E-119	AL134003.1	EST_HUMAN	DK-20-1007010 J1 T82 (synonym: tmsd2) Homo sapiens cDNA clone DKF57604.010.5
5764	18656	31694	0.75	1.0E-119	AL134003.1	EST_HUMAN	DK-20-1007010 J1 T82 (synonym: tmsd2) Homo sapiens cDNA clone DKF57604.010.5
6367	19416	32581	0.58	1.0E-119	AB150703.1	EST_HUMAN	qf76903.1 Soares, Jedd, JH41111 T47601 (synonym: tmsd2) Homo sapiens cDNA clone DKF57604.010.5
6367	19416	32582	0.58	1.0E-119	AB150703.1	EST_HUMAN	SHN1 (CL, MOUSE P26535) PEPATIN T47601 (synonym: tmsd2) Homo sapiens cDNA clone DKF57604.010.5
6536	19480	32762	0.98	1.0E-119	AF159383.1	NT	Homo sapiens insulin-like growth factor 2 (IGF2) mRNA, complete cds
6536	19480	32763	0.98	1.0E-119	AF159383.1	NT	Homo sapiens insulin-like growth factor 2 (IGF2) mRNA, complete cds
9558	16620	32811	1.38	1.0E-119	AA176732.1	EST_HUMAN	Homo sapiens insulin-like growth factor 2 (IGF2) mRNA, complete cds
9732	19768	32976	2.86	1.0E-119	X02325.1	NT	Homo sapiens insulin-like growth factor 2 (IGF2) mRNA, complete cds
5745	19719	32982	4.40	1.0E-119	AF197419.3	EST_HUMAN	EST136826 MAGE, mouse testes, MAGE3 Homo sapiens cDNA
7996	20327	34041	1.09	1.0E-119	BE146014.1	EST_HUMAN	EST136826 MAGE, mouse testes, MAGE3 Homo sapiens cDNA
8021	20327	34292	0.51	1.0E-119	AF175651.1	NT	6016920581 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3446081.5
9226	22148	34501	1.71	1.0E-119	BE15150.1	EST_HUMAN	Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxythiobenzimidazole (dNT-2 gene), occurs 1-6
9226	22148	34501	1.71	1.0E-119	BE15150.1	EST_HUMAN	EST12605465 NIH_MGC_30 Homo sapiens cDNA clone IMAGE:3623508.5
9226	22148	34501	1.71	1.0E-119	BE15150.1	EST_HUMAN	Homo sapiens KIA00477, mRNA

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Top Hit

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Table 4

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Database	Source
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Single Exon Probes Expressed in Adult Liver

Probe Seq ID NO:	Exon Seq ID NO:	ORF Seq ID NO:	Expression Signal	Mean Similar (BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6590	18333	37161	1.01	1.0E-121	AB032481.1	NT	Homo sapiens UOD19 gene for hemochromatosis factor, complete cds
6460	18631	37257	0.8	1.0E-121	BE222250.1	EST HUMAN	homo sapiens UOD19 gene for hemochromatosis factor, complete cds
6753	19526	37923	0.33	1.0E-121	BE271424.1	EST HUMAN	homo sapiens UOD19 gene for hemochromatosis factor, complete cds
6910	19440	38158	0.45	1.0E-121	MB1463.1	NT	Human glutathione S-transferase (GSTA3) gene, complete cds
7215	20716	38278	0.91	1.0E-121	AZ27738.1	EST HUMAN	Human glutathione S-transferase (GSTA3) gene, complete cds
7239	18468	37250	0.77	1.0E-121	AB032481.1	EST HUMAN	homo sapiens UOD19 gene for hemochromatosis factor, complete cds
7289	19463	37250	0.77	1.0E-121	AB032481.1	EST HUMAN	homo sapiens UOD19 gene for hemochromatosis factor, complete cds
8216	21447	37923	0.33	1.0E-121	AB032481.1	EST HUMAN	homo sapiens UOD19 gene for hemochromatosis factor, complete cds
8230	21421	37923	0.33	1.0E-121	AB032481.1	EST HUMAN	homo sapiens UOD19 gene for hemochromatosis factor, complete cds
8523	21421	37923	0.33	1.0E-121	AB032481.1	EST HUMAN	homo sapiens UOD19 gene for hemochromatosis factor, complete cds
8523	21421	37923	0.33	1.0E-121	AB032481.1	EST HUMAN	homo sapiens UOD19 gene for hemochromatosis factor, complete cds
10372	23261	36692	1.16	1.0E-121	AN583558.1	EST HUMAN	homo sapiens UOD19 gene for hemochromatosis factor, complete cds
10372	23261	36692	1.16	1.0E-121	AN583558.1	EST HUMAN	homo sapiens UOD19 gene for hemochromatosis factor, complete cds
11216	24141	37568	2.35	1.0E-121	11427788.1	EST HUMAN	homo sapiens UOD19 gene for hemochromatosis factor, complete cds
11223	24148	37566	13.65	1.0E-121	AF042300.1	NT	Homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA
11007	24233	37773	2.62	1.0E-121	7320334.1	EST HUMAN	homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA
11433	24249	37795	1.57	1.0E-121	N95024.1	EST HUMAN	homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA
297	13391	26295	1.5	1.0E-122	11526770.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TILM1), mRNA
350	13473	26336	2.08	1.0E-122	AF11488.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TILM1), mRNA
378	13403	26330	1.90	1.0E-122	11526776.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TILM1), mRNA
907	13659	26907	3.23	1.0E-122	AF11488.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TILM1), mRNA
1248	14284	27227	5.68	1.0E-122	M20707.1	NT	Human leucocyte immunoglobulin gamma pseudogene (Chr22.4) variable region (subgroup V kappa II)
1719	14747	27715	1.03	1.0E-122	AF10705.1	NT	Homo sapiens cyclin-rich repeat-containing protein S32 precursor, mRNA, complete cds
1741	14708	27759	2.00	1.0E-122	11418424.1	NT	Homo sapiens cyclin-rich repeat-containing protein S32 precursor, mRNA, complete cds
1741	14708	27740	2.00	1.0E-122	11418424.1	NT	Homo sapiens cyclin-rich repeat-containing protein S32 precursor, mRNA, complete cds
1930	14659	27841	0.18	1.0E-122	BE040024.1	EST HUMAN	homo sapiens cyclin-rich repeat-containing protein S32 precursor, mRNA, complete cds
2514	15515	28518	5.03	1.0E-122	BF136170.1	EST HUMAN	homo sapiens cyclin-rich repeat-containing protein S32 precursor, mRNA, complete cds
2514	15515	28518	5.03	1.0E-122	BF136170.1	EST HUMAN	homo sapiens cyclin-rich repeat-containing protein S32 precursor, mRNA, complete cds
4089	17965	30814	1.1	1.0E-122	4524166.1	NT	Homo sapiens amyloid beta (A4) precursor protein (protease resistant, Alzheimer disease) (APP), mRNA
5111	18193		1.52	1.0E-122	AN544545.1	EST HUMAN	homo sapiens amyloid beta (A4) precursor protein (protease resistant, Alzheimer disease) (APP), mRNA

Table 4
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Probes SEQ ID NO.	Enon SEQ ID NO.	ORF SEQ NO.	Expression Signal	Mod Similar (BLAST E Value)	Top Hit Protein No.	Top Hit Database Source	Top Hit Descriptor
5765	18028	31928	1.22	1.0E-122	BE55039.1	EST_HUMAN	6011155971 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:355422.5
5766	18029	31929	1.22	1.0E-122	BE55040.1	EST_HUMAN	6011155971 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:355423.5
7091	18036	31926	0.35	1.0E-122	AB92091.1	EST_HUMAN	at160606.1 Scnraa, isoalt, NIH Homo sapiens cDNA clone IMAGE:140639.3
7981	20517	33805	0.47	1.0E-122	AB92091.1	EST_HUMAN	at160606.1 Scnraa, isoalt, NIH Homo sapiens cDNA clone IMAGE:140639.3
8336	21263	34507	0.48	1.0E-122	AJ24259.1	EST_HUMAN	at150301.1 Scnraa, isoalt, NIH Homo sapiens cDNA clone IMAGE:653439.5 similar to TR:G04070.1 1A-MINOXYCLOPROPANE-1-CARBONYLATE SYNTHASE ;
8339	21263	34508	0.48	1.0E-122	AJ24259.1	EST_HUMAN	at150301.1 Scnraa, isoalt, NIH Homo sapiens cDNA clone IMAGE:653439.5 similar to TR:G04070.1 1A-MINOXYCLOPROPANE-1-CARBONYLATE SYNTHASE ;
8354	22262	39643	0.63	1.0E-122	AJ27690.1	EST_HUMAN	at150301.1 Scnraa, isoalt, NIH Homo sapiens cDNA clone IMAGE:653439.5 similar to TR:G04070.1 1A-MINOXYCLOPROPANE-1-CARBONYLATE SYNTHASE ;
8576	22262	39870	1.42	1.0E-122	114422.9	NT	Homo sapiens mRNA for doubleless and mab-3 related transcription factor 1 (DMRT1)
8683	22778	39166	1.07	1.0E-122	AJ39618.1	EST_HUMAN	962507.1 NCIC_GCAP_Bln23 Homo sapiens cDNA clone IMAGE:251757.3 similar to SH:MTAT1_Homo sapiens Q13330 METAS TASSIS-ASSOCIATED PROTEIN MTAT1 ;
8693	22778	39167	1.07	1.0E-122	AJ39618.1	EST_HUMAN	962507.1 NCIC_GCAP_Bln23 Homo sapiens cDNA clone IMAGE:251757.3 similar to SH:MTAT1_Homo sapiens Q13330 METAS TASSIS-ASSOCIATED PROTEIN MTAT1 ;
10033	23018	39553	0.87	1.0E-122	AJ117854.1	NT	Novel human gene mapping to chromosome X, testis of adult (proboscovian)
11425	24341	37759	1.05	1.0E-122	AY05953.1	EST_HUMAN	EST1307004 IMAGE resequencing, IMAGE: Homo sapiens
12314	26211	41187	0.21	1.0E-122	11418187	NT	Homo sapiens phosphatidylinositol 4-phosphate 5-kinase (PI4K5), mRNA
201	13300	28216	18.2	1.0E-122	U31516.1	NT	Human phosphatidylinositol 4-phosphate 5-kinase (PI4K5), mRNA
764	13448	28783	2.17	1.0E-122	U31516.1	EST_HUMAN	6020160501 NCIC_GCAP_Bln23 Homo sapiens cDNA clone IMAGE:14551930.5
764	13448	28784	2.17	1.0E-122	U31516.1	EST_HUMAN	6020160501 NCIC_GCAP_Bln23 Homo sapiens cDNA clone IMAGE:14551930.5
10340	14068	27025	0.39	1.0E-122	AF34274.1	EST_HUMAN	6020160501 NCIC_GCAP_Bln23 Homo sapiens cDNA clone IMAGE:14551930.5
10340	14068	27025	0.39	1.0E-122	AF34274.1	EST_HUMAN	6020160501 NCIC_GCAP_Bln23 Homo sapiens cDNA clone IMAGE:14551930.5
10340	14068	27025	0.39	1.0E-122	AF34274.1	EST_HUMAN	6020160501 NCIC_GCAP_Bln23 Homo sapiens cDNA clone IMAGE:14551930.5
10340	14068	27025	0.39	1.0E-122	AF34274.1	EST_HUMAN	6020160501 NCIC_GCAP_Bln23 Homo sapiens cDNA clone IMAGE:14551930.5
1286	14330	27247	4.34	1.0E-126	4503816	NT	Homo sapiens testis medullary large ribosomal protein (L60R1B), mRNA
1286	14330	27247	4.34	1.0E-126	4503816	NT	Homo sapiens phosphatidylinositol 4-phosphate 5-kinase, type II, beta (PI4K5B2), mRNA, and translated products
1286	14330	27248	4.34	1.0E-126	4503816	NT	Homo sapiens phosphatidylinositol 4-phosphate 5-kinase, type II, beta (PI4K5B2), mRNA, and translated products
14764	14905	27467	6.94	1.0E-126	AJ39544.1	NT	Human aneuploid (AMELV) gene, 3 and of cdc
14764	14905	27468	6.94	1.0E-126	AJ39544.1	NT	Human aneuploid (AMELV) gene, 3 and of cdc
2111	16124	28128	2.36	1.0E-126	M5541.9.1	NT	Human aneuploid (AMELV) gene, 3 and of cdc
2111	16124	28129	2.36	1.0E-126	M5541.9.1	NT	Human aneuploid (AMELV) gene, 3 and of cdc
2111	16124	28130	2.36	1.0E-126	M5541.9.1	NT	Human aneuploid (AMELV) gene, 3 and of cdc
2396	13544	31607	1.64	1.0E-126	7709602	NT	Homo sapiens Hsp90-like protein (LOC91230), mRNA
2396	13544	31608	1.64	1.0E-126	7709602	NT	Homo sapiens Hsp90-like protein (LOC91230), mRNA
5632	18768	31607	1.64	1.0E-126	134219.1	EST	Homo sapiens retinoblastoma-binding protein (GRABP) gene, complete cds
5632	18768	31608	1.64	1.0E-126	134219.1	EST	Homo sapiens retinoblastoma-binding protein (GRABP) gene, complete cds
5773	18845	31949	1.07	1.0E-126	BE769746.1	NT	U0160110891 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:39414534.5 similar to

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mean Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6742	19776	33269	1.88	1.0E-123	AU18435.1	EST_HUMAN	AU18435.1 H.18431 Homo sapiens cDNA clone H.18431.03351 5'
7447	20343	33509	0.04	1.0E-123	U5198.1	EST_HUMAN	U5198.1 Homo sapiens cDNA clone H.18431.03351 5'
7930	20355	33524	1.35	1.0E-123	U5198.1	EST_HUMAN	U5198.1 Homo sapiens cDNA clone H.18431.03351 5'
7938	20495	33765	0.57	1.0E-123	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
7971	20730	34022	0.88	1.0E-123	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
8601	21003	34326	1.32	1.0E-123	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
8700	21012	34338	1.94	1.0E-123	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
8708	21020	34346	0.37	1.0E-123	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
8282	21187	34524	0.48	1.0E-123	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
8332	21187	34526	0.48	1.0E-123	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
8366	21270	34594	0.47	1.0E-123	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
9066	22028	35028	1.08	1.0E-123	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
9106	22066	35053	1.45	1.0E-123	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
10036	22336	35023	41.79	1.0E-123	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
12142	24662	35482	4.85	1.0E-123	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
12142	24662	35482	4.85	1.0E-123	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
200	13302	26290	1.1	1.0E-124	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
238	13302	26297	1.1	1.0E-124	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
294	13338	26361	1.26	1.0E-124	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
508	13579	26465	2.61	1.0E-124	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
715	13773	26962	4.94	1.0E-124	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
715	13773	26963	4.94	1.0E-124	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
783	13839	26774	4.84	1.0E-124	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
834	13869	26870	1.15	1.0E-124	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
929	13861	26926	1.77	1.0E-124	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
1341	14374	27327	0.85	1.0E-124	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'
1375	14407	27360	4.07	1.0E-124	U5225.1	NT	U5225.1 Homo sapiens cDNA clone H.18431.03351 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar (Top) HN BLAST E Value	Top HN Accession No.	Top HN Database Source	Tap HN Descriptor
1379	14407	27941	4.07	1.0E-124	AF27492.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1837	14860	27642	3.1	1.0E-124	AF171712.1	NT	Homo sapiens insulin-like growth factor receptor kinase 1 gene, exon 11
2075	15098	28098	1.48	1.0E-124	BE57934.1	EST_HUMAN	Homo sapiens insulin-like growth factor receptor kinase 1 gene, exon 11
2461	15463	28484	1.35	1.0E-124	AB52433.1	NT	Homo sapiens insulin-like growth factor receptor kinase 1 gene, exon 11
9420	15462	28599	0.88	1.0E-124	453416	NT	Homo sapiens insulin-like growth factor receptor kinase 1 gene, exon 11
3548	15597	28483	1.16	1.0E-124	S7584.1	NT	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
3549	15597	28483	1.16	1.0E-124	S7584.1	NT	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
3970	15598	28584	0.87	1.0E-124	453750	NT	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
4124	17183	30559	1.02	1.0E-124	453416	NT	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
4856	17635	30756	1.02	1.0E-124	453416	NT	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
5033	17635	30756	1.02	1.0E-124	453416	NT	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
5034	17635	30756	1.02	1.0E-124	453416	NT	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
5560	18240	32295	0.83	1.0E-124	453750	NT	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
5950	18240	32295	0.83	1.0E-124	453750	NT	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
8104	19185	32296	0.88	1.0E-124	BF50813.1	EST_HUMAN	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
8410	19458	32332	0.65	1.0E-124	AV711263.1	EST_HUMAN	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
6701	19737	32939	1.24	1.0E-124	11420694	NT	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
7556	20351	33619	2.92	1.0E-124	V11171.1	NT	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
7407	20437	33717	1.02	1.0E-124	BE271295.1	EST_HUMAN	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
7407	20437	33718	1.02	1.0E-124	BE271295.1	EST_HUMAN	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
7694	20905	34221	0.66	1.0E-124	AA65033.1	EST_HUMAN	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
8834	21794	35111	9.63	1.0E-124	453750	NT	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
9031	21990	35316	2.2	1.0E-124	AW912106.1	EST_HUMAN	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
9031	21990	35320	2.2	1.0E-124	AW912106.1	EST_HUMAN	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
9705	22600	39008	0.67	1.0E-124	AT709994.1	EST_HUMAN	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
9795	22600	39009	0.67	1.0E-124	AT709994.1	EST_HUMAN	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
10023	22623	39511	2.8	1.0E-124	AW46933.1	EST_HUMAN	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
10023	22623	39512	2.8	1.0E-124	AW46933.1	EST_HUMAN	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
10077	22698	39593	0.66	1.0E-124	AF423653.1	NT	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
10107	22698	39594	0.66	1.0E-124	AF423653.1	NT	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11
10135	23029	34222	7.36	1.0E-124	AT707133.1	EST_HUMAN	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ16/IRK1) gene, exon 11

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10135	23029	38423	7.39	1.0E-124/A177133.1	EST_HUMAN	EST_HUMAN	w6802.ct NO1_OGAP_K612 Homo sapiens cDNA clone IMAGE:240891 3'
10383	23272	38695	1.67	1.0E-124/A163755.1	EST_HUMAN	EST_HUMAN	UHF-DNA-abc-504-G-UT NH1 MGCC 50 Homo sapiens cDNA clone IMAGE:307894b 5'
11483	24360	37840	1.49	1.0E-124/A94776.1	NT	NT	Human muscle glycogen phosphorylase (PYGM) gene, exon 8 through 17
11777	24676	38195	3.54	1.0E-124/A100563.1	EST_HUMAN	EST_HUMAN	h05065.ct Source_NEL_T_GBC S1 Homo sapiens cDNA clone IMAGE:398006 3'
11804	24604	37444	2.19	1.0E-124/A46465.1	EST_HUMAN	EST_HUMAN	h19803.ct NO1_OGAP_Gcat4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:031662 031662 YKR5 PROTEIN ;
11804	24604	37445	2.19	1.0E-124/A46465.1	EST_HUMAN	EST_HUMAN	h19803.ct NO1_OGAP_Gcat4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:031662 031662 YKR5 PROTEIN ;
12073	24814	38417	4.99	1.0E-124/A032957.1	NT	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
12083	13773	26692	5.81	1.0E-124/A397851.1	EST_HUMAN	EST_HUMAN	281604.11 Stralagene scRNA brain S11 Homo sapiens cDNA clone IMAGE:729719 5' similar to TR:0300482 0300482 POL-REVERSE TRANSCRIPTASE HOMOLOG RETROVIRAL ELEMENT ;
12083	13773	26699	5.81	1.0E-124/A397851.1	EST_HUMAN	EST_HUMAN	281604.11 Stralagene scRNA brain S11 Homo sapiens cDNA clone IMAGE:729719 5' similar to TR:0300482 0300482 POL-REVERSE TRANSCRIPTASE HOMOLOG RETROVIRAL ELEMENT ;
339	13428		7.35	1.0E-125/A032986.1	NT	NT	Homo sapiens cDNA clone IMAGE:392565 5'
448	13116	26022	4.78	1.0E-125/BE143922.1	EST_HUMAN	EST_HUMAN	h010171 NH1 MGCC 9 Homo sapiens cDNA clone IMAGE:392565 5'
697	13729	26540	22.97	1.0E-125/A110393.1	EST_HUMAN	EST_HUMAN	KIA0038 Human fetal liver cDNA library Homo sapiens cDNA
697	13729	26541	22.97	1.0E-125/A110393.1	EST_HUMAN	EST_HUMAN	KIA0038 Human fetal liver cDNA library Homo sapiens cDNA
751	13605	26133	1.95	1.0E-125/A129476.1	NT	NT	Homo sapiens ALB like protein mRNA, partial cds
885	13038	25885	3.05	1.0E-125/A042813.1	EST_HUMAN	EST_HUMAN	3655cd.71 Source_pregnant uterus_NH4PU Homo sapiens cDNA clone IMAGE:495540 3' similar to h0105857.ct1 Olfactory receptor-like protein HGNP07E (HUMAN);
1029	14375	27013	1.05	1.0E-125/A115310.2	NT	NT	Homo sapiens chromosome 21 segment HS210210
1102	14271	27169	1.32	1.0E-125/A115310.2	NT	NT	Homo sapiens KIAA00744 gene product: Hsane Desci/ase 7 (KIAA0744), mRNA
1898	15907	27593	2.01	1.0E-125/7687180	NT	NT	Homo sapiens Usmrpin-shiba mRNA, complete cds
1833	14856	27593	3.08	1.0E-125/A015490.1	NT	NT	Homo sapiens Usmrpin-shiba mRNA, complete cds
1833	14856	27593	3.08	1.0E-125/A015490.1	NT	NT	Homo sapiens Usmrpin-shiba mRNA, complete cds
2381	15586	28387	1.18	1.0E-125/A011275.1	EST_HUMAN	EST_HUMAN	2405cd.71 Source_fetal liver_NH4PU Homo sapiens cDNA clone IMAGE:429568 5'
2528	15526	28531	1.42	1.0E-125/A042813.1	EST_HUMAN	EST_HUMAN	2405cd.71 Source_pregnant uterus_NH4PU Homo sapiens cDNA clone IMAGE:429568 5'
2938	15832	28532	2.35	1.0E-125/4501809	NT	NT	h0105857.ct1 Olfactory receptor-like protein HGNP07E (HUMAN);
2938	15832	28532	2.35	1.0E-125/4501809	NT	NT	h0105857.ct1 Olfactory receptor-like protein HGNP07E (HUMAN);
3053	18368	29010	1.02	1.0E-125/BE018009.1	EST_HUMAN	EST_HUMAN	h0105857.ct1 Source_pregnant uterus_NH4PU Homo sapiens cDNA clone IMAGE:3248131 5' similar to TR:060504 060504 ZINC FINGER PROTEIN ;
3925	18953	29857	1.32	1.0E-125/A042813.1	EST_HUMAN	EST_HUMAN	h0105857.ct1 Olfactory receptor-like protein HGNP07E (HUMAN);

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Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Mean Similarity (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4666	1767	35541	2.3	1.0E-125	11425114	NT	Homo sapiens zinc finger protein 215/27 (ZNF215), mRNA
4666	1767	35542	2.3	1.0E-125	11425114	NT	Homo sapiens zinc finger protein 215/27 (ZNF215), mRNA
4720	17725	35997	0.84	1.0E-125	BE3154121	EST_HUMAN	Homo sapiens cDNA clone IMAGE3177680 5' similar to TR-Q25058 Q25058
5163	13261	26179	1.13	1.0E-125	BE2196101	EST_HUMAN	Homo sapiens cDNA clone IMAGE3177680 5' similar to TR-Q25058 Q25058
5163	13261	26180	1.13	1.0E-125	BE2196101	EST_HUMAN	Homo sapiens cDNA clone IMAGE3177680 5' similar to TR-Q25058 Q25058
5265	19023	32150	0.68	1.0E-125	BE6232451	EST_HUMAN	Homo sapiens cDNA clone IMAGE3177680 5' similar to TR-Q25058 Q25058
5265	19023	32151	0.68	1.0E-125	BE6232451	EST_HUMAN	Homo sapiens cDNA clone IMAGE3177680 5' similar to TR-Q25058 Q25058
6098	19149	32285	1.3	1.0E-125	11390448	NT	Homo sapiens KIA0095 protein (KIA0095), mRNA
6150	19180	32285	0.98	1.0E-125	BE1751691	EST_HUMAN	Homo sapiens cDNA clone IMAGE3177680 5' similar to TR-Q25058 Q25058
6150	19214	32284	3.77	1.0E-125	BE6239611	EST_HUMAN	Homo sapiens cDNA clone IMAGE3177680 5' similar to TR-Q25058 Q25058
6203	19259	32405	0.85	1.0E-125	AB7300451	EST_HUMAN	Homo sapiens cDNA clone IMAGE3177680 5' similar to TR-Q25058 Q25058
6534	19278	32700	0.49	1.0E-125	BE7300451	EST_HUMAN	Homo sapiens cDNA clone IMAGE3177680 5' similar to TR-Q25058 Q25058
6563	19905	33109	2.04	1.0E-125	BE6232451	EST_HUMAN	Homo sapiens cDNA clone IMAGE3177680 5' similar to TR-Q25058 Q25058
6563	19905	33110	2.04	1.0E-125	BE6232451	EST_HUMAN	Homo sapiens cDNA clone IMAGE3177680 5' similar to TR-Q25058 Q25058
7415	20114	33343	8.45	1.0E-125	X03427.1	NT	Homo sapiens (IGF-II) gene, exon 5
7415	20114	33350	8.45	1.0E-125	X03427.1	NT	Homo sapiens (IGF-II) gene, exon 5
7850	20979	34189	0.57	1.0E-125	BE78523.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE3177680 5' similar to TR-Q25058 Q25058
8223	21728	34459	0.4	1.0E-125	11425672	NT	Homo sapiens adapter-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8319	21724	34648	0.57	1.0E-125	BE15100.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE3177680 5' similar to TR-Q25058 Q25058
9110	22036	35393	1.21	1.0E-125	U00265.1	NT	Human chromosome 10 duplicated adenosine triphosphatase (ALD) gene segment containing exons 8-10
9110	22036	35394	1.21	1.0E-125	U00265.1	NT	Human chromosome 10 duplicated adenosine triphosphatase (ALD) gene segment containing exons 8-10
9652	22565	35959	8.55	1.0E-125	BE161640.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE3177680 5' similar to TR-Q25058 Q25058
9652	22566	35960	8.55	1.0E-125	BE161640.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE3177680 5' similar to TR-Q25058 Q25058
9919	22507	36296	1.16	1.0E-125	U565093.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE3177680 5' similar to TR-Q25058 Q25058
10972	23525	37293	0.85	1.0E-125	U302293.1	NT	Homo sapiens cDNA clone IMAGE3177680 5' similar to TR-Q25058 Q25058
11125	24655	37502	2.88	1.0E-125	AP049458.1	NT	Homo sapiens cDNA clone IMAGE3177680 5' similar to TR-Q25058 Q25058
11210	24165	37585	1.54	1.0E-125	AW131022.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE3177680 5' similar to TR-Q25058 Q25058

Table 4

Single Exon Probes Expressed in Adult Liver

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (%) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2000	15018		2.6	1.0E-130	U04992.1	NT	Human gene for catalase (EC 1.1.1.1.0) exon 9 mapping to chromosome 11, band p13
2821	15510		7.65	1.0E-130	AJ010230.1	NT	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2921	15974	28672	1.30	1.0E-130	BE664218.1	EST_HUMAN	Homo sapiens NIG, MGC_53 Homo sapiens cDNA clone IMAGE:3655468 5'
2921	15974	28672	1.39	1.0E-130	BE664218.1	EST_HUMAN	601343016F1 NIH, MGC_53 Homo sapiens cDNA clone IMAGE:3655468 5'
3559	15974	28672	0.87	1.0E-130	AF240958.1	NT	Homo sapiens refined dehydrogenase homolog, isoform-1 (RDH) mRNA, complete cds
3559	15974	28672	0.64	1.0E-130	BE664218.1	EST_HUMAN	601343016F1 NIH, MGC_53 Homo sapiens cDNA clone IMAGE:3655468 5'
3559	15974	28672	0.64	1.0E-130	BE664218.1	EST_HUMAN	601343016F1 NIH, MGC_53 Homo sapiens cDNA clone IMAGE:3655468 5'
3559	15974	28672	0.64	1.0E-130	BE664218.1	EST_HUMAN	601343016F1 NIH, MGC_53 Homo sapiens cDNA clone IMAGE:3655468 5'
4012	17030	28526	1.52	1.0E-130	AW503500.1	EST_HUMAN	U4HF-SNU-seq-06-03-01-UT NIH, MGC_50 Homo sapiens cDNA clone IMAGE:367931 5'
4012	17030	28526	1.52	1.0E-130	AW503500.1	EST_HUMAN	U4HF-SNU-seq-06-03-01-UT NIH, MGC_50 Homo sapiens cDNA clone IMAGE:367931 5'
4654	17600	30527	10.78	1.0E-130	AW43553.1	EST_HUMAN	GM-CHN048-18026-511-02, C00045 Homo sapiens cDNA
5233	16221	31069	1.32	1.0E-130	AW36238.1	EST_HUMAN	RCC-C10318-201159-03-14-1, C10318 Homo sapiens cDNA
5233	16221	31070	1.32	1.0E-130	AW36238.1	EST_HUMAN	RCC-C10318-201159-03-14-1, C10318 Homo sapiens cDNA
7031	20957	32360	0.98	1.0E-130	X57625.1	NT	Human perlecan transcript, partial
7133	20241	32492	0.85	1.0E-130	AW434261.1	EST_HUMAN	Human perlecan transcript, partial
7133	20241	32492	0.85	1.0E-130	AW434261.1	EST_HUMAN	Human perlecan transcript, partial
7133	20241	32492	0.85	1.0E-130	AW434261.1	EST_HUMAN	Human perlecan transcript, partial
7133	20241	32492	0.85	1.0E-130	AW434261.1	EST_HUMAN	Human perlecan transcript, partial
7146	20251	33310	0.78	1.0E-130	11425446	NT	Homo sapiens estrogen-responsive B box protein (EBBP) mRNA
7625	20560	33459	1.76	1.0E-130	1146777	NT	Homo sapiens solute carrier family 6 (nucleoside/nucleic transporter, L-proline), member 7 (SLC6A7), mRNA
7759	20570	33697	0.97	1.0E-130	AF29737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7759	20570	33698	0.97	1.0E-130	AF29737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8240	22168		0.91	1.0E-130	AF08559.1	NT	Homo sapiens aurora-related kinase 1 (ARK1) mRNA, complete cds
8240	22168		0.91	1.0E-130	AF08559.1	NT	Homo sapiens aurora-related kinase 1 (ARK1) mRNA, complete cds
8765	22519	35064	2.77	1.0E-130	AB03756.1	EST_HUMAN	EST:398312 MAGE, esophageal, MACD Homo sapiens cDNA
8765	22519	35064	2.77	1.0E-130	AB03756.1	EST_HUMAN	EST:398312 MAGE, esophageal, MACD Homo sapiens cDNA
10442	23851	35067	0.72	1.0E-130	AW10549.1	EST_HUMAN	x432945.X1 NC1, CCAP_O23 Homo sapiens cDNA clone IMAGE:2559574 3'
11719	24821	38099	1.77	1.0E-130	AW10549.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ22028 (FLJ22028), mRNA
11719	24821	38100	1.77	1.0E-130	AW10549.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ22028 (FLJ22028), mRNA
12127	24968	38472	1.7	1.0E-130	490142	NT	Homo sapiens glutamate receptor, metabotropic 5 (GRM5) mRNA
12127	24968	38472	1.7	1.0E-130	490142	NT	Homo sapiens glutamate receptor, metabotropic 5 (GRM5) mRNA
4	13120	28000	1.82	0.0E+00	AA228126.1	EST_HUMAN	z18504.11 Source, NIH/NIH, S1 Homo sapiens cDNA clone IMAGE:697590 5' similar to TRC222811
4	13120	28001	1.82	0.0E+00	AA228126.1	EST_HUMAN	z18504.11 Source, NIH/NIH, S1 Homo sapiens cDNA clone IMAGE:697590 5' similar to TRC222811
6	13120	26011	1.44	0.0E+00	4880136	NT	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN ;
6	13120	26011	1.44	0.0E+00	4880136	NT	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN ;
16	13131	26017	3.69	0.0E+00	8923346	NT	Homo sapiens checkpoint suppressor 1 (CHES1), mRNA
16	13131	26017	3.69	0.0E+00	8923346	NT	Homo sapiens checkpoint suppressor 1 (CHES1), mRNA
16	13131	26016	3.89	0.0E+00	8923346	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
22	13136	28025	2.85	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
22	13138	26026	2.66	0.0E+00	383527.1	NT	Homo sapiens DCAF1 mRNA, partial cds
28	13144	26031	18.28	0.0E+00	AF141484.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
30	13152	26041	0.91	0.0E+00	802267.1	NT	Homo sapiens C2orf45 effector protein 2 (CEP2), mRNA
38	13154	26044	15.3	0.0E+00	U55000.1	NT	Human Hepatocellular Carcinoma (HCC) cell line, clone 1 through 8
41	13156	26048	4.2	0.0E+00	U55000.1	NT	Human Hepatocellular Carcinoma (HCC) cell line, clone 1 through 8
43	13158	26050	1.54	0.0E+00	680725.1	NT	Homo sapiens RNA polymerase II, subunit alpha (RNAP2), mRNA
50	13160	26071	18.52	0.0E+00	U71512.1	NT	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
52	13162	26073	1.82	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
53	13164	26083	1.48	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
54	13166	26084	1.48	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
55	13168	26084	1.48	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
56	13170	26084	1.48	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
57	13172	26084	1.48	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
58	13174	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
59	13176	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
60	13178	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
61	13180	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
62	13182	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
63	13184	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
64	13186	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
65	13188	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
66	13190	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
67	13192	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
68	13194	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
69	13196	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
70	13198	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
71	13200	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
72	13202	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
73	13204	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
74	13206	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
75	13208	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
76	13210	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
77	13212	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
78	13214	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
79	13216	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
80	13218	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
81	13220	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
82	13222	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
83	13224	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
84	13226	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
85	13228	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
86	13230	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
87	13232	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
88	13234	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
89	13236	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
90	13238	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
91	13240	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
92	13242	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
93	13244	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
94	13246	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
95	13248	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
96	13250	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
97	13252	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
98	13254	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
99	13256	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
100	13258	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
101	13260	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
102	13262	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
103	13264	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
104	13266	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
105	13268	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
106	13270	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
107	13272	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
108	13274	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
109	13276	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
110	13278	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
111	13280	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
112	13282	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
113	13284	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
114	13286	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
115	13288	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
116	13290	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
117	13292	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
118	13294	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
119	13296	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
120	13298	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
121	13300	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
122	13302	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
123	13304	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
124	13306	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)
125	13308	26087	9.6	0.0E+00	U71512.1	EST HUMAN	Homo sapiens mRNA for putative resistance protein 3 (ABCG3)

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Signal BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
135	13237	28185	3.59	0.0E+00	4605938	NT	Homo sapiens polymerase (RNA) (DNA directed) polymerase A (2200) (POLR2A) mRNA
143	13266	28186	3.59	0.0E+00	4605938	NT	Homo sapiens poly Pz binding protein (POLR2A) mRNA
148	13456	28147	0.65	0.0E+00	4603980	NT	Homo sapiens poly Pz binding protein (POLR2A) mRNA
146	13246	28163	1.04	0.0E+00	1691415	EST_HUMAN	Y83947.2 Stradiolone fetal spleen (8937203) Homo sapiens cDNA, clone IMAGE:38310.8
146	13246	28164	1.04	0.0E+00	1691415	EST_HUMAN	Y83947.2 Stradiolone fetal spleen (8937203) Homo sapiens cDNA, clone IMAGE:38310.8
160	13354	28164	5.97	0.0E+00	4504444	NT	Homo sapiens 5' non-coding nuclear ribonucleoprotein A (NSRP5) mRNA
167	13356	28185	1.19	0.0E+00	4504444	EST_HUMAN	60146337F NIH_MGC_97 Homo sapiens cDNA, clone IMAGE:3833303.8
168	13270	28186	13.52	0.0E+00	4504444	NT	Homo sapiens 5' non-coding nuclear ribonucleoprotein A (NSRP5) mRNA
172	13273	28188	0.93	0.0E+00	1111882	EST_HUMAN	Homo sapiens 5' non-coding nuclear ribonucleoprotein A (NSRP5) mRNA
174	13276	28189	1.38	0.0E+00	1111882	EST_HUMAN	Homo sapiens 5' non-coding nuclear ribonucleoprotein A (NSRP5) mRNA
175	13275	28189	0.93	0.0E+00	1111882	EST_HUMAN	Homo sapiens 5' non-coding nuclear ribonucleoprotein A (NSRP5) mRNA
176	13276	28190	2.32	0.0E+00	1720783	EST_HUMAN	60117270F NIH_MGC_17 Homo sapiens cDNA, clone IMAGE:3159864.8
177	13277	28191	1.26	0.0E+00	1720783	EST_HUMAN	60117270F NIH_MGC_17 Homo sapiens cDNA, clone IMAGE:3159864.8
177	13277	28192	1.26	0.0E+00	1720783	EST_HUMAN	60117270F NIH_MGC_17 Homo sapiens cDNA, clone IMAGE:3159864.8
178	13278	28193	1.59	0.0E+00	1720783	EST_HUMAN	60117270F NIH_MGC_17 Homo sapiens cDNA, clone IMAGE:3159864.8
181	13281	28166	8.26	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS210002
181	13281	28167	8.26	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS210002
182	13290	28204	2.86	0.0E+00	BE018970.1	EST_HUMAN	CE22691.1
192	13260	28205	2.86	0.0E+00	BE018970.1	EST_HUMAN	CE22691.1
197	13265	28206	2.25	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0754 protein, partial cds
197	13265	28209	2.25	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0754 protein, partial cds
198	13266	28210	1.42	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0754 protein, partial cds
198	13266	28211	1.42	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0754 protein, partial cds
207	13306	28223	69.46	0.0E+00	D50956.1	NT	Human gamma-cytoplasmic actin (ACTGAP) pseudogene
212	13311	28226	2.86	0.0E+00	AF275948.1	NT	Homo sapiens CTCL tumor antigen set4.3 mRNA, complete cds
212	13311	28229	2.86	0.0E+00	AF275948.1	NT	Homo sapiens CTCL tumor antigen set4.3 mRNA, complete cds
214	13313	28231	4.87	0.0E+00	AF159714.1	NT	Homo sapiens chromosome X USL3-2 protein mRNA, complete cds
214	13313	28232	4.87	0.0E+00	AF159714.1	NT	Homo sapiens chromosome X USL3-2 protein mRNA, complete cds
224	13666	28239	20.86	0.0E+00	AB273008.1	EST_HUMAN	ig4086x1 NC1_CGAP_L88 Homo sapiens cDNA, clone IMAGE:2207847.8 similar to gpJ05167 (PROFLIN) (HUMAN)

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Table 4

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Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Med Similar (Top) HR BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
347	13456	26330	0.7	0.0E+00	U14687	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (B1B AND CHC HOMOLOGY 1) (P44530)
348	13457	26331	3.25	0.0E+00	7657213	NT	Homo sapiens homologue of Drosophila melanogaster protein 1 (HOMOLOG 1) (P44530)
349	13457	26331	2.05	0.0E+00	7657213	NT	Homo sapiens homologue of Drosophila melanogaster protein 1 (HOMOLOG 1) (P44530)
354	13461	26389	3.4	0.0E+00	5474624	NT	Homo sapiens homologue of Drosophila melanogaster protein 1 (HOMOLOG 1) (P44530)
355	13462	26390	0.71	0.0E+00	4555596	NT	Homo sapiens homologue of Drosophila melanogaster protein 1 (HOMOLOG 1) (P44530)
356	13462	26390	24.03	0.0E+00	4922705	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
358	13465	26398	24.03	0.0E+00	4922705	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
371	13468	26379	1.18	0.0E+00	U17601	NT	Human zinc finger protein 2637 (ZFP263) mRNA, partial cds
373	13469	26377	2.49	0.0E+00	AF231619.1	NT	Homo sapiens chromosome 21 unknown mRNA
375	13469	26377	2.49	0.0E+00	AF231619.1	NT	Homo sapiens chromosome 21 unknown mRNA
376	13469	26378	2.61	0.0E+00	AF231619.1	NT	Homo sapiens chromosome 21 unknown mRNA
377	13473	26376	2.61	0.0E+00	AF231619.1	NT	Homo sapiens chromosome 21 unknown mRNA
379	13464	26381	0.88	0.0E+00	4507602	NT	Homo sapiens chromosome 21 unknown mRNA
382	13467	26385	1.32	0.0E+00	4503864	NT	Homo sapiens chromosome 21 unknown mRNA
383	13468	26386	1.30	0.0E+00	286006.1	NT	Homo sapiens chromosome 21 unknown mRNA
384	13468	26386	1.04	0.0E+00	286006.1	NT	Homo sapiens chromosome 21 unknown mRNA
386	13470	26388	0.73	0.0E+00	4507602	NT	Homo sapiens chromosome 21 unknown mRNA
397	13476	26359	1.4	0.0E+00	AU343693.1	EST_HUMAN	Human mRNA for KIAA0184 gene, partial cds
408	13521	26443	5.29	0.0E+00	AB028942.1	NT	Human mRNA for KIAA0184 gene, partial cds
409	13522	26444	1.49	0.0E+00	AB03014.1	EST_HUMAN	Human mRNA for KIAA0184 gene, partial cds
414	13487	26406	1.89	0.0E+00	AW754180.1	EST_HUMAN	Human mRNA for KIAA0184 gene, partial cds
417	13486	26409	1.34	0.0E+00	4503980	NT	Human mRNA for KIAA0184 gene, partial cds
418	13490	26410	2.22	0.0E+00	4503980	NT	Human mRNA for KIAA0184 gene, partial cds
419	13490	26411	2.22	0.0E+00	4503980	NT	Human mRNA for KIAA0184 gene, partial cds
418	13490	26412	1.39	0.0E+00	4503980	NT	Human mRNA for KIAA0184 gene, partial cds
420	13492	26413	1.41	0.0E+00	4503980	NT	Human mRNA for KIAA0184 gene, partial cds
420	13492	26414	1.41	0.0E+00	4503980	NT	Human mRNA for KIAA0184 gene, partial cds
421	13493	26415	0.71	0.0E+00	4503980	NT	Human mRNA for KIAA0184 gene, partial cds
422	13494	26416	2.6	0.0E+00	4503980	NT	Human mRNA for KIAA0184 gene, partial cds
423	13495	26417	1.12	0.0E+00	4503980	NT	Human mRNA for KIAA0184 gene, partial cds
424	13496	26418	1.38	0.0E+00	U74970.1	NT	Human mRNA for KIAA0184 gene, partial cds
424	13496	26418	1.38	0.0E+00	U74970.1	NT	Human mRNA for KIAA0184 gene, partial cds
425	13496	26418	1.38	0.0E+00	U74970.1	NT	Human mRNA for KIAA0184 gene, partial cds
425	13496	26418	1.14	0.0E+00	U74970.1	NT	Human mRNA for KIAA0184 gene, partial cds
425	13496	26418	1.14	0.0E+00	U74970.1	NT	Human mRNA for KIAA0184 gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	OF-SEQ ID NO:	Expression Signal	Mean Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
429	13310	29592	36.83	0.0E+00	4506998	NT	Homo sapiens fibronectin protein 1 (FN1, FN1) mRNA
431	13311		1.01	0.0E+00	R17795.1	EST HUMAN	X73562.11 Sources: initial brain 1 (NB) Homo sapiens cDNA clone IMAGE:31852.9 Homo sapiens phosphatidylethanolamine transferase, phosphatidylethanolamine synthetase, phosphatidylethanolamine transferase (PLETH) mRNA
451	13523	26445	0.85	0.0E+00	4503074	NT	Homo sapiens nuclear protein 53 (RPS53) mRNA
452	13524		8.84	0.0E+00	4506728	NT	Homo sapiens nuclear protein 53 (RPS53) mRNA
453	13526	26446	2.71	0.0E+00	A03296.4	EST HUMAN	Homo sapiens mRNA for KIAA1019 protein, partial cds
454	13528	26447	3.19	0.0E+00	A03182.1	EST HUMAN	Homo sapiens SON DNA binding protein (SON) mRNA
455	13529	26448	2.03	0.0E+00	A03182.1	EST HUMAN	Homo sapiens SON DNA binding protein (SON) mRNA
456	13530	26449	2.33	0.0E+00	AF163697.1	NT	Mus musculus truncated SON protein (SON) mRNA, complete cds
457	13531	26450	3.81	0.0E+00	4501079	NT	Homo sapiens interleukin 6 receptor 1 (IL6R) mRNA
458	13544		0.61	0.0E+00	A1331292.1	EST HUMAN	ES127034.1 Cerebellum 11 Homo sapiens cDNA 9 and
459	13545		1.11	0.0E+00	BE244447.1	EST HUMAN	901111530F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3592348.9
460	13561	26476	4.19	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
461	13562	26477	4.19	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
462	13566	26486	14.63	0.0E+00	4507887	NT	Homo sapiens keratin 18 (KR18) mRNA
463	13568	26486	14.63	0.0E+00	4507887	NT	Homo sapiens keratin 18 (KR18) mRNA
464	13571	26492	2.13	0.0E+00	AL163243.2	NT	Homo sapiens chromosome 21 segment HS21C048
465	13572	26493	5.69	0.0E+00	AL163243.2	NT	Homo sapiens chromosome 21 segment HS21C048
466	13573	26494	5.69	0.0E+00	AL163243.2	NT	Homo sapiens chromosome 21 segment HS21C048
467	13578	26494	5.69	0.0E+00	AL163243.2	NT	Homo sapiens chromosome 21 segment HS21C048
468	13585	26499	5.84	0.0E+00	A032035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
469	13588	26501	1.02	0.0E+00	AU12268.1	EST HUMAN	ALU52896 NT2694 Homo sapiens cDNA clone NT2694-200837.5
470	13590	26507	3.08	0.0E+00	AF163697.1	EST HUMAN	601274050F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3610750.5
471	13592	26508	1.98	0.0E+00	A0328825.1	EST HUMAN	PMC-DT0065-130400-002-00 DT0065 Homo sapiens cDNA
472	13593	26508	1.98	0.0E+00	A0328825.1	EST HUMAN	Novel human gene mapping to chromosome 1
473	13599	26510	1.36	0.0E+00	AL117233.1	NT	Homo sapiens F320 protein (F320), mRNA
474	13600	26511	1.18	0.0E+00	AL117233.1	NT	IL2-F10150-070600-125-F07 F10150 Homo sapiens cDNA
475	13601		0.81	0.0E+00	BF373403.1	EST HUMAN	Homo sapiens chromosome 21 segment HS21C010
476	13611	26521	1.01	0.0E+00	AL163210.2	EST HUMAN	QV25-070605-180400-142105 BT0303 Homo sapiens cDNA
477	13617	26526	1.01	0.0E+00	BF028005.1	EST HUMAN	601765695F1 NIH_MGC_30 Homo sapiens cDNA clone IMAGE:365608.5
478	13623	26531	1.5	0.0E+00	BF028005.1	EST HUMAN	601765695F1 NIH_MGC_30 Homo sapiens cDNA clone IMAGE:365608.5
479	13624	26531	1.5	0.0E+00	BF028005.1	EST HUMAN	Homo sapiens transcription elongation factor 2 (SII), poly(A)+, full length (CEIL) mRNA
480	13626	26538	0.94	0.0E+00	A040693.1	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNAT11) mRNA
481	13629	26541	7.91	0.0E+00	60030300	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNAT11) mRNA
482	13632	26541	7.91	0.0E+00	60030300	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNAT11) mRNA
483	13633	26542	3.95	0.0E+00	4504590	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNAT11) mRNA
484	13633	26543	3.95	0.0E+00	4504590	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNAT11) mRNA

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Table 4

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Probe Seq ID Seq ID NO:	Exon Seq ID Seq ID NO:	QRF SEQ ID NO:	Expression Signal	Mean Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
828	13883	28620	2.26	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
828	13883	28621	2.25	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
832	13887	28605	7.99	0.0E+00	5174718	NT	Homo sapiens perlecan (PCN1) mRNA
833	13888	28606	8.26	0.0E+00	4507530	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
849	13904	28646	1.86	0.0E+00	7687215	NT	Homo sapiens homophilic glycoprotein associated kinase (HUNK) mRNA
850	13905	28647	2.23	0.0E+00	7687215	NT	Homo sapiens homophilic glycoprotein associated kinase (HUNK) mRNA
852	13907	28648	3.59	0.0E+00	7687215	NT	Homo sapiens homophilic glycoprotein associated kinase (HUNK) mRNA
853	13912	28650	1.09	0.0E+00	4507530	NT	Homo sapiens perlecan (PCN1) mRNA
855	13912	28650	1.09	0.0E+00	4507530	NT	Homo sapiens perlecan (PCN1) mRNA
856	13913	28651	0.88	0.0E+00	4507530	NT	Homo sapiens perlecan (PCN1) mRNA
857	13913	28652	0.88	0.0E+00	4507530	NT	Homo sapiens perlecan (PCN1) mRNA
859	13921	28637	1.63	0.0E+00	4507530	NT	Homo sapiens perlecan (PCN1) mRNA
860	13921	28638	2.13	0.0E+00	4507530	NT	Homo sapiens perlecan (PCN1) mRNA
861	13921	28639	2.13	0.0E+00	4507530	NT	Homo sapiens perlecan (PCN1) mRNA
875	13928	28670	3.48	0.0E+00	AF027103.1	NT	Homo sapiens sodium/hydro-neutral cotransporter (SLC9A3) gene, complete cds
879	13932	28680	3.48	0.0E+00	AF027103.1	NT	Homo sapiens sodium/hydro-neutral cotransporter (SLC9A3) gene, complete cds
880	13933	28680	3.48	0.0E+00	AF027103.1	NT	Homo sapiens sodium/hydro-neutral cotransporter (SLC9A3) gene, complete cds
881	13944	28682	8.07	0.0E+00	4507150	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
881	13944	28682	8.07	0.0E+00	4507150	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
882	13945	28681	2.29	0.0E+00	AB02842.1	NT	Homo sapiens SON DNA binding protein (SON) mRNA
883	13945	28682	6.77	0.0E+00	AB02842.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
885	13959	28686	1.07	0.0E+00	4500728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
886	13960	28687	1.07	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
887	13943	28685	1.53	0.0E+00	AF020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
888	13941	28689	1.53	0.0E+00	AF020717.1	EST HUMAN	Homo sapiens mRNA for KIAA0910 protein, partial cds
889	13941	28689	1.53	0.0E+00	AF020717.1	EST HUMAN	Homo sapiens mRNA for KIAA0910 protein, partial cds
890	13945	28681	1.59	0.0E+00	AF02842.1	EST HUMAN	Homo sapiens mRNA for KIAA0910 protein, partial cds
892	13945	28681	1.59	0.0E+00	AF02842.1	EST HUMAN	Homo sapiens mRNA for KIAA0910 protein, partial cds
893	13945	28682	2.57	0.0E+00	7657215	NT	Homo sapiens homophilic glycoprotein associated kinase (HUNK) mRNA
893	13945	28682	2.57	0.0E+00	7657215	NT	Homo sapiens homophilic glycoprotein associated kinase (HUNK) mRNA
893	13945	28683	2.57	0.0E+00	7657215	NT	Homo sapiens homophilic glycoprotein associated kinase (HUNK) mRNA
893	13945	28683	2.57	0.0E+00	7657215	NT	Homo sapiens homophilic glycoprotein associated kinase (HUNK) mRNA
916	13966	28716	0.99	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21-009
923	13970	28622	1.19	0.0E+00	BE069692.1	EST HUMAN	Homo sapiens chromosome 21 segment HS21-009
923	13970	28622	1.19	0.0E+00	BE069692.1	EST HUMAN	Homo sapiens chromosome 21 segment HS21-009
933	13986	28651	3.75	0.0E+00	AL163203.2	NT	Homo sapiens lamin receptor 1 (LR1), ribosomal protein S4 (LAMP1) mRNA
943	13994	28651	19.56	0.0E+00	4504958	NT	Homo sapiens lamin receptor 1 (LR1), ribosomal protein S4 (LAMP1) mRNA
946	13997	28639	3.17	0.0E+00	35494.1	NT	Human protein C inhibitor (PCI-6) mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similarity BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1176	14216	27165	1.26	0.0E+00	U020710.1	NT	Homo sapiens mRNA for KIAA0509 protein, partial cds
1183	14233	27161	1.51	0.0E+00	969944	NT	Homo sapiens chromosome 12 open reading frame S2 (ORF52), mRNA
1168	14235	27174	1.16	0.0E+00	705078	NT	Homo sapiens glutathione S-transferase 1 (Gsta1, GSTO1), transcript variant GAD25, mRNA
1166	14235	27175	1.15	0.0E+00	705078	NT	Homo sapiens glutathione S-transferase 1 (Gsta1, GSTO1), transcript variant GAD25, mRNA
1190	14238	27178	1.15	0.0E+00	AB037815.1	NT	Homo sapiens mRNA for KIAA1414 gene, partial cds
1205	14245	27197	13.55	0.0E+00	4557807	NT	Homo sapiens intron 18 (KAT18), mRNA
1237	14273		1.09	0.0E+00	7657305	NT	Homo sapiens intron 1E (cds) homolog 3 (IL13), mRNA
1254	14350	27233	0.98	0.0E+00	AF284730.1	NT	Homo sapiens ALF-3 protein, mRNA, partial cds
1284	14360	27234	0.95	0.0E+00	AF284730.1	NT	Homo sapiens ALF-3 protein, mRNA, partial cds
1293	14361	27233	1.31	0.0E+00	AF284730.1	NT	Homo sapiens ALF-3 protein, mRNA, partial cds
1293	14363	27230	0.89	0.0E+00	AF284730.1	NT	Homo sapiens ALF-3 protein, mRNA, partial cds
1274	14355	27235	1.71	0.0E+00	AF102118.1	NT	Homo sapiens ALF-3 protein, mRNA, partial cds
1273	14356	27230	1.71	0.0E+00	AF102118.1	NT	Homo sapiens ALF-3 protein, mRNA, partial cds
1281	14359	27226	1.72	0.0E+00	4602068	NT	Homo sapiens chromosome 3 subtelomeric region
1281	14359	27226	1.72	0.0E+00	4602068	NT	Homo sapiens chromosome 3 subtelomeric region
1301	14354	27230	80.99	0.0E+00	183001.1	NT	Homo sapiens NF2 gene
1307	14340	27269	2.17	0.0E+00	AF08479.1	NT	Homo sapiens ribosomal protein S2 (RP52), mRNA
1314	14347	27263	1.54	0.0E+00	AB040940.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCH9), mRNA, complete cds
1314	14347	27264	1.44	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
1326	14360	27307	2.76	0.0E+00	5174748	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
1326	14360	27308	2.76	0.0E+00	5174748	NT	Homo sapiens Wolfman syndrome (WFS), mRNA
1326	14360	27309	2.76	0.0E+00	5174748	NT	Homo sapiens Wolfman syndrome (WFS), mRNA
1327	14361	27321	2.24	0.0E+00	AF090150.1	NT	Homo sapiens Wolfman syndrome (WFS), mRNA
1337	13997	27321	1.32	0.0E+00	7657623	NT	Homo sapiens ribosomal protein phosphatase 2A, large gamma subunit gene, exon 5
1337	13997	27322	1.32	0.0E+00	7657623	NT	Homo sapiens ribosomal protein phosphatase 2A, large gamma subunit gene, exon 5
1343	13951	27328	0.69	0.0E+00	U07620.2	NT	Homo sapiens RPS30 gene for RING finger protein
1344	14376	27326	1.84	0.0E+00	5803149	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1345	14377	27330	2.23	0.0E+00	4903004	NT	Homo sapiens zinc finger protein 9 (ZNF173), mRNA
1347	14379	27331	0.9	0.0E+00	5803149	NT	Homo sapiens zinc finger protein 9 (RNF9), mRNA
1348	14380	27332	1.83	0.0E+00	4500004	NT	Homo sapiens zinc finger protein 9 (ZNF173), mRNA
1350	14382	27334	3.86	0.0E+00	AB011146.1	NT	Homo sapiens KIAA0577 protein, complete cds
1351	14383	27353	2.69	0.0E+00	7681095	NT	Homo sapiens KIAA0577 gene product (KIAA0577), mRNA
1352	14384	27360	5.09	0.0E+00	7681095	NT	Homo sapiens KIAA0577 gene product (KIAA0577), mRNA
1353	14385	27387	3.86	0.0E+00	5567357	NT	Homo sapiens period (Decapitell) homolog 3 (PER3), mRNA
1353	14385	27388	3.86	0.0E+00	5567357	NT	Homo sapiens period (Decapitell) homolog 3 (PER3), mRNA

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Table 4

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Probe SEQ ID NO.	Enon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1670	14601	27560	1.96	0.0E+00	4507720	NT	Homo sapiens bin (TTN) mRNA
1671	14601	27561	1.96	0.0E+00	4507720	NT	Homo sapiens bin (TTN) mRNA
1672	14601	27562	1.96	0.0E+00	4507720	NT	Homo sapiens bin (TTN) mRNA
1673	14601	27563	1.96	0.0E+00	4507720	NT	Homo sapiens bin (TTN) mRNA
1674	14601	27564	1.96	0.0E+00	4507720	NT	Homo sapiens bin (TTN) mRNA
1675	14601	27565	1.96	0.0E+00	4507720	NT	Homo sapiens bin (TTN) mRNA
1676	14601	27566	1.96	0.0E+00	4507720	NT	Homo sapiens bin (TTN) mRNA
1677	14601	27567	1.96	0.0E+00	4507720	NT	Homo sapiens bin (TTN) mRNA
1678	14601	27568	1.96	0.0E+00	4507720	NT	Homo sapiens bin (TTN) mRNA
1679	14601	27569	1.96	0.0E+00	4507720	NT	Homo sapiens bin (TTN) mRNA
1680	14726	27699	1.1	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1681	14726	27700	2.36	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1682	14726	27701	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1683	14726	27702	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1684	14894	27694	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1685	14894	27695	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1686	14894	27696	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1687	14721	27688	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1688	14721	27689	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1689	14721	27690	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1690	14721	27691	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1691	14721	27692	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1692	14721	27693	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1693	14721	27694	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1694	14721	27695	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1695	14721	27696	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1696	14721	27697	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1697	14721	27698	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1698	14721	27699	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1699	14721	27700	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1700	14721	27701	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1701	14721	27702	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1702	14721	27703	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1703	14721	27704	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1704	14721	27705	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1705	14721	27706	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1706	14721	27707	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1707	14721	27708	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1708	14721	27709	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1709	14721	27710	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1710	14721	27711	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1711	14721	27712	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1712	14721	27713	1.17	0.0E+00	AF048104.1	EST_HUMAN	Human skeletal muscle (KRT18) mRNA
1713	14721						

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1707	14736	27702	1.31	0.0E+00	D52227.4.1	EST_HUMAN	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1710	14758	27708	3.74	0.0E+00	R5132.1	EST_HUMAN	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1710	14738	27707	3.74	0.0E+00	R5132.1	EST_HUMAN	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1712	14740	27709	1.21	0.0E+00	H165830.1	EST_HUMAN	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1713	14741	27710	2.18	0.0E+00	280783.1	EST_HUMAN	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1713	14741	27710	2.18	0.0E+00	280783.1	EST_HUMAN	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1716	14744	27713	9.49	0.0E+00	5031748.NT	NT	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1728	14753	27720	4.63	0.0E+00	8923841.NT	NT	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1729	14759	27726	3.03	0.0E+00	5453583.NT	NT	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1730	14763	27734	1.22	0.0E+00	4523873.NT	NT	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1742	14768	27741	4.43	0.0E+00	8584403.1	NT	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1744	14771	27743	2.22	0.0E+00	8584403.1	NT	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1753	14780	27750	0.63	0.0E+00	4557333.NT	NT	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1761	15008	27758	0.62	0.0E+00	11543911.NT	NT	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1772	14785	27763	2.15	0.0E+00	A573341.1	NT	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1809	15910	27768	20.59	0.0E+00	450719.NT	NT	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1812	14837	27800	2.18	0.0E+00	4557333.NT	NT	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1815	14839	27813	1.64	0.0E+00	U62063.1	NT	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1818	14842	27816	0.69	0.0E+00	U62063.1	NT	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1819	15911	27817	3.07	0.0E+00	U14967.1	EST_HUMAN	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1829	14852	27830	10.54	0.0E+00	450332.NT	NT	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1831	14854	27833	3.31	0.0E+00	A5002331.1	NT	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1832	14855	27834	6	0.0E+00	4502394.NT	NT	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1832	14855	27835	6	0.0E+00	4502394.NT	NT	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1832	14855	27836	6	0.0E+00	4502394.NT	NT	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1843	14860	27851	1	0.0E+00	450332.NT	NT	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147
1848	14869	27852	1	0.0E+00	450332.NT	NT	hprt1:cbstx1 NC1, GMAP_L1624 Homo sapiens cDNA clone IMAGE:316281.3 similar to TRC05147 055147

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similarity (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2059	15107	28109	3.38	0.0E+00	BE097725.1	EST_HUMAN	RC3-C10A13-27070-022-410 C10A13 Homo sapiens cDNA
2060	15113	28117	2.95	0.0E+00	U09020.1	NT	Human plasma membrane calcium ATPase isoform 2 (ATP1B2) mRNA, complete cds
2060	15113	28118	2.95	0.0E+00	U09020.1	NT	Human plasma membrane calcium ATPase isoform 2 (ATP1B2) mRNA, complete cds
2104	15118	28122	0.62	0.0E+00	4759488	EST_HUMAN	Human GAP-binding protein 1 (GTPBP1) mRNA, complete cds
2126	15130		3.8	0.0E+00	BE07894.1	EST_HUMAN	QVY-CH0065-15-1 Homo sapiens cDNA clone IMAGE:384738 5'
2127	15140		1.41	0.0E+00	AF070963.1	EST_HUMAN	Human Y-box1-20 nucleoprotein protein (Y-BOX1) gene, exon 6 and complete cds
2128	15142	28145	3.73	0.0E+00	BF027382.1	EST_HUMAN	AF027382F1 NH_MGC_20 Homo sapiens cDNA clone IMAGE:384738 5'
2130	15145	28148	1.57	0.0E+00	BE07262.1	EST_HUMAN	AF034705-47-21000-044-64 BT0547 Homo sapiens cDNA
2132	15146	28147	1.29	0.0E+00	AF040788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2133	15146	28148	2.69	0.0E+00	BF072708.1	EST_HUMAN	IL3-CT021b2-271099-022-510 CT0219 Homo sapiens cDNA
2137	15150	28151	2.67	0.0E+00	U04490.1	EST_HUMAN	QV-BT065-020390-092 BT0653 Homo sapiens cDNA
2137	15150	28152	2.97	0.0E+00	U04490.1	EST_HUMAN	QV-BT065-020390-092 BT0653 Homo sapiens cDNA
2171	15163		1	0.0E+00	7657262	NT	Homo sapiens polypeptide large conductance calcium-activated channel, subfamily M, beta member 3-like (KCNMB3L) mRNA
2193	15204		1.04	0.0E+00	U14767.1	EST_HUMAN	Human DNA-binding protein mRNA, 3' end
2207	15212	28214	0.98	0.0E+00	BE274664.1	EST_HUMAN	G0112233F1 NH_MGC_20 Homo sapiens cDNA clone IMAGE:3346938 5'
2207	15214	28217	1.01	0.0E+00	U07985.1	NT	Human mRNA for KIAA0244 gene, partial cds
2204	15215	28218	6.93	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CERNB0208 5'
2204	15215	28218	6.93	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CERNB0208 5'
2204	15215	28219	8.93	0.0E+00	AV738288.1	EST_HUMAN	es35067.1 AT NCL CGAP_105 Homo sapiens cDNA clone IMAGE:1567940 3'
2208	15217	28221	1.34	0.0E+00	AA031001.1	EST_HUMAN	Human apolipoprotein B-100 (apoB) gene, exons 22 through 24
2208	15219		29.79	0.0E+00	U19825.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 22 through 24
2210	15221	28224	15.47	0.0E+00	BF044434.1	EST_HUMAN	902091820F1 NCL CGAP_Bn64-1 Homo sapiens cDNA clone IMAGE:4150734 5'
2211	15222	28225	17.81	0.0E+00	BE748599.1	EST_HUMAN	90197218F1 NH_MGC_35 Homo sapiens cDNA clone IMAGE:3330412 3'
2214	15225	28228	11.4	0.0E+00	BF077897.1	EST_HUMAN	GMI-1N0741-250500-439-048 T10741 Homo sapiens cDNA
2214	15225	28229	11.4	0.0E+00	BF077897.1	EST_HUMAN	GMI-1N0741-250500-439-048 T10741 Homo sapiens cDNA
2218	15219	28234	3.1	0.0E+00	BF013817.1	EST_HUMAN	90100207F1 NH_MGC_19 Homo sapiens cDNA clone IMAGE:3346938 5'
2221	15231	28237	1.27	0.0E+00	BE018750.1	EST_HUMAN	90346237 NH_MGC_10 Homo sapiens cDNA clone IMAGE:3346938 5'
2222	15232	28238	1.89	0.0E+00	AA042913.1	EST_HUMAN	9035007.1 S. Scars, argonaut, uterus, NIPU1 Homo sapiens cDNA clone IMAGE:466640 3' similar to
2222	15232	28239	1.89	0.0E+00	AA042913.1	EST_HUMAN	9035007.1 S. Scars, argonaut, uterus, NIPU1 Homo sapiens cDNA clone IMAGE:466640 3' similar to
2222	15232	28240	1.89	0.0E+00	AA042913.1	EST_HUMAN	9035007.1 S. Scars, argonaut, uterus, NIPU1 Homo sapiens cDNA clone IMAGE:466640 3' similar to
2220	15240	28247	2.52	0.0E+00	AL103304.2	NT	Human sapiens chromosome 21 segment HS210304

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Probe SEQ ID NO:	Exon NO:	Q9F SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2376	15383	25394	3.80	0.0E+00	7652017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2379	15383	25395	2.37	0.0E+00	4759467	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose-6-phosphate dehydrogenase) (H6PD), mRNA
2379	15384	25396	2.37	0.0E+00	4759467	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose-6-phosphate dehydrogenase) (H6PD), mRNA
2380	15385		8.43	0.0E+00	A129107.1	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose-6-phosphate dehydrogenase) (H6PD), mRNA
2381	15387	25398	7.8	0.0E+00	AUT18032.1	EST: HUMAN	Human hexose-6-phosphate dehydrogenase (glucose-6-phosphate dehydrogenase) (H6PD), mRNA
2382	15387	25399	7.8	0.0E+00	AUT18032.1	EST: HUMAN	Human hexose-6-phosphate dehydrogenase (glucose-6-phosphate dehydrogenase) (H6PD), mRNA
2383	15387	25399	7.8	0.0E+00	AUT18032.1	EST: HUMAN	Human hexose-6-phosphate dehydrogenase (glucose-6-phosphate dehydrogenase) (H6PD), mRNA
2383	15388	25399	0.68	0.0E+00	6620068	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose-6-phosphate dehydrogenase) (H6PD), mRNA
2389	15443	25443	1.62	0.0E+00	AUT18032.1	EST: HUMAN	Human hexose-6-phosphate dehydrogenase (glucose-6-phosphate dehydrogenase) (H6PD), mRNA
2441	15445		4.5	0.0E+00	AB12035.1	EST: HUMAN	O68892.29XDA PHOSPHATIDYLINOSITOL-4-KINASE 1
2442	15446	25446	0.91	0.0E+00	6620020	NT	Homo sapiens hypothetical protein FLJ23633 (FLJ23633), mRNA
2445	15448		1.20	0.0E+00	BE65505.1	EST: HUMAN	Homo sapiens hypothetical protein FLJ23633 (FLJ23633), mRNA
2448	15452	25448	1.76	0.0E+00	BE65762.1	EST: HUMAN	MR1-TH00021-280000-001-H05 TH00021 Homo sapiens cDNA
2457	15461		2.64	0.0E+00	AB02622.1	EST: HUMAN	AB005622 HLA cDNA (T Nomo) Homo sapiens cDNA similar to adenylylase kinase leucine 2
2459	15463	25450	5.79	0.0E+00	6006902	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA
2463	15468	25464	1.83	0.0E+00	D63006.1	NT	Homo sapiens gene for cholesteryltransferin type-A receptor, complete cds
2463	15468	25465	1.83	0.0E+00	D63006.1	NT	Homo sapiens gene for cholesteryltransferin type-A receptor, complete cds
2472	15470	25475	2.34	0.0E+00	AF10675.1	NT	Homo sapiens immunoglobulin-like transcript 10, variant 4 (LIT4) gene, exon 8
2477	15479	25480	1.46	0.0E+00	BF45274.1	EST: HUMAN	AB027805F1 NCI CGAP 37667 Homo sapiens cDNA clone IMAGE:415970.6
2483	15485	25487	4.12	0.0E+00	5729777	NT	AB027805F1 NCI CGAP 37667 Homo sapiens cDNA clone IMAGE:415970.6
2487	15493	25493	12.66	0.0E+00	BF709144.1	EST: HUMAN	AB027805F1 NCI CGAP 37667 Homo sapiens cDNA clone IMAGE:415970.6
2500	15502	25502	2.95	0.0E+00	AW409922.1	EST: HUMAN	AB027805F1 NCI CGAP 37667 Homo sapiens cDNA clone IMAGE:415970.6
2502	15504	25504	3.27	0.0E+00	AW40910.1	EST: HUMAN	AB027805F1 NCI CGAP 37667 Homo sapiens cDNA clone IMAGE:415970.6
2530	15531		2.29	0.0E+00	BE70542.1	EST: HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2535	15538	25538	15.31	0.0E+00	BE70542.1	EST: HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2536	15547	27957	1.39	0.0E+00	7657038	NT	UHL-94-4024-08-01-01 NCI CGAP 37667 Homo sapiens cDNA clone IMAGE:306555.9
2537	15537	25537	1.76	0.0E+00	AB304462.1	EST: HUMAN	Homo sapiens protein for membrane transport protein (XK gene)
2540	15540	25539	2.44	0.0E+00	U33984.2	NT	Homo sapiens putative growth factor receptor-like (PGRFL), mRNA
2542	15542		5.02	0.0E+00	545397.1	NT	Homo sapiens putative growth factor receptor-like (PGRFL), mRNA
2545	15549	25543	0.91	0.0E+00	BE91078.1	EST: HUMAN	AB027805F1 NCI CGAP 37667 Homo sapiens cDNA clone IMAGE:415970.6
2548	15548	25544	8.02	0.0E+00	7957488	NT	Homo sapiens similar to rat integral membrane glycoprotein PON121 (PON121), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	OPF SEC ID NO:	Expression Signal	Mean Similar BLAST E Value	Top Hit Accession No.	Top Hit (Top Hit) Database Source	Top Hit Descriptor
2547	15547	29545	1.21	0.0E+00	BE160655.1	EST_HUMAN	RC4H10276.103200.015-c08.H107/8 Homo sapiens cDNA
2548	15548	29546	1.78	0.0E+00	BE23540	NT	Homo sapiens myo-doesmin protein FL32056 (F-23056), mRNA
2549	15549	29547	4.11	0.0E+00	U9326.1	NT	Human S622 (S622), mRNA, complete cds
2550	15550	29548	1.34	0.0E+00	BE39640.1	EST_HUMAN	00130521T1F1.N1.M1.MGC.31 Homo sapiens cDNA clone IMAGE:3509068.5
2551	15551	29549	0.48	0.0E+00	BE37831.1	EST_HUMAN	00130521T1F1.N1.M1.MGC.30 Homo sapiens cDNA clone IMAGE:3603371.5
2552	15552	29550	0.48	0.0E+00	BE267851.1	EST_HUMAN	00130521T1F1.N1.M1.MGC.29 Homo sapiens cDNA clone IMAGE:3603371.5
2553	15553	29551	1.09	0.0E+00	AF114627.1	EST_HUMAN	AF114027 Homo sapiens lung fibroblast Homo sapiens cDNA clone ESF5
2554	15554	29552	1.43	0.0E+00	AF245355.1	EST_HUMAN	Homo sapiens actinin mRNA, complete cds
2555	15555	29553	1.43	0.0E+00	AF245355.1	EST_HUMAN	301049734F1.N1.M1.MGC.10 Homo sapiens cDNA clone IMAGE:3461101.5
2556	15556	29554	1.33	0.0E+00	BE16367.1	EST_HUMAN	ALJ43271.79AA41 Homo sapiens cDNA clone J79AA1001673.5
2557	15557	29555	16.71	0.0E+00	ALJ13277.1	EST_HUMAN	ALJ43271.79AA41 Homo sapiens cDNA clone J79AA1001673.5
2558	15558	29556	1.77	0.0E+00	BE22826.1	EST_HUMAN	901103512F1.N1.M1.MGC.15 Homo sapiens cDNA clone IMAGE:2607035.5
2559	15559	29557	1.25	0.0E+00	BE22826.1	EST_HUMAN	901103512F1.N1.M1.MGC.13 Homo sapiens cDNA clone IMAGE:2607035.5
2560	15560	29558	1.25	0.0E+00	BE232890.1	EST_HUMAN	901103512F1.N1.M1.MGC.13 Homo sapiens cDNA clone IMAGE:2607035.5
2561	15561	29559	1.21	0.0E+00	BF22041.1	EST_HUMAN	HYPO1ETHICAL.9.3 NO PROTEIN ;
2562	15562	29560	1.21	0.0E+00	BF22041.1	EST_HUMAN	Homo sapiens actinin mRNA, complete cds
2563	15563	29561	1.21	0.0E+00	AF245051.1	EST_HUMAN	601173031F1.N1.M1.MGC.17 Homo sapiens cDNA clone IMAGE:3529150.5
2564	15564	29562	9.30	0.0E+00	AF245051.1	EST_HUMAN	Homo sapiens actinin mRNA, complete cds
2565	15565	29563	1.31	0.0E+00	BE260613.1	EST_HUMAN	Homo sapiens mRNA for KIAA1415 protein, partial cds
2566	15566	29564	1.96	0.0E+00	AB027836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2567	15567	29565	1.96	0.0E+00	AB027836.1	NT	UH-BW1-hamp-412-DJ-L1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3070531.3
2568	15568	29566	3.24	0.0E+00	U931835.1	EST_HUMAN	60255053F1.N1.M1.MGC.31 Homo sapiens cDNA clone IMAGE:4285012.5
2569	15569	29567	1.89	0.0E+00	BF672018.1	EST_HUMAN	Homo sapiens mRNA for KIAA1321 protein, partial cds
2570	15570	29568	1.23	0.0E+00	AB027142.1	NT	In18008.x1 NCI CGAP Bn25 Homo sapiens cDNA clone IMAGE:2180055.3 similar to gbL20977
2571	15571	29569	1.5	0.0E+00	AB17737.1	EST_HUMAN	CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, BRAIN ISOFORM 2 (HUMAN);
2572	15572	29570	1.5	0.0E+00	AB17737.1	EST_HUMAN	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 28KD (TA-21)
2573	15573	29571	1.5	0.0E+00	AB17737.1	EST_HUMAN	mRNA
2574	15574	29572	2.67	0.0E+00	5032150	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
2575	15575	29573	5.07	0.0E+00	AB027890.1	EST_HUMAN	601090108F1.N1.M1.MGC.7 Homo sapiens cDNA clone IMAGE:3644304.3
2576	15576	29574	1.0	0.0E+00	BE789445.1	EST_HUMAN	601090108F1.N1.M1.MGC.7 Homo sapiens cDNA clone IMAGE:3644304.3
2577	15577	29575	1.0	0.0E+00	BE789445.1	EST_HUMAN	001143722F1.N1.M1.MGC.10 Homo sapiens cDNA clone IMAGE:3001380.5
2578	15578	29576	0.92	0.0E+00	BE2993328.1	EST_HUMAN	001094605F1.N1.M1.MGC.7 Homo sapiens cDNA clone IMAGE:353222.5
2579	15579	29577	0.92	0.0E+00	BE792472.1	EST_HUMAN	001094605F1.N1.M1.MGC.7 Homo sapiens cDNA clone IMAGE:353222.5
2580	15580	29578	4.1	0.0E+00	BE792472.1	EST_HUMAN	Homo sapiens mRNA for KIAA0603 protein, partial cds
2581	15581	29579	1.29	0.0E+00	AB020710.1	NT	Homo sapiens MP (maternal non-phosphorylated) dehydrogenase 1 (MPDH1) mRNA
2582	15582	29580	1.29	0.0E+00	AB020710.1	NT	Homo sapiens MP (maternal non-phosphorylated) dehydrogenase 1 (MPDH1) mRNA
2583	15583	29581	2.44	0.0E+00	4504692	NT	Homo sapiens MP (maternal non-phosphorylated) dehydrogenase 1 (MPDH1) mRNA

Single Exon Probe Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	QPCR ID NO:	Expression Signal	Most Similar (BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2653	16587		1.12	0.0E+00	U76027.1	NT	Homo sapiens Brd4-like kinase (BTK), alpha-D-galactosidase A (GLA), L4-Hilla fibronectin protein (L4L) and PTP3 (P173) genes, complete cds
2654	16588	26585	5.54	0.0E+00	AF175277.1	NT	Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2656	16592	26586	1.11	0.0E+00	A5011108.1	NT	Homo sapiens mRNA for KIAA0359 protein, partial cds
2701	16593	26589	1.37	0.0E+00	AU133585.1	EST_HUMAN	AL133585 NT264-Homo sapiens cDNA, NT582-03184.5
2702	16598	26590	1.57	0.0E+00	N95283.1	NT	Human Bcl-2 homologous antigen (BCL2) mRNA, complete cds
2704	16598	26592	1.02	0.0E+00	AU130403.1	EST_HUMAN	AL130403 NT263-Homo sapiens cDNA, clone NT582-000779.5
2704	16598	26592	1.02	0.0E+00	AU130403.1	EST_HUMAN	AL130403 NT263-Homo sapiens cDNA, clone NT582-000779.5
2706	16598	26595	1.4	0.0E+00	AY865151.1	EST_HUMAN	SC1-OT0089-220003-011-407 O10589 Homo sapiens cDNA
2710	16704	26700	0.9	0.0E+00	BF300181.1	EST_HUMAN	7A18053-X1 NG3 QGAP, Corin Homo sapiens cDNA, clone IMAGE:331080.3
2711	16705	26701	4.81	0.0E+00	BE531883.1	EST_HUMAN	401380741F1 NH1_MGC, 19 Homo sapiens cDNA, clone IMAGE:3628823.5
2712	16705	26701	3.28	0.0E+00	BE531883.1	EST_HUMAN	401380741F1 NH1_MGC, 19 Homo sapiens cDNA, clone IMAGE:3628823.5
2748	16740	26735	0.92	0.0E+00	AB527152.1	NT	Homo sapiens mRNA for KIAA1311 protein, partial cds
2769	16761		6.42	0.0E+00	AA316723.1	EST_HUMAN	EST18641 HCC cell line (retrievals to liver in mouse) Homo sapiens cDNA 5' and similar to ribosomal protein L29
2770	16762	26734	7.64	0.0E+00	BE74484.1	EST_HUMAN	62185023BF1 NH1_MGC, 7 Homo sapiens cDNA, clone IMAGE:3943567.5
2771	16768	26735	2.98	0.0E+00	U82563.1	NT	Human beta-primo-saphin (BAM22) gene, exon 5
2772	16768	26735	2.98	0.0E+00	U82563.1	NT	Homo sapiens neuregulin 1 (NRG1) transcript variant SMC2F, mRNA
2783	16770	26736	1.26	0.0E+00	AF107063.1	NT	Homo sapiens skeletal muscle UN-protein 1 (FHL1) gene, complete cds
2783	16771	26736	1.41	0.0E+00	AF107063.1	EST_HUMAN	601801991F1 NH1_MGC, 7 Homo sapiens cDNA, clone IMAGE:3944953.5
2787	16771	26737	7.68	0.0E+00	BE66343.1	EST_HUMAN	601853485F1 NH1_MGC, 30 Homo sapiens cDNA, clone IMAGE:3580504.5
2790	16834	26777	5.97	0.0E+00	BE66343.1	EST_HUMAN	601853485F1 NH1_MGC, 30 Homo sapiens cDNA, clone IMAGE:3580504.5
2791	16780		1.22	0.0E+00	AV172147.1	EST_HUMAN	AV172147 HTB Homo sapiens cDNA, clone HTB8759.5
2793	16782	26780	2.43	0.0E+00	AV174485.1	NT	Homo sapiens spermatogenesis-associated PDI (KIAA0787) mRNA
2793	16782	26781	2.43	0.0E+00	5174485.1	NT	Homo sapiens spermatogenesis-associated PDI (KIAA0787) mRNA
2794	16783	26782	1.18	0.0E+00	8622441.1	NT	Homo sapiens hypophyseal protein FU20477 (FLJ20477), mRNA
2794	16783	26783	1.18	0.0E+00	8622441.1	NT	Homo sapiens hypophyseal protein FU20477 (FLJ20477), mRNA
2796	16784	26784	2.92	0.0E+00	AF17901.5	NT	Homo sapiens hyperplasia-related calcium-regulated gene mRNA, complete cds
2796	16785		99.03	0.0E+00	AV691093.1	EST_HUMAN	AV691096 GLC Homo sapiens cDNA, clone GLC007.3
2797	16786	26785	10.79	0.0E+00	BF377897.1	EST_HUMAN	CMT-TN0141-260900-499-008 TN0141 Homo sapiens cDNA
2707	16786	26785	10.79	0.0E+00	BF377897.1	EST_HUMAN	CMT-TN0141-260900-499-008 TN0141 Homo sapiens cDNA
2804	16793	26783	3.97	0.0E+00	BE74193.1	EST_HUMAN	601580005F1 NH1_MGC, 9 Homo sapiens cDNA, clone IMAGE:3929472.5
2804	16793	26783	3.97	0.0E+00	BE74193.1	EST_HUMAN	601580005F1 NH1_MGC, 9 Homo sapiens cDNA, clone IMAGE:3929472.5
2806	16764	26784	0.92	0.0E+00	MA4914.1	EST_HUMAN	W69H01.1 Soares melanocyte 20H04 Homo sapiens cDNA, clone IMAGE:275288.5 similar to PIR.A48773 A-6073 ketch protein, long form - fruit fly
2808	16767	26787	0.91	0.0E+00	BE176938.1	EST_HUMAN	RG4-110597-70050-072-411 HT0597 Homo sapiens cDNA

Single Exon Probes Expressed in Adult Liver

[illegible]

Table 4

Single Exon Probes Expressed in Adult Liver

Pedia ID	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) HIT BLAST E Value	Top HIT Accession No.	Top HIT Defense Source	Top HIT Descriptor
20905	152698	286936	0.0E+00/D50697.1	NT		Homo sapiens gamma-oxaloacetic acid (AC1/GP3) pseudogene
20906	152699	286939	0.0E+00/D50697.1	NT		Homo sapiens gamma-oxaloacetic acid (AC1/GP3) pseudogene
20907	152699	286940	0.0E+00/D50697.1	NT		Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
20910	152693	286902	0.0E+00/J10254.1	NT		H-sapiens mRNA for nuclear DNA helicase II
20911	152694	286903	0.0E+00/J162303.1	NT		Homo sapiens proteasome alpha C1 (POD4-alphaCCT) mRNA, complete cds
20912	152695	286903	0.0E+00/A030470.1	NT		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20913	152695	286904	0.0E+00/A030470.1	NT		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20925	152758	286793	0.0E+00/A030470.1	NT		Homo sapiens sarin/tetrahymene kinase 8 (STK8) mRNA
20926	152759	286794	0.0E+00/A030470.1	EST - HUMAN		KOZS256G05027.1 t588 (synonym: hule5) Homo sapiens cDNA clone DKFZ5466G0581
20929	152691	286789	0.0E+00/B041868.1	EST - HUMAN		Homo sapiens chondroitin sulfate proteoglycan 4 (melanocyte-associated) (CSPO4) mRNA
20930	152692	286789	0.0E+00/B041868.1	EST - HUMAN		DVJ219T0006-130400-138-H3g BT0693 Homo sapiens cDNA
20932	152690	286840	0.0E+00/B041868.1	EST - HUMAN		DVJ219T0006-130400-138-H3g BT0693 Homo sapiens cDNA
20933	152688	286840	0.0E+00/B041868.1	EST - HUMAN		Homo sapiens low density lipoprotein-related protein 2 (LRP2) mRNA
20934	152688	286840	0.0E+00/B041868.1	EST - HUMAN		Homo sapiens low density lipoprotein-related protein 2 (LRP2) mRNA
20935	152688	286840	0.0E+00/B041868.1	EST - HUMAN		Homo sapiens low density lipoprotein-related protein 2 (LRP2) mRNA
20936	152688	286840	0.0E+00/B041868.1	EST - HUMAN		Homo sapiens chromosome 21 segment HS21C008
20938	152691	286854	0.0E+00/AL163206.2	NT		Homo sapiens chromosome 21 segment HS21C008
20939	152692	286895	0.0E+00/AA16879.1	EST - HUMAN		2098B11.1 NCI-GARP_GCB31 Homo sapiens cDNA clone IMAGE56937.3 similar to cointatins AII negative element
20940	152692	286895	0.0E+00/Y19210.1	EST - HUMAN		Homo sapiens HR23 gene for testis tumor, exons 1 to 9
20941	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens EPHA4 (EPHA4) mRNA
20942	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20943	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20944	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20945	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20946	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20947	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20948	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20949	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20950	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20951	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20952	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20953	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20954	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20955	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20956	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20957	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20958	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20959	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20960	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20961	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20962	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20963	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20964	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20965	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20966	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20967	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20968	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20969	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20970	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20971	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20972	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20973	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20974	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20975	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20976	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20977	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20978	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20979	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20980	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20981	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20982	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20983	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20984	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20985	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20986	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20987	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20988	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20989	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20990	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20991	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20992	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20993	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20994	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20995	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20996	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20997	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20998	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
20999	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
21000	152693	286905	0.0E+00/A030470.1	EST - HUMAN		Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe Seq ID No.	Exon Seq ID No.	ORF Seq ID No.	Exposition Signal	Mod Strain (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2595	16047	28650	1.95	0.0E+00	475827	NT	Homo sapiens neurexin III (NRX3) mRNA
2596	16050	28653	1.05	0.0E+00	X15305.1	NT	H. sapiens NF1 gene, exon 4
2598	16050	28654	1.05	0.0E+00	X15305.1	NT	H. sapiens NF1 gene, exon 4
3000	16052	28655	12.3	0.0E+00	AF102731	NT	Homo sapiens neurokinin-like transcript 1 to variant 4 (L11a) gene, exon 8
3071	16056	28657	0.87	0.0E+00	AF102731	EST_HUMAN	Q6389.41 Sarcosine, beta-NH-Homo sapiens cDNA (from IMAGE 1755602 3'
3074	16074	28676	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3075	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3076	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3077	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3078	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3079	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3080	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3081	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3082	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3083	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3084	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3085	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3086	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3087	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3088	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3089	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3090	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3091	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3092	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3093	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3094	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3095	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3096	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3097	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3098	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3099	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3100	16074	28677	0.87	0.0E+00	AF24074.1	NT	Homo sapiens neurokinin 2 (NR2) gene, complete cds, alternatively spliced
3101	16152	29048	2.35	0.0E+00	AF07433.1	NT	Homo sapiens putative transcription factor CHS3 (CHS3) mRNA, partial cds
3102	16152	29048	2.35	0.0E+00	AF07433.1	NT	Homo sapiens putative transcription factor CHS3 (CHS3) mRNA, partial cds
3103	16152	29048	2.35	0.0E+00	AF07433.1	NT	Homo sapiens putative transcription factor CHS3 (CHS3) mRNA, partial cds
3104	16155		3.12	0.0E+00	AF160770.1	NT	Human gamma1 gene 16.1 for Ig lambda L chain C region [ig-C16.1]
3125	16176	29071	4.45	0.0E+00	X03529.1	NT	Human gamma1 gene 16.1 for Ig lambda L chain C region [ig-C16.1]
3131	16181		2	0.0E+00	AF166955.1	NT	Human gamma1 gene 16.1 for Ig lambda L chain C region [ig-C16.1]
3136	16185	29078	1.53	0.0E+00	AF044583.1	NT	Human gamma1 gene 16.1 for Ig lambda L chain C region [ig-C16.1]
3153	16203	29084	1.58	0.0E+00	AF255208.1	NT	Human gamma1 gene 16.1 for Ig lambda L chain C region [ig-C16.1]
3154	16204	29085	4.81	0.0E+00	AF149773.1	NT	Human gamma1 gene 16.1 for Ig lambda L chain C region [ig-C16.1]
3160	16205	29086	4.85	0.0E+00	7602159	NT	Human gamma1 gene 16.1 for Ig lambda L chain C region [ig-C16.1]
3169	16209	29089	1.35	0.0E+00	AF042075.1	NT	Human gamma1 gene 16.1 for Ig lambda L chain C region [ig-C16.1]

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acquisition No.	Top Hit Database Source	Top Hit Description
31195	15204	29129	3.4	4026763	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCMB1) mRNA
31195	15204	29129	3.4	0.0E+00	NT	Human fruit fly heavy chain mRNA, complete cds
31633	15641	29136	21.09	20941.1	NT	Homo sapiens heavy chain mRNA, complete cds
31633	15641	29136	21.09	0.0E+00	AB011121.1	Homo sapiens mRNA for KIA0349 protein, partial cds
31977	16245	29140	1.13	0.0E+00	AB011121.1	Homo sapiens mRNA for KIA0349 protein, partial cds
31977	16245	29141	1.13	0.0E+00	AB011121.1	Homo sapiens mRNA for KIA0349 protein, partial cds
32031	16251	29147	3.74	0.0E+00	T64070.1	yeS2063 at Stragelung lung [5632722] Homo sapiens cDNA clone IMAGE:592939
32031	16251	29147	3.74	0.0E+00	T64070.1	yeS2063 BASIC Protein, 28k. ;
32128	16268	29165	1.35	0.0E+00	BF43368.1	081676507F1 NC1 JM3C 35 Homo sapiens cDNA clone IMAGE:4107433 5'
32128	16268	29166	1.42	0.0E+00	BF43368.1	WTJ210.10.1 NC1 CGAP CG38 Homo sapiens cDNA clone IMAGE:2816803 3'
32225	16273	29173	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29174	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29175	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29176	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29177	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29178	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29179	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29180	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29181	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29182	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29183	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29184	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29185	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29186	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29187	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29188	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29189	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29190	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29191	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29192	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29193	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29194	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29195	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29196	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29197	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29198	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29199	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29200	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29201	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29202	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29203	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29204	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29205	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29206	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29207	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29208	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29209	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29210	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29211	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29212	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29213	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29214	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29215	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29216	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29217	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29218	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29219	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29220	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29221	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29222	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29223	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29224	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29225	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29226	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29227	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29228	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29229	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29230	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29231	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29232	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29233	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29234	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29235	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29236	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29237	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29238	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29239	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29240	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29241	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29242	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29243	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29244	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29245	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29246	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29247	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29248	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29249	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29250	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29251	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29252	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29253	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29254	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29255	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29256	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29257	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29258	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29259	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29260	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29261	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29262	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29263	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29264	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29265	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29266	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29267	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29268	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29269	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29270	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29271	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29272	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29273	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29274	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29275	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29276	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29277	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29278	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29279	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29280	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29281	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29282	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29283	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29284	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29285	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29286	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29287	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29288	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29289	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29290	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29291	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29292	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29293	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29294	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29295	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29296	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29297	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29298	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29299	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29300	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29301	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29302	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29303	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29304	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29305	5.65	0.0E+00	0088022.1	Hsapiens mRNA for gamma-glutamyltransferase
32225	16273	29306	5.65	0.0E+00	0088022.1	Hsapiens

Table 4

[illegible][illegible]

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Table 4

Single Exon Probes Expressed in Adult Liver

[illegible]

Single Exon Probe Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3827	16596	25746	1.67	0.0E+00	4955894	NT	Homo sapiens plasminogen activator inhibitor, type I (ephrin-terp) (PA12) mRNA
3828	16596	25781	3.66	0.0E+00	7051897	NT	Homo sapiens KIAA0022 gene product (KIA0022) mRNA
3829	16596	25782	3.66	0.0E+00	7051897	NT	Homo sapiens KIAA0022 gene product (KIA0022) mRNA
3830	16599	25796	1.06	0.0E+00	AF145712	NT	Homo sapiens double nucleotide-1 mRNA, complete cds
3831	16621	25798	1.06	0.0E+00	AF145712	NT	Homo sapiens double nucleotide-1 mRNA, complete cds
3832	16621	25798	2.87	0.0E+00	AF17933.1	NT	Homo sapiens DNA mismatch repair protein (ML1) gene, complete cds
3833	16622	25798	2.87	0.0E+00	AF17933.1	NT	Homo sapiens DNA mismatch repair protein (ML1) gene, complete cds
3834	16626	25803	2.12	0.0E+00	7057468	NT	Homo sapiens calcium/calmodulin-dependent protein kinase type II (POM121L1) mRNA
3835	16626	25804	2.12	0.0E+00	7057468	NT	Homo sapiens calcium/calmodulin-dependent protein kinase type II (POM121L1) mRNA
3836	16631	25810	1.04	0.0E+00	10718139	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1) mRNA
3837	16631	25810	1.04	0.0E+00	10718139	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1) mRNA
3838	16634	25813	1.46	0.0E+00	AF17285.1	NT	Homo sapiens musculetis juncophilis 1 (Apl-pending), mRNA
3839	16634	25814	1.46	0.0E+00	AF17285.1	NT	Homo sapiens musculetis juncophilis 1 (Apl-pending), mRNA
3840	16653	25816	1.05	0.0E+00	AF17989.1	EST - HUMAN	Gottlia griffia olfactory receptor (GG071) gene, partial cds
3841	16653	25816	1.23	0.0E+00	4758188	NT	homo sapiens desmoglein (DPL DPL1) (DSF) mRNA
3842	16656	25817	4.06	0.0E+00	S76985.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ1B1) gene, complete cds
3843	16656	25818	2.43	0.0E+00	7710148	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ1B1) gene, complete cds
3844	16659	25819	1.43	0.0E+00	7082183	NT	Homo sapiens KIA00659 gene product (KIA00659) mRNA
3845	16659	25819	1.43	0.0E+00	7082183	NT	Homo sapiens KIA00659 gene product (KIA00659) mRNA
3846	16664	25823	1.13	0.0E+00	6912766	NT	Homo sapiens transient receptor potential channel 5 (TRP5), mRNA
3847	16664	25823	8.59	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3848	16669	25832	8.59	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3849	16687	25835	4.66	0.0E+00	U05412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3850	16687	25835	4.66	0.0E+00	U05412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3851	16692	25936	0.58	0.0E+00	AF14488.1	NT	Homo sapiens threosidin short isoform (TSH) mRNA, complete cds
3852	16692	25936	0.58	0.0E+00	AF14488.1	NT	Homo sapiens threosidin short isoform (TSH) mRNA, complete cds
3853	16693	25938	1.44	0.0E+00	4520783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCMB1) mRNA
3854	16693	25938	1.44	0.0E+00	4520783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCMB1) mRNA
3855	16695	25941	1.76	0.0E+00	AF072815.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3856	16695	25941	1.76	0.0E+00	AF072815.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3857	16695	25942	1.76	0.0E+00	4759171	NT	Homo sapiens SCG5-interacting protein 1 (SRRP128) mRNA
3858	16695	25942	0.73	0.0E+00	4759171	NT	Homo sapiens SCG5-interacting protein 1 (SRRP128) mRNA
3859	16697	25945	2.01	0.0E+00	AF04727.1	EST - HUMAN	W61801.1 NC_034P_Lym21 Homo sapiens cDNA clone IMAGE3411065 3' similar to TRC-03340
3860	16697	25945	2.01	0.0E+00	AF04727.1	EST - HUMAN	W61801.1 NC_034P_Lym21 Homo sapiens cDNA clone IMAGE3411065 3' similar to TRC-03340
3861	16697	25946	1.34	0.0E+00	AF163248.2	NT	Homo sapiens chromosome 21 segment RS21048
3862	16697	25946	1.34	0.0E+00	AF163248.2	NT	Homo sapiens chromosome 21 segment RS21048
3863	16697	25946	3.67	0.0E+00	4505742	NT	Homo sapiens chromosome 21 segment RS21048
3864	16697	25946	3.67	0.0E+00	4505742	NT	Homo sapiens chromosome 21 segment RS21048
3865	16697	25946	1.68	0.0E+00	AF046338.1	EST - HUMAN	U73725.1 NC_041043.1 T134 (synonym: hinc5) Homo sapiens cDNA clone DKFZP384N0415 5'
3866	16697	25946	1.19	0.0E+00	AF046338.1	EST - HUMAN	U73725.1 NC_041043.1 T134 (synonym: hinc5) Homo sapiens cDNA clone DKFZP384N0415 5'
3867	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3868	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3869	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3870	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3871	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3872	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3873	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3874	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3875	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3876	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3877	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3878	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3879	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3880	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3881	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3882	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3883	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3884	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3885	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3886	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3887	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3888	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3889	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3890	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3891	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3892	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3893	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3894	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3895	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3896	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3897	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3898	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3899	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3900	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3901	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3902	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3903	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3904	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3905	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3906	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3907	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3908	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3909	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3910	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3911	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3912	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3913	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3914	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3915	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3916	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3917	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3918	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3919	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3920	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3921	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3922	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3923	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3924	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3925	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3926	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3927	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3928	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3929	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3930	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3931	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3932	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3933	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3934	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3935	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3936	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3937	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3938	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3939	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3940	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3941	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3942	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3943	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3944	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens APT1 gamma subunit binding protein 1 (APT1 GBP1) mRNA
3945	16697	25946	1.19	0.0E+00	60058827	NT	Homo sapiens A

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe Seq ID NO:	Exon Seq ID NO:	Q95 SEQ ID NO:	Expression Signal	Max Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3659	16087	28873	3.54	0.0E+00	4504738	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
3661	16169	28877	2.02	0.0E+00	4505078	NT	Homo sapiens melanoma antigen, family 3, 1 (MAGE3) mRNA
3665	16163	28877	0.5	0.0E+00	AF164412.1	NT	Homo sapiens HSP17 hepatitis-B virus and P37-binding protein gene, complete cds
3662	17010	25688	1.79	0.0E+00	4538942	NT	Homo sapiens zinc finger protein (ZNF404-12) mRNA
3669	17016	25605	1.4	0.0E+00	EF350253.1	EST_HUMAN	RC3H1 10850-17100-31-412.11 (085) Homo sapiens cDNA
3681	17018	25607	1.25	0.0E+00	AF168221.1	EST_HUMAN	MPK45 Human mitotic kinase expression library Homo sapiens cDNA, clone hcycle 1608728 similar to U95A5 [M168221.1] Human mitotic kinase expression library Homo sapiens cDNA, clone hcycle 1608728 similar to U95A5 [M168221.1] Human mitotic kinase expression library Homo sapiens cDNA, clone hcycle 1608728 similar to U95A5 [M168221.1] Human mitotic kinase expression library Homo sapiens cDNA, clone hcycle 1608728 similar to U95A5
3691	17021	25608	1.25	0.0E+00	AF168221.1	EST_HUMAN	MPK45 Human mitotic kinase expression library Homo sapiens cDNA, clone hcycle 1608728 similar to U95A5
3693	17026	25918	1.23	0.0E+00	AF169533.1	NT	Homo sapiens F-box protein FBX5 (FBX5) mRNA, partial cds
4022	17028	25918	1.12	0.0E+00	AF164108.1	EST_HUMAN	U1H315-3a10-07-00-01.31 N31 G3AP, S455 Homo sapiens cDNA clone IMAGE2739946.3
4033	17030	25910	1	0.0E+00	U06281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
4034	17031	25910	1	0.0E+00	U06281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
4037	17034	25924	4.96	0.0E+00	EF378902.1	EST_HUMAN	601235056F1 NH: M3C: 43 Homo sapiens cDNA clone IMAGE3508800.3
4069	17036	25928	0.76	0.0E+00	EF313148.1	EST_HUMAN	601183727F1 NH: M3C: 19 Homo sapiens cDNA clone IMAGE3508743.5
4071	17044	25934	1.13	0.0E+00	AF168740.1	EST_HUMAN	PKA.L110031-100100-003-H30.L10031 Homo sapiens cDNA
4073	17046	25934	1.13	0.0E+00	U10891.1	NT	Human G2 protein mRNA, partial cds
4073	17046	25934	1.13	0.0E+00	U10891.1	NT	Human G2 protein mRNA, partial cds
4053	17060	25905	0.72	0.0E+00	U10891.1	NT	Human G2 protein mRNA, partial cds
4053	17060	25905	0.72	0.0E+00	U10891.1	NT	Human G2 protein mRNA, partial cds
4060	17068	25909	4.6	0.0E+00	AF161655.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4060	17068	25909	4.6	0.0E+00	AF161655.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4071	17097	25970	3.41	0.0E+00	U123910.1	NT	Homo sapiens class II lymphocyte antigen DP-psi-bale-2 pseudogene, exon 2
4073	17099	25981	7.21	0.0E+00	AF163303.2	NT	Homo sapiens chromosome 21 segment RS21C103
4053	17108	25988	3.70	0.0E+00	AF163284.2	NT	Homo sapiens chromosome 21 segment RS21C084
4053	17116	25984	1.76	0.0E+00	AF163284.2	NT	Homo sapiens chromosome 21 segment RS21C084
4065	17120	25987	1.18	0.0E+00	U78493.1	NT	Homo sapiens chromosome 21 segment RS21C084
4104	17126	30008	9.34	0.0E+00	400247.0	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EF1A1) mRNA
4111	17134	30008	0.89	0.0E+00	U06356.1	NT	Human zinc finger protein, ZNF133
4130	17152	30026	4.46	0.0E+00	AB016010.1	NT	Chlorobaculage mRNA for ribosomal protein S4X, complete cds
4140	17161	30026	4.72	0.0E+00	U238517.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (RNA46 gene)
4152	17173	30045	1.14	0.0E+00	AF163023.14.2	NT	Homo sapiens mRNA for KIAA0316 protein, partial cds
4153	17174	30046	1.43	0.0E+00	AF163023.2	NT	Homo sapiens chromosome 21 segment RS21C003
4154	17175	30047	1.85	0.0E+00	AF163023.2	NT	Homo sapiens mRNA for raga-2 (raga gene)
4154	17175	30048	1.85	0.0E+00	AF163023.2	NT	Homo sapiens mRNA for raga-2 (raga gene)

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Table 4

Single Exon Probe Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	OFF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source
4160	17161	30033	8.32	0.0E+00	5032026	NT
4160	17161	30034	8.32	0.0E+00	5032026	NT
4172	17193	30035	0.1	0.0E+00	453314	NT
4178	17198	30038	7.1	0.0E+00	453314	NT
4179	17199	30039	1.38	0.0E+00	453314	NT
4181	17203	30071	7.65	0.0E+00	453314	NT
4184	17204	30072	2.63	0.0E+00	453314	NT
4185	17295		1.07	0.0E+00	453314	NT
4185	17295		1.07	0.0E+00	453314	NT
4186	17293	30039	3.09	0.0E+00	453314	NT
4186	17293	30039	3.09	0.0E+00	453314	NT
4191	17244		0.98	0.0E+00	453314	NT
4201	18404	30045	1.05	0.0E+00	453314	NT
4205	14200	27137	0.92	0.0E+00	453314	NT
4205	14200	27138	0.92	0.0E+00	453314	NT
4211	17228	30095	1.26	0.0E+00	453314	NT
4213	17230	30096	0.89	0.0E+00	453314	NT
4213	17230	30096	0.89	0.0E+00	453314	NT
4216	16039	29545	0.75	0.0E+00	453314	NT
4218	17234	30102	1.19	0.0E+00	453314	NT
4218	17234	30103	1.19	0.0E+00	453314	NT
4224	17240	30107	0.77	0.0E+00	453314	NT
4232	17248	30110	5.7	0.0E+00	453314	NT
4232	17248	30111	5.7	0.0E+00	453314	NT
4234	17250	30117	0.87	0.0E+00	453314	NT
4234	17250	30118	0.87	0.0E+00	453314	NT
4238	17254		2.9	0.0E+00	453314	NT
4240	17252	30128	2.49	0.0E+00	453314	NT
4253	17259		5.17	0.0E+00	453314	NT
4258	17274	30142	1.12	0.0E+00	453314	NT
4259	17275	30143	2	0.0E+00	453314	NT
4259	17275	30144	2	0.0E+00	453314	NT

Expressed in Adult Liver

Expressed in Adult Liver

[illegible]

Table 4

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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Probe SEQ ID NO.	Expn SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4450	17460	30317	10.93	0.0E+00	6912283	NT	Homo sapiens COMPLEMENT C1q RECEPTOR (C1QA), mRNA
4458	17478		1.39	0.0E+00 AF15047.2		NT	Homo sapiens gap Junction protein connexin-33 (CX33) gene, complete cds
4471	17488	30347	5.28	0.0E+00 1.4091.1		NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4481	17492	30332	3.62	0.0E+00 20780.1		NT	H-sapiens H2Bf11 gene
4491	17492	30333	3.62	0.0E+00 20780.1		NT	H-sapiens H2Bf11 gene
4492	17493	30354	0.65	0.0E+00 AW160833.1		EST_HUMAN	yyb8b10.1 NC1_CGAP_1144 Homo sapiens cDNA IMAGE:2839514 3' similar to TP979345 P97365
4498	17493	30330	0.95	0.0E+00 X00483.1		EST_HUMAN	ZINC FINGER PROTEIN 64
4488	17499	30391	0.95	0.0E+00 X00483.1		EST_HUMAN	H-sapiens H4d1 genes for H4 histone
4483	17503	30397	10.13	0.0E+00 7962091		NT	Homo sapiens KIAA0350 gene product (KIAA0350), mRNA
4483	17503	30338	10.13	0.0E+00 7962091		NT	Homo sapiens KIAA0350 gene product (KIAA0350), mRNA
4494	17514	30331	14.29	0.0E+00 196920.1		NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4508	17518	30382	0.93	0.0E+00 AJ271738.1		NT	Homo sapiens X4 pseudautosomal region, segment 2/2
4508	17518	30384	1.12	0.0E+00 J0503781.1		NT	Homo sapiens H2A1 gene for alpha-AcH11 2, exon 10
4558	17560		0.89	0.0E+00 AF16563.1		NT	Homo sapiens ACTIN2 gene for alpha-AcH11 2, exon 10
4598	17567	30425	1.22	0.0E+00 AJ249716.1		NT	Homo sapiens ACTIN2 gene for alpha-AcH11 2, exon 10
4598	17567	30426	1.22	0.0E+00 AJ249716.1		NT	Homo sapiens ACTIN2 gene for alpha-AcH11 2, exon 10
4593	17570	30432	0.98	0.0E+00 J028176.1		EST_HUMAN	2497 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4592	17570	30433	0.98	0.0E+00 J028176.1		EST_HUMAN	2497 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4590	17588		1.97	0.0E+00 AF205930.1		NT	Homo sapiens HPS1 gene, exon 5
4600	17608	30405	0.74	0.0E+00 J102323.1		EST_HUMAN	347323 HESR3Aa CDS1788 Homo sapiens cDNA clone HESR3Aa, COT-HUP P2038 B'
4600	17608	30405	0.74	0.0E+00 J102323.1		EST_HUMAN	347323 HESR3Aa CDS1788 Homo sapiens cDNA clone HESR3Aa, COT-HUP P2038 B'
4610	17608	30405	0.74	0.0E+00 J102323.1		EST_HUMAN	347323 HESR3Aa CDS1788 Homo sapiens cDNA clone HESR3Aa, COT-HUP P2038 B'
4622	17620	30409	3.15	0.0E+00 AF106564.1		EST_HUMAN	CG0595 HETEROCAST DIFFERENTIATION ASSOCIATED PROTEIN ANNAK
4624			1.38	0.0E+00	8051619.1	NT	Homo sapiens UTR coxs2b nuclear cell growth factor 18S rRNA, complete cds
4638	17632	30468	1.11	0.0E+00 AF10950.1		NT	Homo sapiens nucleolar endothelial cell growth factor 18S rRNA, complete cds
4639	17632		1.11	0.0E+00 AF10950.1		NT	Homo sapiens chromosome 21 segment HS210A7
4639	17637		11.42	0.0E+00 AL103307.2		NT	Homo sapiens G protein-coupled receptor 50 (GPCR2) mRNA
4634	17645	30509	0.97	0.0E+00	4759487	NT	Homo sapiens serine-threonine protein kinase (MNBIH) mRNA, complete cds
4640	17646	30510	2.81	0.0E+00 AF108310.1		NT	Homo sapiens pyrin (MEP1) gene, complete cds
4646	17652	30517	1.93	0.0E+00 AF111083.1		NT	Homo sapiens pyrin (MEP1) gene, complete cds
4646	17652	30518	1.93	0.0E+00 AF111083.1		NT	Homo sapiens pyrin (MEP1) gene, complete cds
4651	18407	30528	3.98	0.0E+00 AF111083.1		NT	Homo sapiens zinc finger protein 195 (ZNF195), mRNA
4655	18407	30528	3.98	0.0E+00 AF111083.1		NT	Homo sapiens zinc finger protein 195 (ZNF195), mRNA

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	Q5-SEQ ID NO.	Expression Signal	Mean Single (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4690	17696	30583	5.72	0.0E+00	AF206161.1	NT	Homo sapiens apolipoprotein precursor, mRNA, complete cds
4695	17670	30540	1.35	0.0E+00	AF15337.1	NT	Homo sapiens polyoma virus gamma C3 (PCP-gamma C3) mRNA, complete cds
4678	17683	30551	4.57	0.0E+00	4983470	NT	Homo sapiens early gene 1 translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4688	17691	30558	0.8	0.0E+00	4655016	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4690	17695	30551	1.31	0.0E+00	4633358	NT	Homo sapiens alpha-2-macroglobulin (A2M) mRNA, complete cds
4683	17698	30554	1.24	0.0E+00	4622558	NT	Homo sapiens alpha-2-macroglobulin (A2M) mRNA, complete cds
4688	17703	30557	3.12	0.0E+00	336185	NT	Homo sapiens alpha-2-macroglobulin (A2M) protein kinase IV (GAMK4) mRNA
4703	17703	30557	14.59	0.0E+00	7632054	NT	Homo sapiens alpha-2-macroglobulin (A2M) protein kinase IV (GAMK4) mRNA
4703	17703	30558	14.59	0.0E+00	7632054	NT	Homo sapiens KIAA0350 gene product (KIAA0350) mRNA
4712	17717	30576	1.16	0.0E+00	AF14314.1	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 5
4715	17720	30582	13.35	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for GTC protein (GTC) gene located in the class III region of the major histocompatibility complex
4715	17720	30583	13.35	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for GTC protein (GTC) gene located in the class III region of the major histocompatibility complex
4737	17742	30592	1.67	0.0E+00	AA147072.1	EST_HUMAN	2p18p30.3 at Sinalagene fetal retina 937202 Homo sapiens cDNA clone KIAA0398S4 3'
4739	17742	30592	2.35	0.0E+00	7657410	NT	Homo sapiens cdc (cdc) Orlan-1n, Drosophila) homolog 1 (ODZ1) mRNA
4741	17746	30607	2.91	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4742	17747	30607	2.91	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C100
4743	17748	30608	2.24	0.0E+00	AB37521.1	NT	Homo sapiens gene for nuclear pore protein, partial cds
4745	17750	30608	1.12	0.0E+00	AF163568.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
4751	17750	30616	1.03	0.0E+00	AF162381.1	NT	Novel human gene mapping to chromosome 1
4753	17758	30618	4.94	0.0E+00	4557687	NT	Homo sapiens keratin 18 (KRT18) mRNA
4753	17758	30619	4.94	0.0E+00	4557687	NT	Homo sapiens keratin 18 (KRT18) mRNA
4754	17759	30620	1.01	0.0E+00	AF163819.1	NT	Homo sapiens inward-rectifying potassium channel K22.1 (KCNJ2) gene, exon 2 and complete cds
4754	17759	30621	1.01	0.0E+00	AF163819.1	NT	Homo sapiens inward-rectifying potassium channel K22.1 (KCNJ2) gene, exon 2 and complete cds
4753	17760	30652	0.90	0.0E+00	AB029570.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4753	17768	30653	0.90	0.0E+00	AB029570.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4768	17774	30641	23.91	0.0E+00	Y18900.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
4777	17782	30652	1	0.0E+00	BE081627.1	EST_HUMAN	QV2411000-10000-142403 310555 Homo sapiens cDNA
4782	17787	30652	2.05	0.0E+00	AF168564.1	NT	Homo sapiens nucleolar lamin X8 (NOL8) gene, partial cds and TNOA gene recombination breakpoint region

Table 4

Express

Single Exon Probes Expressed in Adult Liver

Protein ID	Enzyme ID	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4720	17764	30661	2.6	0.0E+00	AB037620.1	NT	Homo sapiens mRNA for KIAA1389 protein, partial cds
4720	17764	30661	2.6	0.0E+00	AB037620.1	NT	Homo sapiens mRNA for KIAA1389 protein, partial cds
4720	17764	30662	3.1	0.0E+00	AB037620.1	NT	Human displacement protein (CCMAT) mRNA
4721	17765	30663	1.81	0.0E+00	U74698.1	NT	Homo sapiens dyfophlin, subfamily 2, member A2 (BTND2A2), mRNA
4726	17769	30666	2.27	0.0E+00	64433812	NT	Homo sapiens dyfophlin, subfamily 2, member A2 (BTND2A2), mRNA
4726	17769	30667	2.27	0.0E+00	64433812	NT	Homo sapiens dyfophlin, subfamily 2, member A2 (BTND2A2), mRNA
4727	17773	30668	2.10	0.0E+00	TG0849.1	EST HUMAN	gagp504.23 transgene full apison (gag57205) Homo sapiens cDNA clone IMAGE:6810.6
4727	17773	30668	2.10	0.0E+00	TG0849.1	EST HUMAN	gagp504.23 transgene full apison (gag57205) Homo sapiens cDNA clone IMAGE:6810.6
4728	17782	30671	0.77	0.0E+00	U050050.1	EST HUMAN	gagp504.23 transgene full apison (gag57205) Homo sapiens cDNA clone IMAGE:6810.6
4728	17782	30671	0.77	0.0E+00	U050050.1	EST HUMAN	gagp504.23 transgene full apison (gag57205) Homo sapiens cDNA clone IMAGE:6810.6
4729	17783	30672	8.23	0.0E+00	U050050.1	EST HUMAN	gagp504.23 transgene full apison (gag57205) Homo sapiens cDNA clone IMAGE:6810.6
4729	17783	30672	8.23	0.0E+00	U050050.1	EST HUMAN	gagp504.23 transgene full apison (gag57205) Homo sapiens cDNA clone IMAGE:6810.6
4730	17784	30673	8.83	0.0E+00	U050050.1	EST HUMAN	gagp504.23 transgene full apison (gag57205) Homo sapiens cDNA clone IMAGE:6810.6
4730	17784	30673	8.83	0.0E+00	U050050.1	EST HUMAN	gagp504.23 transgene full apison (gag57205) Homo sapiens cDNA clone IMAGE:6810.6
4731	17785	30704	1.94	0.0E+00	U74698.1	NT	Homo sapiens dyfophlin, subfamily 2, member A2 (BTND2A2), mRNA
4731	17785	30704	1.94	0.0E+00	U74698.1	NT	Homo sapiens dyfophlin, subfamily 2, member A2 (BTND2A2), mRNA
4732	17786	30706	1.85	0.0E+00	U74698.1	NT	Homo sapiens dyfophlin, subfamily 2, member A2 (BTND2A2), mRNA
4732	17786	30706	1.85	0.0E+00	U74698.1	NT	Homo sapiens dyfophlin, subfamily 2, member A2 (BTND2A2), mRNA
4733	17787	30708	1.08	0.0E+00	U050050.1	EST HUMAN	gagp504.23 transgene full apison (gag57205) Homo sapiens cDNA clone IMAGE:6810.6
4733	17787	30708	1.08	0.0E+00	U050050.1	EST HUMAN	gagp504.23 transgene full apison (gag57205) Homo sapiens cDNA clone IMAGE:6810.6
4734	17788	30716	1.02	0.0E+00	U050050.1	EST HUMAN	gagp504.23 transgene full apison (gag57205) Homo sapiens cDNA clone IMAGE:6810.6
4734	17788	30716	1.02	0.0E+00	U050050.1	EST HUMAN	gagp504.23 transgene full apison (gag57205) Homo sapiens cDNA clone IMAGE:6810.6
4735	17788	30735	1.06	0.0E+00	U050050.1	EST HUMAN	gagp504.23 transgene full apison (gag57205) Homo sapiens cDNA clone IMAGE:6810.6
4735	17788	30735	1.06	0.0E+00	U050050.1	EST HUMAN	gagp504.23 transgene full apison (gag57205) Homo sapiens cDNA clone IMAGE:6810.6
4736	17789	30738	0.97	0.0E+00	697700	NT	Homo sapiens alpha-3 type IX collagen (COL3A3), gene, promoter region, and exons 1-26
4736	17789	30738	0.97	0.0E+00	697700	NT	Homo sapiens alpha-3 type IX collagen (COL3A3), gene, promoter region, and exons 1-26
4737	17791	30739	0.87	0.0E+00	697700	NT	Homo sapiens alpha-3 type IX collagen (COL3A3), gene, promoter region, and exons 1-26
4737	17791	30739	0.87	0.0E+00	697700	NT	Homo sapiens alpha-3 type IX collagen (COL3A3), gene, promoter region, and exons 1-26
4738	17792	30741	0.96	0.0E+00	7018320	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4738	17792	30741	0.96	0.0E+00	7018320	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4739	17793	30742	0.86	0.0E+00	7018320	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4739	17793	30742	0.86	0.0E+00	7018320	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4740	17794	30743	1.07	0.0E+00	U050050.1	EST HUMAN	gagp504.23 transgene full apison (gag57205) Homo sapiens cDNA clone IMAGE:6810.6
4740	17794	30743	1.07	0.0E+00	U050050.1	EST HUMAN	gagp504.23 transgene full apison (gag57205) Homo sapiens cDNA clone IMAGE:6810.6
4741	17795	30744	1.84	0.0E+00	U050050.1	EST HUMAN	gagp504.23 transgene full apison (gag57205) Homo sapiens cDNA clone IMAGE:6810.6
4741	17795	30744	1.84	0.0E+00	U050050.1	EST HUMAN	gagp504.23 transgene full apison (gag57205) Homo sapiens cDNA clone IMAGE:6810.6
4742	17796	30745	1.57	0.0E+			

Table 4

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Table 4

Single Exon Probes Expressed in Adult Liver

Protein SEQ ID NO.	Expn SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) HT BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6190	18126	30667	1.98	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FL230477 (FL230477). mRNA
6191	18126	30668	1.98	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FL230477 (FL230477). mRNA
6192	18126	30669	1.98	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FL230477 (FL230477). mRNA
6193	18143	30986	0.85	0.0E+00	A691246.1	EST	ncf1508.91 NCBI CGAP. P1rat Homo sapiens cDNA clone IMAGE:1100704.3 similar to TR-E239140
6194	18143	30986	0.85	0.0E+00	A691246.1	EST	ncf1508.91 NCBI CGAP. P1rat Homo sapiens cDNA clone IMAGE:1100704.3 similar to TR-E239140
6195	18143	30989	0.85	0.0E+00	A691246.1	EST	ncf1508.91 NCBI CGAP. P1rat Homo sapiens cDNA clone IMAGE:1100704.3 similar to TR-E239140
6196	18150	31000	0.85	0.0E+00	A691246.1	EST	ncf1508.91 NCBI CGAP. P1rat Homo sapiens cDNA clone IMAGE:1100704.3 similar to TR-E239140
6197	18172	31017	0.71	0.0E+00	U51598.1	NT	Homo sapiens E2F transcription factor 2 (E2F52) mRNA
6198	18179	31071	1.6	0.0E+00	AL16300.2	NT	Homo sapiens MHC class I region
6199	18186	31171	1.1	0.0E+00	D50467.1	NT	Homo sapiens chromosome 21 segment H8210309
6200	18198	32164	1.34	0.0E+00	4507720	NT	Homo sapiens gamma-globulin chain (A1010-3) pseudogene
6201	18217	32168	1.34	0.0E+00	4507720	NT	Homo sapiens beta (11N) mRNA
6202	18230	32168	1.34	0.0E+00	4507720	NT	Homo sapiens beta (11N) mRNA
6203	18237	32168	1.34	0.0E+00	4507720	NT	Homo sapiens beta (11N) mRNA
6204	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6205	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6206	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6207	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6208	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6209	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6210	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6211	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6212	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6213	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6214	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6215	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6216	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6217	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6218	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6219	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6220	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6221	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6222	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6223	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6224	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6225	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6226	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6227	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6228	18242	31071	0.88	0.0E+00	363984.1	NT	Bacillus anthracis toxin gene for spore-associated EG 2.41.10
6229	18242	3107					

Table 4

Express

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WO 01/57273

PCT/US01/00664

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Table 4

Single Exon Probe Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Dietitese Source	Top Hit Description
5688	18667	32078	0.56	0.0E+00	A035298.1	NT	Homo sapiens mRNA for neuron II, complete cds
5690	18669	32078	1.97	0.0E+00	U9361.1	NT	Human beta-prime-subunit (CACNG3) gene, exon 13
5692	18691	32110	0.77	0.0E+00	A040361.1	NT	Homo sapiens mRNA for KNOT161 protein, partial cds
5696	19073	32193	0.53	0.0E+00	A114293.1	EST_HUMAN	H41433 Human fetal liver cDNA library Homo sapiens cDNA
5697	19032	32177	0.47	0.0E+00	A163605.1	EST_HUMAN	420361171 Shiga toxin nucleoside 193201 Homo sapiens cDNA clone IMAGE327933 5' similar to gb:003740
5698	19033	32178	1.46	0.0E+00	A003535.1	NT	AF050184 HUMAN, SKELETAL MUSCLE (HUMAN)
5699	19033	32179	1.46	0.0E+00	A003536.1	NT	Homo sapiens KNOT1 gene
5700	19031	32169	1.24	0.0E+00	A020761.1	EST_HUMAN	H43281 Human fetal liver cDNA library Homo sapiens cDNA
5701	19031	32169	1.24	0.0E+00	A020761.1	EST_HUMAN	Homo sapiens protein subunit beta 2 (P53H42) cDNA
5702	19035	32200	1.24	0.0E+00	BE72173.1	EST_HUMAN	H01584032F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE330551 5'
5703	19035	32200	1.24	0.0E+00	BE72173.1	EST_HUMAN	Homo sapiens anilloide-sensitive calcium channel 1, neuronal (deponenr)(AOCN1), mRNA
5704	19036	32223	1.27	0.0E+00	9586943	NT	H01345141F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE3377643 5'
5705	19036	32223	1.12	0.0E+00	BE50092.1	EST_HUMAN	Mus musculus axonin / Axin, mRNA
5706	19037	32224	1.26	0.0E+00	U046478	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta1B, complete cds
5707	19038	32225	2.03	0.0E+00	U9361.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta1B, complete cds
5708	19038	32226	2.83	0.0E+00	U9361.1	NT	602396272F1 NCI_CGAP_Bm94 Homo sapiens cDNA clone IMAGE4784321 5'
5709	19116	32247	2.56	0.0E+00	BF348535.1	EST_HUMAN	Homo sapiens calcium channel gamma 5 subunit (CACNG3) gene, exon 4 and complete cds
5710	19122	32280	1.03	0.0E+00	A114021.1	NT	H01584032F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE3347463 5'
5711	19123	32291	3.84	0.0E+00	BE773983.1	EST_HUMAN	H283411.L1 NCI_CGAP_Lu64 Homo sapiens cDNA clone IMAGE3214581 3' similar to TR:Q62647 Q62084
5712	19134	32298	0.91	0.0E+00	BE500963.1	EST_HUMAN	PHOSPHOLIPASE C NEIGHBORING
5713	19139	32275	2.41	0.0E+00	BF596005.1	EST_HUMAN	602396252F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE4510076 5'
5714	19144	32279	0.96	0.0E+00	A1464642.1	EST_HUMAN	92050061.1 Sorens_NIH.WFPL S1 Homo sapiens cDNA clone IMAGE871883 3'
5715	19148	32313	2.44	0.0E+00	A127289.1	NT	Homo sapiens cyclin 20 (CEN20) mRNA, complete cds
5716	19160	32315	2.00	0.0E+00	BF628144.1	EST_HUMAN	RC51E10027.210000-222-03.0 E10027 Homo sapiens cDNA
5717	19165	32320	1.12	0.0E+00	BE500930.1	EST_HUMAN	H01584032F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE3300463 5'
5718	19191	32326	0.53	0.0E+00	A125660.1	NT	Homo sapiens KNOT161 gene (partial), XTS gene and LZTFL1 gene
5719	19204	32341	0.46	0.0E+00	BF596085.1	EST_HUMAN	H01584032F1 NCI_CGAP_Lu64 Homo sapiens cDNA clone IMAGE3278540 3' similar to SW:DA1X1_HUMAN
5720	19204	32341	0.46	0.0E+00	BF596085.1	EST_HUMAN	P51643 ORPHAN NUCLEAR RECEPTOR DAX-1 [1]
5721	19204	32342	0.46	0.0E+00	BE593868.1	EST_HUMAN	P51643 ORPHAN NUCLEAR RECEPTOR DAX-1 [1]

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) hit BLAST E- Value	Top Hit Accession	Top Hit Database Source	Top Hit Descriptor
6150	19200	32348	0.78	0.0E+00/AW192760.1	EST_HUMAN	EST_HUMAN	yf5953.AT1.NC1_GCAF_Orb38 Homo sapiens cDNA clone IMAGE:2746248 3' similar to TRP78336 P78338
6151	19200	32348	0.78	0.0E+00/AW192760.1	EST_HUMAN	EST_HUMAN	GLYMATATE KINASE ASSOCIATED PROTEIN ;
6162	19219	32352	2.16	0.0E+00/BF031742.1	EST_HUMAN	EST_HUMAN	Q01559060F1 NH_MGC_58 Homo sapiens cDNA clone IMAGE:3627775 5'
6162	19219	32352	2.16	0.0E+00/BF031742.1	EST_HUMAN	EST_HUMAN	Q01559060F1 NH_MGC_58 Homo sapiens cDNA clone IMAGE:3627775 5'
6162	19219	32353	2.16	0.0E+00/BF031742.1	EST_HUMAN	EST_HUMAN	h344063.AT1.NC1_GCAF_Orb32 Homo sapiens cDNA clone IMAGE:2675596 3' similar to TRC09Z/N3
6183	19231	32378	1.51	0.0E+00/BF16507.1	EST_HUMAN	EST_HUMAN	Q02413 MYOSIN-RHO-GAP PROTEIN 1, NMR 7 ;
6188	19245	32390	1.04	0.0E+00/BF16507.1	EST_HUMAN	EST_HUMAN	Q04104 HSP60A-200000-369.a.t10 H0394 Homo sapiens cDNA
6188	19245	32391	1.04	0.0E+00/BF16507.1	EST_HUMAN	EST_HUMAN	Q04104 HSP60A-200000-369.a.t10 H0394 Homo sapiens cDNA
6190	19242	32397	1.35	0.0E+00/V33039.1	EST_HUMAN	EST_HUMAN	z004906.AT1.Scores_purifiedHydromorpha_NorParha Homo sapiens cDNA clone IMAGE:321756 5'
6190	19242	32398	1.35	0.0E+00/V33039.1	EST_HUMAN	EST_HUMAN	z004906.AT1.Scores_purifiedHydromorpha_NorParha Homo sapiens cDNA clone IMAGE:321756 5'
6197	19293	32438	1.26	0.0E+00/V472618.1	NT	NT	Homo sapiens putative neural regeneration protein 2 (NRG2) gene, exon 14
6201	19297	32443	2.79	0.0E+00/BE16071.1	EST_HUMAN	EST_HUMAN	Q0115951.F1 NH_MGC_71 Homo sapiens cDNA clone IMAGE:36112338 5'
6205	19293	32443	2.4	0.0E+00/BE16071.1	EST_HUMAN	EST_HUMAN	Q0115951.F1 NH_MGC_71 Homo sapiens cDNA clone IMAGE:36112338 5'
6210	19295	32416	0.54	0.0E+00/BE16071.1	EST_HUMAN	EST_HUMAN	Q01285332F1 NH_MGC_57 Homo sapiens cDNA clone IMAGE:3611095 5'
6226	19281	32438	0.68	0.0E+00/W758481.1	EST_HUMAN	EST_HUMAN	L3-C170231-110300-027-a9 C170231 Homo sapiens cDNA
6229	19283	32438	1.47	0.0E+00/L145307.1	NT	NT	Homo sapiens plectin 12 gene product, cytoplasmic vesicle protein 2B variant (K140735). mRNA
6229	19283	32438	1.47	0.0E+00/L145307.1	NT	NT	Homo sapiens plectin 12 gene product, cytoplasmic vesicle protein 2B variant (K140735). mRNA
6230	19294	32440	1.09	0.0E+00/BE01063.1	EST_HUMAN	EST_HUMAN	Q0167759F1 NH_MGC_21 Homo sapiens cDNA clone IMAGE:360200 5'
6230	19294	32441	1.09	0.0E+00/BE01063.1	EST_HUMAN	EST_HUMAN	Q0167759F1 NH_MGC_21 Homo sapiens cDNA clone IMAGE:360200 5'
6230	19294	32442	1.09	0.0E+00/BE01063.1	EST_HUMAN	EST_HUMAN	Q0167759F1 NH_MGC_21 Homo sapiens cDNA clone IMAGE:360200 5'
6246	20644	32456	10.74	0.0E+00/57939896.1	EST_HUMAN	EST_HUMAN	-Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), mRNA
6249	19302	32462	1.3	0.0E+00/AA193506.1	EST_HUMAN	EST_HUMAN	Q00001.1 Scores_NHAM_P24P-S1 Homo sapiens cDNA clone IMAGE:656050 5' similar to SW-Y705.HUMAN.P24P-S1 Homo sapiens cDNA CELL LINE PLASMID CELL LINE PROTEIN 6 ;
6249	19302	32463	1.3	0.0E+00/AA193506.1	EST_HUMAN	EST_HUMAN	SW-Y705.HUMAN.P24P-S1 Homo sapiens cDNA clone IMAGE:656050 5' similar to
6272	19321	32468	12.66	0.0E+00/U24625.1	NT	NT	SW-Y705.HUMAN.P24P-S1 Homo sapiens cDNA clone IMAGE:656050 5' similar to Human T cell surface glycoprotein CD-5 mRNA, complete cds
6272	19321	32466	12.66	0.0E+00/U24625.1	NT	NT	Human T cell surface glycoprotein CD-5 mRNA, complete cds
6274	19326	32491	0.41	0.0E+00/AW463093.1	EST_HUMAN	EST_HUMAN	RCS-C170254-110300-027-a9 C170254 Homo sapiens cDNA
6274	19326	32492	0.41	0.0E+00/AW463093.1	EST_HUMAN	EST_HUMAN	RC3-C170254-110300-027-a9 C170254 Homo sapiens cDNA
6316	19305	32536	1.07	0.0E+00/BE26636.1	EST_HUMAN	EST_HUMAN	Q01114702F1 NH_MGC_19 Homo sapiens cDNA clone IMAGE:3345696 5'
6316	19305	32536	1.07	0.0E+00/BE26636.1	EST_HUMAN	EST_HUMAN	Q01114702F1 NH_MGC_19 Homo sapiens cDNA clone IMAGE:3345696 5'
6326	19375	32543	4.4	0.0E+00/M38107.1	EST_HUMAN	EST_HUMAN	Q01710309-090200-059-a9 Q17038 Homo sapiens cDNA (NF-1) mRNA, 3' end of cds
6336	19365	32543	4.4	0.0E+00/M38107.1	EST_HUMAN	EST_HUMAN	Q01710309-090200-059-a9 Q17038 Homo sapiens cDNA (NF-1) mRNA, 3' end of cds
6356	19390	32585	0.49	0.0E+00/BE370007.1	NT	NT	Q01298270F1 NH_Miscellaneous type 1 (NF-1) mRNA, 3' end of cds
6371	19402	32586	1.44	0.0E+00/BE370007.1	EST_HUMAN	EST_HUMAN	Q01298270F1 NH_Miscellaneous type 1 (NF-1) mRNA, 3' end of cds

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Table 4

Single Exon Probe Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	QPF SEQ ID NO:	Expression Signal	Mean Single Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6377	19426	32562	1.31	0.0E+00	AI19772.1	EST_HUMAN	AI19772.1 PLACE1 Homo sapiens cDNA clone PLACE1007201 5'
6396	19447	32618	3.48	0.0E+00	A14982.1	NT	Human G protein-coupled receptor GPR105 gene, complete cds
6428	19474	32650	4.17	0.0E+00	A124740.1	EST_HUMAN	248166311 Stragene full length cDNA clone IMAGE:54805 5' similar to
6429	19476	32651	3.87	0.0E+00	U1245915	NT	TC0351193 cDNA library from Drosophila melanogaster cDNA clone IMAGE:54805 5' similar to
6450	19496	32652	3.87	0.0E+00	U1246915	NT	Human alpha-2-macroglobulin (A2M) mRNA
6451	19496	32671	0.84	0.0E+00	U07223	NT	Human alpha-2-macroglobulin (A2M) mRNA
6465	19513	32688	3.91	0.0E+00	U123997	NT	Human alpha-2-macroglobulin (A2M) mRNA
6472	19517	32693	3.71	0.0E+00	BE527173.1	EST_HUMAN	Human alpha-2-macroglobulin (A2M) mRNA
6490	19533		0.76	0.0E+00	A195048.1	EST_HUMAN	Human alpha-2-macroglobulin (A2M) mRNA
6492	19537	32714	1.65	0.0E+00	U136300.1	EST_HUMAN	Human alpha-2-macroglobulin (A2M) mRNA
6502	19548	32722	1.07	0.0E+00	BE72785.1	EST_HUMAN	Human alpha-2-macroglobulin (A2M) mRNA
6502	19548	32728	1.07	0.0E+00	BE727355.1	EST_HUMAN	Human alpha-2-macroglobulin (A2M) mRNA
6514	19559	32736	0.54	0.0E+00	A119925.1	EST_HUMAN	Human alpha-2-macroglobulin (A2M) mRNA
6514	19568	32740	0.54	0.0E+00	A119925.1	EST_HUMAN	Human alpha-2-macroglobulin (A2M) mRNA
6517	19591	32742	1.21	0.0E+00	BF357123.1	EST_HUMAN	Human alpha-2-macroglobulin (A2M) mRNA
6525	19590	32752	1.81	0.0E+00	U1455930	NT	Human alpha-2-macroglobulin (A2M) mRNA
6535	19579	32761	0.76	0.0E+00	U55549.1	NT	Human alpha-2-macroglobulin (A2M) mRNA
6554	19590	32764	1.15	0.0E+00	AW176142.1	EST_HUMAN	Human alpha-2-macroglobulin (A2M) mRNA
6576	19591	32801	0.7	0.0E+00	BE574544.1	EST_HUMAN	Human alpha-2-macroglobulin (A2M) mRNA
6581	19622	32807	1.05	0.0E+00	76202039	NT	Human alpha-2-macroglobulin (A2M) mRNA
6585	19636		0.88	0.0E+00	A1650020.1	EST_HUMAN	Human alpha-2-macroglobulin (A2M) mRNA
6594	19649	32828	3.82	0.0E+00	A1657658.1	EST_HUMAN	Human alpha-2-macroglobulin (A2M) mRNA
6607	19659	32831	5.76	0.0E+00	A01255.1	EST_HUMAN	Human alpha-2-macroglobulin (A2M) mRNA
6617	19650	32842	0.55	0.0E+00	U112693	NT	Human alpha-2-macroglobulin (A2M) mRNA
6622	19652	32847	1.50	0.0E+00	X13377.1	NT	Human alpha-2-macroglobulin (A2M) mRNA
6624	19664	32849	0.71	0.0E+00	A1465576.1	EST_HUMAN	Human alpha-2-macroglobulin (A2M) mRNA
6625	19666	32850	1.09	0.0E+00	A0812541.1	EST_HUMAN	Human alpha-2-macroglobulin (A2M) mRNA
6631	19671	32855	4.46	0.0E+00	BE735568.1	EST_HUMAN	Human alpha-2-macroglobulin (A2M) mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO;	Exon SEQ ID NO;	OPF SEQ ID NO;	Expression Signal	Mean Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6631	16671	32957	4.46	0.0E+00	BE75969.1	EST HUMAN	361305588F1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:365616 5'
6632	16673	32958	0.84	0.0E+00	AW746596.1	EST HUMAN	MF0-B10264-221165-022111 E10251 Homo sapiens cDNA
6633	16675	32959	0.84	0.0E+00	AW748066.1	EST HUMAN	MF0-B10264-221165-022111 E10251 Homo sapiens cDNA
6636	16676			0.0E+00	U77026.1	NT	Homo sapiens (Homo sapiens) complete cds
6638	16678	32960	129.09	0.0E+00	AU110235.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'
6638	16678	32957	129.09	0.0E+00	AU110235.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'
6643	16682	32973	0.69	0.0E+00	BE759463.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'
6644	16683	32974	1.07	0.0E+00	U52577.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'
6652	16700	32996	2.94	0.0E+00	BE759463.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'
6671	16714	33005	2.88	0.0E+00	BE759463.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'
6671	16714	32970	2.88	0.0E+00	BE759463.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'
6711	16747	32950	0.61	0.0E+00	BE767097.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'
6717	16759	32956	0.46	0.0E+00	BE767493.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'
6754	16788	33001	1.48	0.0E+00	AW769483.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'
6754	16788	33002	1.48	0.0E+00	AW769483.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'
6754	16788	33003	1.48	0.0E+00	AW769483.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'
6754	16788	33004	1.48	0.0E+00	AW769483.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'
6758	16801	33041	0.8	0.0E+00	BE768840.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'
6758	16801	33042	0.8	0.0E+00	BE768840.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'
6801	16834	33045	2.59	0.0E+00	AF106850.1	NT	Homo sapiens low voltage-activated L-type calcium channel alpha 1C splice variant Cav7.1a (CACNA1C) mRNA, complete cds
6804	16837	33048	0.47	0.0E+00	LA8540.1	NT	Homo sapiens tubulin (TUB2) gene, exons 38, 39, 40 and 41
6805	16859	33046	1.14	0.0E+00	11420558	NT	Homo sapiens transferrin/transferrin receptor domain-associated protein (TRFRAP) mRNA
6813	16849	33056	4.34	0.0E+00	AW769483.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'
6813	16849	33057	4.34	0.0E+00	AW769483.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'
6817	16860	33060	1.07	0.0E+00	M37103.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'
6817	16860	33061	1.07	0.0E+00	M37103.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'
6835	16907	33081	4.3	0.0E+00	BE769483.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'
6842	16874	33088	4.78	0.0E+00	BE769483.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'
6843	16875	33089	0.79	0.0E+00	BE769483.1	EST HUMAN	U771026-106063-11 Homo sapiens cDNA clone IMAGE:365620 5'

Single Exon Probe Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	QPF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6643	16876	33090	0.79	0.0E+00	BE767955.1	EST_HUMAN	QY7-CA10055-14050-315-402 GN0355 Homo sapiens cDNA
6647	16879	33093	7.27	0.0E+00	BE568813.1	EST_HUMAN	601512058F1 NH1_MGC_71 Homo sapiens cDNA clone IMAGE:391311 5'
6647	16879	33094	7.27	0.0E+00	BE568813.1	EST_HUMAN	601512058F1 NH1_MGC_71 Homo sapiens cDNA clone IMAGE:391311 5'
6657	16889	33103	3.56	0.0E+00	124483.1	NT	Human salivary CD22 gene, exon 1-2
6662	16894	33107	2.55	0.0E+00	AL103304.2	NT	Homo sapiens chromosome 21 segment 11557000
6662	16894	33108	2.55	0.0E+00	AL103304.2	NT	Homo sapiens chromosome 21 segment 11557000
6668	16900	33115	3.77	0.0E+00	603983	NT	Human salivary CD22 gene, exon 3A (spare receptor) ZP94A mRNA
6672	16903	33116	4.3	0.0E+00	AB28412.1	EST_HUMAN	PI7653 VCL COAP_G03 Homo sapiens cDNA clone IMAGE:242415 5' similar to SW-WNT3_MOUSE
6674	16905	33120	1.71	0.0E+00	133923.1	EST_HUMAN	Homo sapiens zinc finger homeodomain protein (ATBFLA) mRNA, complete cds
6674	16905	33120	0.72	0.0E+00	AV1925420.1	EST_HUMAN	U1HF-BNU-anno-c1-c1-U1T1 NH1_MGC_30 Homo sapiens cDNA clone IMAGE:308721 5'
6680	16910	33133	4.48	0.0E+00	AA145894.1	EST_HUMAN	2065635.11 Swine, fetal, N2HFB_3v Homo sapiens cDNA clone IMAGE:793685 5'
6684	16914	33134	1.1	0.0E+00	BE272200.1	EST_HUMAN	60168517F1 NH1_MGC_57 Homo sapiens cDNA clone IMAGE:4103663 5'
6690	16926	33136	1.84	0.0E+00	BE252875.1	EST_HUMAN	QY3-BN001730000-278-028 BN0017 Homo sapiens cDNA
6643	16972	33195	0.76	0.0E+00	11420759	NT	Homo sapiens scalin carrier family 1 (high affinity aspartylglutamate transporter), member 9 (SLC1A9), mRNA
6643	16972	33196	0.76	0.0E+00	11420759	NT	Homo sapiens scalin carrier family 1 (high affinity aspartylglutamate transporter), member 9 (SLC1A9), mRNA
6644	16973	33196	0.62	0.0E+00	AJ230823.1	EST_HUMAN	AL230823 Homo sapiens library (Serassi P) Homo sapiens cDNA clone PS15D7 3'
6645	16974	33198	0.57	0.0E+00	AV115594.1	EST_HUMAN	hg32604AT NCL COAP_K011 Homo sapiens cDNA clone IMAGE:2952128 3'
6655	16993	33221	1.32	0.0E+00	AUT126023.1	EST_HUMAN	AUT126023 Homo sapiens cDNA clone NT2RMA02430 5'
6657	16995	33223	0.63	0.0E+00	BE1701494.1	EST_HUMAN	PM2-NN0174230700-001-H10 NN0174 Homo sapiens cDNA
6657	16995	33224	0.63	0.0E+00	BE1701494.1	EST_HUMAN	PM2-NN0174230700-001-H10 NN0174 Homo sapiens cDNA
6660	20017	33249	1.29	0.0E+00	BE142363.1	EST_HUMAN	OMA-HT013-270996-002-008 HT013 Homo sapiens cDNA
7012	20039	33272	0.63	0.0E+00	BE200612.1	EST_HUMAN	RCO-BN0171-203000-032-004 BN0171 Homo sapiens cDNA
7012	20039	33272	0.63	0.0E+00	BE200612.1	EST_HUMAN	RCO-BN0171-203000-032-004 BN0171 Homo sapiens cDNA
7041	20067	33301	7.63	0.0E+00	BE109191.1	EST_HUMAN	PM3-HT0500-293000-032-008 HT0500 Homo sapiens cDNA
7043	20069	33303	1.46	0.0E+00	BE109191.1	EST_HUMAN	PM3-HT0500-293000-032-008 HT0500 Homo sapiens cDNA
7063	20269	33545	3.08	0.0E+00	BE160597.1	EST_HUMAN	IL6 GN0352-100000-145-407 GN0352 Homo sapiens cDNA
7063	20269	33545	3.08	0.0E+00	BE160597.1	EST_HUMAN	IL6 GN0352-100000-145-407 GN0352 Homo sapiens cDNA
7065	20301	33552	1.07	0.0E+00	U08713.1	NT	Human salivary peroxidase mRNA, complete cds
7068	20305	33564	0.77	0.0E+00	BE571697.1	EST_HUMAN	746807.X1 NCL COAP_G03 Homo sapiens cDNA clone IMAGE:322207 3' similar to TR_062286 C92286
7111	20315	33578	6.63	0.0E+00	AJ940521.1	EST_HUMAN	1K310224-230799-001-B01 S10524 Homo sapiens cDNA
7111	20315	33578	6.63	0.0E+00	AJ940521.1	EST_HUMAN	1K310224-230799-001-B01 S10524 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7123	20245	33952	1.89	0.0E+00	1143626	NT	Homo sapiens CUB antigen (CUB), mRNA
7127	20246	33497	0.81	0.0E+00	AD4243.1	EST: HUMAN	ORF2p3432221.1 f44 (epoxyglt: hns2) Homo sapiens cDNA clone D4F4349.D0201.6
7138	20249	33498	4.06	0.0E+00	X56103.1	NT	1, alpha immunoglobulin heavy chain gene, variable region
7141	20249	33501	0.84	0.0E+00	A166270.1	EST: HUMAN	NR000001.1 Homo sapiens cDNA clone IMAGE:342080.6
7141	20244	33505	0.81	0.0E+00	BE74367.1	EST: HUMAN	301595770F1 NH1_MGC_21 Homo sapiens cDNA clone IMAGE:342080.6
7171	18443	31312	1.16	0.0E+00	BE74369.1	EST: HUMAN	301595770F1 NH1_MGC_21 Homo sapiens cDNA clone IMAGE:342080.6
7181	18453	31322	1.32	0.0E+00	BE56788.1	EST: HUMAN	301439070F1 NH1_MGC_21 Homo sapiens cDNA clone IMAGE:342080.6
7181	18453	31323	1.32	0.0E+00	BE56788.1	EST: HUMAN	301439070F1 NH1_MGC_21 Homo sapiens cDNA clone IMAGE:342080.6
7189	20189	33432	2.33	0.0E+00	BE590192.1	EST: HUMAN	749493.1 NOL CGAP_L104 Homo sapiens cDNA clone IMAGE:3321681.3 similar to SW:G085_HUMAN
7190	20189	33433	2.33	0.0E+00	BE590192.1	EST: HUMAN	749493.1 NOL CGAP_L104 Homo sapiens cDNA clone IMAGE:3321681.3 similar to SW:G085_HUMAN
7203	20201	33436	0.65	0.0E+00	BF700780.1	EST: HUMAN	302128958F1 NH1_MGC_21 Homo sapiens cDNA clone IMAGE:4285532.6
7217	20217	33464	1.43	0.0E+00	BF708376.1	EST: HUMAN	CM1-HT07077.000000-397-911 HT0877 Homo sapiens cDNA
7224	20223	33471	2.11	0.0E+00	AA105705.1	EST: HUMAN	Z34933.1 Scores, NH1_MGC_21 Homo sapiens cDNA clone IMAGE:336332.6
7232	20141		11.86	0.0E+00	11634810	NT	Homo sapiens calretinin (calretinin-associated protein), delta 2 (neurite filopodium-related arm-repeat protein) (CTNND2), mRNA
7234	20143	33332	1.04	0.0E+00	11481474	NT	Homo sapiens sodium channel, nonvoltage-gated 1, beta (Liddle syndrome) (SCNN1B), mRNA
7290	20196	33396	2.57	0.0E+00	BF599605.1	EST: HUMAN	302189532F1 NH1_MGC_21 Homo sapiens cDNA clone IMAGE:4310076.6
7290	20197	33405	0.96	0.0E+00	4567364	NT	Homo sapiens Bloem syndrome (BLM) mRNA
7295	20176		1.94	0.0E+00	J03036.1	NT	Human MYCL2 gene, complete cds
7276	20224	33477	2.97	0.0E+00	AF217288.1	NT	Homo sapiens cyclin 20 (CDH20) mRNA, complete cds
7276	20224	33475	2.97	0.0E+00	AF217288.1	NT	Homo sapiens cyclin 20 (CDH20) mRNA, complete cds
7277	20220	33479	0.86	0.0E+00	M83113.1	NT	Human neurofilament type 1 gene, exon 4b
7290	18459	31329	3.15	0.0E+00	11420716	NT	Homo sapiens melanoma antigen, family 5, 2 (MAGE5), mRNA
7251	18461	31330	0.58	0.0E+00	AJ10596.1	EST: HUMAN	1635406.1 Scores, NH1_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112499.3 similar to SW:OXR1_HUMAN P2269 OX151 LERO-LINDING PROTEIN.1
7291	18460	31331	0.58	0.0E+00	AJ10606.1	EST: HUMAN	1635406.1 Scores, NH1_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112499.3 similar to SW:OXR1_HUMAN P2269 OX151 LERO-LINDING PROTEIN.1
7295	18465	31335	0.88	0.0E+00	BE759705.1	EST: HUMAN	301150150F1 NH1_MGC_21 Homo sapiens cDNA clone IMAGE:3316533.6
7308	18478	31298	0.95	0.0E+00	BE549465.1	EST: HUMAN	301165145F1 NH1_MGC_21 Homo sapiens cDNA clone IMAGE:3868739.6

Single Exon Probes Expressed in Adult Liver

[illegible]

Table 4

Single Exon Probes Express

Pools	Emo	ORF SEQ	Expression	Most Similar	Top Hit Annotation	Top Hit Database Source	Top Hit Description
NO.	BEID NO.	ID NO.	Signal	Value	No.		
7476	20419	33698	1.08	0.0E+00	BE2543.031	EST_HUMAN	00111938P1 NIH MG-26 Homo sapiens cDNA clone IMAGE:3354586 5'
7483	20433	33712	1.27	0.0E+00	010173.1	NT	Human type IV sodium channel alpha polypeptide (SCN4A) gene, exon 14
7501	20430	33722	0.93	0.0E+00	AB007835.1	NT	Homo sapiens mRNA for KIA0466 protein, partial cds
7601	20440	33723	0.71	0.0E+00	AB007835.1	NT	Homo sapiens mRNA for KIA0466 protein, partial cds
7607	20446	33730	2.16	0.0E+00	AU133213.1	EST_HUMAN	AU133213 NT25P4 Homo sapiens cDNA clone NT25P4-4001565 5'
7524	20453	33751	0.86	0.0E+00	11428387	NT	Homo sapiens membrane protein CH1 (CH1), mRNA
7626	20468	33763	0.64	0.0E+00	AU145312.1	EST_HUMAN	EST162318 Jurkat T-cells V17 Homo sapiens cDNA 5' end
7532	20471	33765	2.81	0.0E+00	AU145705.1	EST_HUMAN	AU145706 Y76AA1 Homo sapiens cDNA clone Y76AA1002605 5'
7533	20472	33760	0.82	0.0E+00	4759333	EST_HUMAN	Homo sapiens netrin 1 (NTN1), mRNA
7543	20482	33770	0.62	0.0E+00	BE061286.1	EST_HUMAN	00143181P1 NIH MG-72 Homo sapiens cDNA clone IMAGE:3917164 5'
7545	20482	33772	1.24	0.0E+00	BE061286.1	EST_HUMAN	00143181P1 NIH MG-72 Homo sapiens cDNA clone IMAGE:3917164 5'
7600	20485	33728	2.46	0.0E+00	AF132953.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7606	18515	31240	2.48	0.0E+00	AF132953.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7678	20514	33801	0.66	0.0E+00	AF132953.1	EST_HUMAN	00158504P1 NIH MG-33 Homo sapiens cDNA clone IMAGE:392222 5'
7576	20514	33802	0.66	0.0E+00	BE147231.1	EST_HUMAN	00158504P1 NIH MG-33 Homo sapiens cDNA clone IMAGE:392222 5'
7601	20527	33816	4.28	0.0E+00	11439399	NT	Homo sapiens vitamin D125-dihydroxyvitamin D3 receptor (VDR), mRNA
7607	20527	33817	4.28	0.0E+00	11439399	NT	Homo sapiens vitamin D125-dihydroxyvitamin D3 receptor (VDR), mRNA
7600	20641	33831	0.53	0.0E+00	AF227144.1	NT	Homo sapiens voltage-dependent calcium channel alpha 1B subunit isoform 6 (CACNA1B) mRNA, complete cds
7626	20583	33836	36.3	0.0E+00	A1183444.1	EST_HUMAN	sp1407142 Sacchar. glaberrima, Rb140w10 Homo sapiens cDNA clone IMAGE:174644 3' similar to SW-ARS2_HUMAN PF1689 ARY15ULFATASE D PRECURSOR, consense element HGR repetitive element
7528	20593	33837	39.3	0.0E+00	A1183434.1	EST_HUMAN	sp1407142 Sacchar. glaberrima, Rb140w10 Homo sapiens cDNA clone IMAGE:174644 3' similar to SW-ARS2_HUMAN PF1689 ARY15ULFATASE D PRECURSOR, consense element HGR repetitive element
7631	20598	33840	0.58	0.0E+00	AF227138.1	NT	Homo sapiens candidate taste receptor 12/50 gene, complete cds
7631	20598	33841	0.58	0.0E+00	AF227138.1	NT	Homo sapiens candidate taste receptor 12/50 gene, complete cds
7634	20598	33844	3.68	0.0E+00	AF227138.1	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7634	20598	33844	3.68	0.0E+00	AF227138.1	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7634	20598	33845	3.46	0.0E+00	11428392	NT	00203506P1 NCI C63AF Brm4 Homo sapiens cDNA clone IMAGE:4162938 5'
7638	20578	33873	13.17	0.0E+00	H33375.1	EST_HUMAN	zmf004711 Strategene muscle 9517203 Homo sapiens cDNA clone IMAGE:592601 5' similar to TR_G063952 G060582 NEBULIN ;
7641	20578	33870	2.83	0.0E+00	AY124183.1	EST_HUMAN	UK-Z65454B0226 1.1 c34 (eyenrich: Nhe33) Homo sapiens cDNA clone DKFZ23448225 5'
7646	20580	33876	2.2	0.0E+00	AU179497.1	EST_HUMAN	UK-Z65454B0226 1.1 c34 (eyenrich: Nhe33) Homo sap. cDNA clone DKFZ23448225 5'
7646	20580	33877	2.2	0.0E+00	AU179497.1	EST_HUMAN	UK-Z65454B0226 1.1 c34 (eyenrich: Nhe33) Homo sap. cDNA clone DKFZ23448225 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Meat Similarity (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Databases Source	Top Hit Descriptor
7657	20591	33985	0.5	0.0E+00	AJ275668.1	NT	Homo sapiens partial mRNA for LIPPC5 protein (LIPPC5 gene)
7662	20524	33924	1.16	0.0E+00	BE295469.1	EST_HUMAN	U01146/27 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529794.5
7664	20526	33925	0.87	0.0E+00	11427953	NT	Homo sapiens hypothetical protein (FLJ3281), mRNA
7667	20529	33928	2.91	0.0E+00	AU118607.1	EST_HUMAN	AU118607 HEBRA1 Homo sapiens cDNA clone HEBRA1033969.5
7668	20530	33928	2.12	0.0E+00	AF053213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7669	20530	33928	2.12	0.0E+00	AF053213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7710	20542	33939	0.83	0.0E+00	AF246605.1	NT	Homo sapiens RNA for 20G22 protein, complete cds
7716	20550	33944	14.21	0.0E+00	X70172.1	NT	Homo sapiens RNA for 20G22 protein, complete cds
7720	20553	33945	0.51	0.0E+00	U05414.1	NT	Homo sapiens RNA for 20G22 protein, complete cds
7721	20553	33947	0.8	0.0E+00	U05414.1	NT	Homo sapiens RNA for 20G22 protein, complete cds
7731	20559	33953	0.88	0.0E+00	U1755603.1	EST_HUMAN	EST:395573 IMAGE resources, MAGO Homo sapiens cDNA
7736	20569	33955	0.54	0.0E+00	BE072445.1	EST_HUMAN	Ts640a x1 NCL CGAP_G8 Homo sapiens cDNA clone IMAGE:3223167.3 similar to gb:M5461.1_maf1.IG
7737	20569	33956	2.27	0.0E+00	AU1560510.1	EST_HUMAN	HEAVY CHAIN PRECURSOR V.I REGION (HUMAN)
7768	20568	33956	0.89	0.0E+00	AF001543.1	EST_HUMAN	EST:395568 IMAGE resources, MAGA Homo sapiens cDNA
7769	20568	33956	0.89	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chondroectodermal apoa.S.C.) Homo sapiens cDNA clone laappa_200
7769	20568	33956	0.89	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chondroectodermal apoa.S.C.) Homo sapiens cDNA clone laappa_200
7769	20568	33957	0.88	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chondroectodermal apoa.S.C.) Homo sapiens cDNA clone laappa_200
7791	20720	33962	0.88	0.0E+00	AF001543.1	NT	Human BT3 protein homologue gene, complete cds
7792	20721	34024	0.59	0.0E+00	BE408203.1	EST_HUMAN	5015025767 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3837434.5
7792	20721	34024	0.59	0.0E+00	BE408203.1	EST_HUMAN	UHF-BKO-mae-9-07-U-1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3064924.5
7804	20733	34035	0.6	0.0E+00	AU142942.1	EST_HUMAN	YMSHST017 Soesma adult brain NZB4H18597 Homo sapiens cDNA clone IMAGE:100051.5
7823	20752	34035	1.01	0.0E+00	BE7130.1	EST_HUMAN	YMSHST017 Soesma adult brain NZB4H18597 Homo sapiens cDNA clone IMAGE:2879940.5 similar to TR-Q08650 Q08650
7824	20763	34056	1.09	0.0E+00	AF129626.1	EST_HUMAN	AF129626 NIH_MGC_1301 Homo sapiens cDNA clone IMAGE:100051.5
7846	20773	34079	1.37	0.0E+00	AU117583.1	EST_HUMAN	AF117583 HEMBA1 Homo sapiens cDNA clone HEMBA1001861.5
7846	20779	34076	4.35	0.0E+00	11427184	NT	Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA
7870	20797	34100	0.54	0.0E+00	AA211893.1	EST_HUMAN	z59802.1 Stradiolone muscle 537206 Homo sapiens cDNA clone IMAGE:462203.5 similar to gb:303740
7873	20804	34107	0.83	0.0E+00	BF220255.1	EST_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN)
7893	20809	34115	0.82	0.0E+00	AF045827.1	EST_HUMAN	MRO-AN0085-27090-304-07 AN0083 Homo sapiens cDNA
7896	20811	34121	0.89	0.0E+00	AF045827.1	EST_HUMAN	UHF-BKO-mae-9-07-U-1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3057495.5
7896	20811	34121	0.89	0.0E+00	AF045827.1	EST_HUMAN	UHF-BKO-mae-9-07-U-1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3057495.5
7982	20818	34124	0.71	0.0E+00	X32832.1	NT	Q13-BN0046-22000-125-04 BN0048 Homo sapiens cDNA
7982	20818	34124	0.71	0.0E+00	X32832.1	NT	Q13-BN0046-22000-125-04 BN0048 Homo sapiens cDNA
7919	20842	34145	0.79	0.0E+00	BF306966.1	EST_HUMAN	Homo sapiens zona finger homeodomain protein (ATBF-1) mRNA, complete cds
7919	20842	34145	0.79	0.0E+00	BF306966.1	EST_HUMAN	UHF-BKO-mae-9-07-U-1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4173348.5
7919	20842	34145	0.79	0.0E+00	BF306966.1	EST_HUMAN	UHF-BKO-mae-9-07-U-1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4173348.5
7923	20851	34158	1.35	0.0E+00	AU118767.1	EST_HUMAN	AU118767 HEMBA1 Homo sapiens cDNA clone HEMBA1004314.5

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	CPG SEQ ID NO:	Expression Signal	Mean Similarity BLAST E Value	Top Hit Accession No.	Top Hit Database Source	*top Hit Descriptor
8201	21107	34437	6.76	0.0E+00	490148	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABC1A), mRNA
8208	21114	34444	0.97	0.0E+00	AV759467.1	EST HUMAN	AV759467 B1 Homo sapiens cDNA clone B1AF5005 5'
8211	21116	34446	6.99	0.0E+00	BE75670.1	EST HUMAN	941833159F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
8211	21116	34447	6.86	0.0E+00	BE75670.1	EST HUMAN	941833159F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
8212	21117	34448	0.76	0.0E+00	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; atrophin receptor interacting protein 1 (K14A0705), mRNA
8212	21117	34449	0.76	0.0E+00	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; atrophin receptor interacting protein 1 (K14A0705), mRNA
8213	21118	34450	0.88	0.0E+00	AU120424.1	EST HUMAN	AU120424 HEUB81 Homo sapiens cDNA clone HEMB1000555 5'
8213	21118	34451	0.88	0.0E+00	AU120424.1	EST HUMAN	AU120424 HEUB81 Homo sapiens cDNA clone HEMB1000555 5'
8240	21145	34477	0.63	0.0E+00	BF59287.1	EST HUMAN	nc0224x.v1 Srares NSF FL3_WL OTL PA_351 Homo sapiens cDNA clone IMAGE:320321 3' similar to contains element TART negative element
8244	21159	34482	1.56	0.0E+00	BE77070.1	EST HUMAN	901181713F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3864258 5'
8244	21159	34483	1.56	0.0E+00	BE77070.1	EST HUMAN	901181713F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3864258 5'
8297	21181	34528	0.47	0.0E+00	A027216.1	EST HUMAN	W06207.x1 NCL CGAP_U1 Homo sapiens cDNA clone IMAGE:2424366 3' similar to TRQ90808 Q90808
8298	21181	34529	0.47	0.0E+00	A027216.1	EST HUMAN	W06207.x1 NCL CGAP_U1 Homo sapiens cDNA clone IMAGE:2424366 3' similar to TRQ90808 Q90808
8298	21181	34535	0.63	0.0E+00	X12224.1	NT	OLFACTORY RECEPTOR 4
8298	21181	34535	0.63	0.0E+00	X12224.1	NT	H sapiens germline immunoglobulin heavy chain, variable region, (6-1G)
8298	21223	34538	0.56	0.0E+00	BE790034.1	EST HUMAN	901130933F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3900041 5'
8304	21268	34643	0.42	0.0E+00	AV1402189.1	EST HUMAN	U1HF-BK0-as1-c-0-JUL1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3054733 5'
8309	21213	34650	0.53	0.0E+00	AV195307.1	EST HUMAN	EST98337 MAGC resequences, MAGD Homo sapiens cDNA
8317	21222		0.46	0.0E+00	BE539884.1	EST HUMAN	743194.x1 NCL CGAP_G05 Homo sapiens cDNA clone IMAGE:322002 3' similar to gb-507796
8322	21227	34632	0.43	0.0E+00	Y16765.1	NT	HYALURONIDASE PRECURSOR (H-1MANX)
8350	21255	34590	0.57	0.0E+00	W52675.1	EST HUMAN	Homo sapiens pathHAA pseudogene
8351	21256	34591	0.76	0.0E+00	11425126	NT	z38010.1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:338443 5'
8352	21257	34592	0.63	0.0E+00	AU117333.1	EST HUMAN	Homo sapiens similar to ER to nucleus signalling 1 (H sapiens) (L0038433), mRNA
8352	21258		0.43	0.0E+00	BE791863.1	EST HUMAN	AU117333 HEMBA1 Homo sapiens cDNA clone HEMBA1001716 5'
8379	21283	34674	0.53	0.0E+00	AV1958044.1	EST HUMAN	EST90110 MAGC resequences, MAGJ Homo sapiens cDNA
8380	21284	34675	0.46	0.0E+00	A1134345.1	EST HUMAN	HP2049 Human fetal liver cDNA library Homo sapiens cDNA
8388	21293	34676	0.46	0.0E+00	BE500733.1	EST HUMAN	NC1-B10721-050400-Q1-H105 B10721 Homo sapiens cDNA
8403	21300	34637	0.44	0.0E+00	6905995	NT	Homo sapiens cyclic fibroblast transmembrane conductance regulator, A TP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8403	21300	34638	0.44	0.0E+00	6905995	NT	Homo sapiens cyclic fibroblast transmembrane conductance regulator, A TP-binding cassette (sub-family C, member 7) (CFTR), mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	QPCR SEQ ID NO:	Expression Signal	Most Similar (BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8405	21308	34640	0.51	0.0E+00	AW03280.1	EST_HUMAN	UHRF-50K-antp-84-04-UT1 NH_MGC_35 Homo sapiens cDNA clone IMAGE:304510 5'
8417	21320	34652	2.76	0.0E+00	AW070162.1	EST_HUMAN	AW070162 AD8 Homo sapiens cDNA clone ADPNT167 5'
8419	21322	34665	2.76	0.0E+00	AW070162.1	EST_HUMAN	UHRF-50K-antp-84-04-UT1 NH_MGC_35 Homo sapiens cDNA clone ADPNT167 5'
8419	21322	34666	0.44	0.0E+00	AW03280.1	EST_HUMAN	UHRF-50K-antp-84-04-UT1 NH_MGC_35 Homo sapiens cDNA clone IMAGE:305008 5'
8450	21359	34709	0.87	0.0E+00	AW03187.1	EST_HUMAN	AT318171 NH_MGC_67 Homo sapiens cDNA clone IMAGE:30187 5'
8479	21410		0.71	0.0E+00	BF21200.1	EST_HUMAN	90185311 NH_MGC_19 Homo sapiens cDNA clone IMAGE:419363 5'
8479	21410	34791	0.76	0.0E+00	BE53703.1	EST_HUMAN	90185311 NH_MGC_19 Homo sapiens cDNA clone IMAGE:355359 5'
8502	21433	34774	1.81	0.0E+00	AA149791.1	EST_HUMAN	90185311 NH_MGC_19 Homo sapiens cDNA clone IMAGE:408410 5'
8516	21438	34798	0.88	0.0E+00	BF02626.1	EST_HUMAN	90185311 NH_MGC_19 Homo sapiens cDNA clone IMAGE:365131 5'
8544	21475	34817	2.41	0.0E+00	BE173546.1	EST_HUMAN	90185311 NH_MGC_19 Homo sapiens cDNA clone IMAGE:365131 5'
8551	21492	34833	3.01	0.0E+00	BE173546.1	EST_HUMAN	90185311 NH_MGC_19 Homo sapiens cDNA clone IMAGE:365131 5'
8551	21492	34834	7.37	0.0E+00	BE48762.1	NT	Human amyloid-beta protein (APP) gene, exon 11
8580	21520	34884	0.77	0.0E+00	AW074881.1	EST_HUMAN	90185311 NH_MGC_19 Homo sapiens cDNA clone IMAGE:365131 5'
8580	21520	34885	0.77	0.0E+00	AW074881.1	EST_HUMAN	90185311 NH_MGC_19 Homo sapiens cDNA clone IMAGE:365131 5'
8596	21527	34871	2.86	0.0E+00	AA397551.1	EST_HUMAN	90185311 NH_MGC_19 Homo sapiens cDNA clone IMAGE:365131 5'
8596	21527	34872	0.83	0.0E+00	AW387131.1	EST_HUMAN	90185311 NH_MGC_19 Homo sapiens cDNA clone IMAGE:365131 5'
8600	21591		0.68	0.0E+00	AB020691.1	NT	Human sapiens mRNA for KIAA0354 protein, partial cds
8601	21532	34873	2.57	0.0E+00	AA142002.1	EST_HUMAN	90185311 NH_MGC_19 Homo sapiens cDNA clone IMAGE:365131 5'
8601	21532	34877	2.57	0.0E+00	BE399421.1	EST_HUMAN	90185311 NH_MGC_19 Homo sapiens cDNA clone IMAGE:365131 5'
8605	21530	34877	1	0.0E+00	BE398421.1	EST_HUMAN	90185311 NH_MGC_19 Homo sapiens cDNA clone IMAGE:365131 5'
8619	21550	34891	0.33	0.0E+00		NT	Human sapiens killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1 (KIR2DS1), mRNA
8621	21552	34893	0.9	0.0E+00	W94278.1	EST_HUMAN	90185311 NH_MGC_19 Homo sapiens cDNA clone IMAGE:365131 5'
8621	21552	34894	0.9	0.0E+00	W94278.1	EST_HUMAN	90185311 NH_MGC_19 Homo sapiens cDNA clone IMAGE:365131 5'
8623	21554		6.23	0.0E+00	BF075060.1	EST_HUMAN	90185311 NH_MGC_19 Homo sapiens cDNA clone IMAGE:4294128 5'
8627	21559		0.53	0.0E+00	AA134114.1	EST_HUMAN	90185311 NH_MGC_19 Homo sapiens cDNA clone IMAGE:365131 5'
8672	21603	34843	1.61	0.0E+00	AA132024.1	EST_HUMAN	90185311 NH_MGC_19 Homo sapiens cDNA clone IMAGE:365131 5'
8672	21603	34844	1.61	0.0E+00	AA132024.1	EST_HUMAN	90185311 NH_MGC_19 Homo sapiens cDNA clone IMAGE:365131 5'
8712	21643		1.18	0.0E+00	BE177603.1	EST_HUMAN	90185311 NH_MGC_19 Homo sapiens cDNA clone IMAGE:365131 5'
8735	21655	35010	1.44	0.0E+00	AW009491.1	EST_HUMAN	90185311 NH_MGC_19 Homo sapiens cDNA clone IMAGE:365131 5'

Table 4

Single Exon Probes Expressed in Adult Liver

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Table 4

[illegible]628

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Max Similar (BLAST E) Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9588	22614		0.74	0.0E+00	H75937.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:232077 8
9589	22625	35859	4.06	0.0E+00	BE315402.1	EST_HUMAN	601141191 NH_MGC_9 Homo sapiens cDNA clone IMAGE:314740 5
9590	22625	35900	4.06	0.0E+00	BE315402.1	EST_HUMAN	601141191 NH_MGC_9 Homo sapiens cDNA clone IMAGE:314740 5
9591	22634	35904	0.71	0.0E+00	BE312721.1	EST_HUMAN	601423821 NH_MGC_9 Homo sapiens cDNA clone IMAGE:358100 5
9592	22634	35905	0.71	0.0E+00	BE312721.1	EST_HUMAN	601423821 NH_MGC_9 Homo sapiens cDNA clone IMAGE:358100 5
9593	22637		0.86	0.0E+00	M59980.1	NT	Human polyomavirus strain JCPy82
9594	22639	35906	1.86	0.0E+00	X14703.1	EST_HUMAN	Human mRNA for CD44, a cell surface alpha 5 beta 1 subunit
9595	22654	35924	2.36	0.0E+00	A061395.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:170094 3
9596	22659		2.3	0.0E+00	A064071.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9597	22659	35927	0.23	0.0E+00	CG86968	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9598	22673	35944	0.2	0.0E+00	AV15521.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9599	22683	35972	3.26	0.0E+00	CG38487	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9600	22691	35972	1.26	0.0E+00	AV12862.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9601	22692	35986	1.21	0.0E+00	11436995	NT	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9602	22713		0.94	0.0E+00	BE410788.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9603	22629	36005	1.57	0.0E+00	BF002024.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9604	22669	36016	1.46	0.0E+00	AB011150.1	NT	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9605	22669	36016	1.46	0.0E+00	BE744823.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9606	22669	36025	0.98	0.0E+00	BE510252.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9607	22644	36025	0.98	0.0E+00	BE510252.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9608	22644	36025	0.98	0.0E+00	BE510252.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9609	22647	36025	0.71	0.0E+00	AU136220.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9610	22651	36033	1.23	0.0E+00	BE693843.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9611	22651	36033	1.23	0.0E+00	BE693843.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9612	22651	36033	1.23	0.0E+00	BE693843.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9613	22659	36050	0.75	0.0E+00	AB011195.1	NT	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9614	22659	36050	0.75	0.0E+00	AB011195.1	NT	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9615	22671	36051	1.85	0.0E+00	AA344691.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9616	22671	36055	1.85	0.0E+00	AA344691.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9617	22671	36055	1.85	0.0E+00	AA344691.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9618	22711	36063	0.89	0.0E+00	AW974493.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9619	22711	36064	0.89	0.0E+00	AW974493.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9620	22711	36064	0.89	0.0E+00	AW974493.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN
9621	22743	36124	1.86	0.0E+00	BE207065.1	EST_HUMAN	IMAGE3340271 Scores fetal liver spleen (NH) Homo sapiens cDNA clone IMAGE:2473150 3 similar to SVI-MG63_HUMAN

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	QPS SEQ ID NO.	Expression Signal	Mean Signal BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8938	22743	39125	1.06	0.0E+00	BE267093.1	EST HUMAN	hs0086.y1 NH_105277 Homo sapiens cDNA clone IMAGE:282873 5' similar to gp135(0.9) Mus musculus beta-4 mRNA, complete cds (M0506).
8940	22657	39346	1.93	0.0E+00	BF349713.1	EST HUMAN	362023150P1 NCI COA_134077 Homo sapiens cDNA clone IMAGE:1158300 5'
8983	22758	39184	3.23	0.0E+00	BE727513.1	EST HUMAN	Q12111088-200 Homo sapiens cDNA clone IMAGE:1110387 Homo sapiens cDNA
8915	22594	39591	0.72	0.0E+00	BF034377.1	EST HUMAN	361416108-200 Homo sapiens cDNA clone IMAGE:3645035 5'
8916	22594	39592	0.72	0.0E+00	BF034377.1	EST HUMAN	361416108-200 Homo sapiens cDNA clone IMAGE:3645035 5'
8921	22911	36299	0.76	0.0E+00	5830099	NT	361416108-200 Homo sapiens cDNA clone IMAGE:3645035 5'
8923	22911	36299	0.76	0.0E+00	5830099	NT	361416108-200 Homo sapiens cDNA clone IMAGE:3645035 5'
8923	22911	36300	0.70	0.0E+00	5830099	NT	361416108-200 Homo sapiens cDNA clone IMAGE:3645035 5'
8923	22931	39238	1.20	0.0E+00	AL042278.1	EST HUMAN	DXF52434.01200.1 (384 (synonym: class) Homo sapiens cDNA clone DKFZ26434.0120 5'
8965	22870	39259	1.86	0.0E+00	AW89043.1	EST HUMAN	0616041.x1 Sawee, NSF FR_2W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1158300 5'
8972	21330	34682	0.67	0.0E+00	BF35592.1	EST HUMAN	TRQ14677 Q14677 KIA0171 PROTEIN ;
8973	21331	34693	4.02	0.0E+00	11550161	NT	361182248F1 NH_105277 Homo sapiens cDNA clone IMAGE:1136068 5'
8973	21331	34694	4.02	0.0E+00	11550161	NT	Homo sapiens hypothetical C2H4 zinc finger protein FLJ22504 (FLJ22504), mRNA
8975	21333	34697	8.83	0.0E+00	AJ220069.1	EST HUMAN	3610946.x1 NCI COA_P_105 Homo sapiens cDNA clone IMAGE:3670007 5'
8975	21333	34697	8.83	0.0E+00	AJ220069.1	EST HUMAN	P28316 005 RIBOSOMAL PROTEIN L29A ;
8976	21333	34698	8.83	0.0E+00	AJ220069.1	EST HUMAN	3610946.x1 NCI COA_P_105 Homo sapiens cDNA clone IMAGE:3670007 5'
8976	21334	34699	1.41	0.0E+00	AW683836.1	EST HUMAN	P28316 005 RIBOSOMAL PROTEIN L29A ;
8976	21334	34699	1.41	0.0E+00	AW683836.1	EST HUMAN	EST3500203 IMAGE:residues, MAGO Homo sapiens cDNA
10003	22520	39207	4.26	0.0E+00	AF163496.1	NT	Homo sapiens polycystic kidney/diseases 2-like protein (PKD2) gene, exon 8
10006	22923	39211	0.73	0.0E+00	BE184528.1	EST HUMAN	601E10882F1 NH_105277 Homo sapiens cDNA clone IMAGE:3612105 5'
10006	22923	39212	0.73	0.0E+00	BE184528.1	EST HUMAN	601E10882F1 NH_105277 Homo sapiens cDNA clone IMAGE:3612105 5'
10015	22915	39311	0.93	0.0E+00	BE255620.1	EST HUMAN	501108642F1 NH_105277 Homo sapiens cDNA clone IMAGE:360722 5'
10015	22915	39311	0.93	0.0E+00	BE255620.1	EST HUMAN	501108642F1 NH_105277 Homo sapiens cDNA clone IMAGE:360722 5'
10018	22918	39307	1.72	0.0E+00	BE719138.1	EST HUMAN	501146823F1 NH_105277 Homo sapiens cDNA clone IMAGE:3670007 5'
10018	22918	39308	1.72	0.0E+00	BE719138.1	EST HUMAN	501146823F1 NH_105277 Homo sapiens cDNA clone IMAGE:3670007 5'
10020	22920	39309	15.09	0.0E+00	AW183779.1	EST HUMAN	501146823F1 NH_105277 Homo sapiens cDNA clone IMAGE:3670007 5'
10040	22940	39329	3.44	0.0E+00	BE293191.1	EST HUMAN	501146823F1 NH_105277 Homo sapiens cDNA clone IMAGE:3670007 5'
10057	22979	39593	6.14	0.0E+00	C06158.1	EST HUMAN	C06158 Human paracatalin, full Homo sapiens cDNA clone IMAGE:3670007 5'
10057	22979	39594	6.14	0.0E+00	C06158.1	EST HUMAN	C06158 Human paracatalin, full Homo sapiens cDNA clone IMAGE:3670007 5'
10069	22979	39597	2.71	0.0E+00	BE749515.1	EST HUMAN	501108642F1 NH_105277 Homo sapiens cDNA clone IMAGE:3621648 5'
10069	22984	39376	2.2	0.0E+00	11437262	NT	Homo sapiens, salivary gland, family 21 (Organic anion transporter), member 1 (SLC21A9), mRNA

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10098	22684	38578	2.2	0.0E+00	11437282	NT	Homo sapiens ucdh1c cluster family 21 (organic anion transporter) member 8 (SLC7149), mRNA
10098	22684	38577	2.3	0.0E+00	11437282	NT	Homo sapiens ucdh1c cluster family 21 (organic anion transporter) member 8 (SLC7149), mRNA
10098	22681	38597	1.92	0.0E+00	SE600548.1	EST_HUMAN	Homo sapiens ucdh1c cluster family 21 (organic anion transporter) member 8 (SLC7149), mRNA
10105	22666	38591	1.14	0.0E+00	AV176328.1	EST_HUMAN	AV176328 AD31 Homo sapiens ucdh1c cluster family 21 (organic anion transporter) member 8 (SLC7149), mRNA
10117	22308	38403	2.68	0.0E+00	AF003094.1	NT	Homo sapiens ucdh1c cluster family 21 (organic anion transporter) member 8 (SLC7149), mRNA
10177	22308	38404	2.08	0.0E+00	AF003094.1	NT	Homo sapiens ucdh1c cluster family 21 (organic anion transporter) member 8 (SLC7149), mRNA
10148	22339	38438	1.16	0.0E+00	SE525771.1	EST_HUMAN	UCP2B10642-133000-017-c01.8 (UCP2) Homo sapiens cDNA
10161	22381	38448	2.11	0.0E+00	AF003093.1	EST_HUMAN	UHF-FBN0-qlg-b-12-04.1.1 NIH_MGC_30 Homo sapiens cDNA clone IMAGE:3076943.5
10167	22358	38468	2.11	0.0E+00	AF150255.1	EST_HUMAN	UHF-FBN0-qlg-b-12-04.1.1 NIH_MGC_30 Homo sapiens cDNA clone IMAGE:3076943.5
10176	22097	38466	1.5	0.0E+00	AF003093.1	NT	Homo sapiens chromosome 8 duplication of the T cell receptor beta locus and tyrosinase gene families
10176	22097	38466	1.5	0.0E+00	AF003093.1	NT	Homo sapiens chromosome 8 duplication of the T cell receptor beta locus and tyrosinase gene families
10176	22096	38467	0.88	0.0E+00	BE783272.1	EST_HUMAN	801470624F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874037.5
10176	22096	38468	0.88	0.0E+00	BE783272.1	EST_HUMAN	801470624F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874037.5
10185	23076	38477	0.82	0.0E+00	W66925.1	EST_HUMAN	ZF1841.1 L1 Scores_fairl heart_NH-H16W Homo sapiens cDNA clone IMAGE:340644.5
10185	23076	38478	0.82	0.0E+00	W66925.1	EST_HUMAN	ZF1841.1 L1 Scores_fairl heart_NH-H16W Homo sapiens cDNA clone IMAGE:340644.5
10188	22069	38460	1.09	0.0E+00	AB013535.1	NT	Homo sapiens mRNA for neuronal alpha protein, complete cds
10202	22063	38405	0.84	0.0E+00	AF1124780.1	EST_HUMAN	am59a1.1 x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1839548.5
10204	22065	38406	2.27	0.0E+00	AF1500526.1	EST_HUMAN	UHF-FBN0-qlg-b-07-04.1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077984.5
10246	22336	38541	2.24	0.0E+00	AF006988.1	NT	MULTIPLE scaffolds associated retrovirus poliovirus (pol) mRNA, partial cds
10272	22162	38572	2.9	0.0E+00	SF78466.1	NT	AGF=hydrogen-induced growth factor AGF Human, placenta, GenomimRNA, 498 nt, segment 5 of 5
10272	22162	38573	2.9	0.0E+00	SF78466.1	NT	AGF=hydrogen-induced growth factor AGF Human, placenta, GenomimRNA, 498 nt, segment 5 of 5
10279	22165	38576	3.07	0.0E+00	BE750320.1	EST_HUMAN	GM1344063F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:388886.5
10283	22183	38684	1.9	0.0E+00	AW363133.1	EST_HUMAN	GM1344063F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:388886.5
10319	22208	38619	0.96	0.0E+00	BE206710.1	EST_HUMAN	9528001 x1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:2664903.3
10334	22229	38637	2.47	0.0E+00	AU103249.1	EST_HUMAN	AU103249 NT2623 Homo sapiens cDNA clone NT2673004260.5
10334	22232	38650	2.47	0.0E+00	AU103249.1	EST_HUMAN	AU103249 NT2623 Homo sapiens cDNA clone NT2673004260.5
10343	22232	38650	0.84	0.0E+00	AW600569.1	EST_HUMAN	UHF-FBN0-qlg-b-05-04.1.1 NIH_MGC_31 Homo sapiens cDNA clone IMAGE:3072387.5
10349	22238	38656	19.64	0.0E+00	BE744000.1	EST_HUMAN	90186658F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:346333.5
10349	22238	38657	19.64	0.0E+00	BE744000.1	EST_HUMAN	90186658F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:346333.5
10381	22250	38570	1.96	0.0E+00	7602097	NT	Homo sapiens KIA00340 gene product (NAA0345), mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

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Single Exon Probe Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10722	23008	37038	1.14	0.0E+00	BE586511.1	EST HUMAN	301645534F1 NH1_MGC_581 Homo sapiens cDNA clone IMAGE:530177.5
10738	23024	37035	0.66	0.0E+00	BE587487.1	EST HUMAN	301642217F1 NH1_MGC_72 Homo sapiens cDNA clone IMAGE:367463.5
10747	23033	37095	0.64	0.0E+00	A311624.1	EST HUMAN	EST162355 Jurek1 cells 11 Homo sapiens cDNA 3' end
10748	23034	37095	0.68	0.0E+00	4794827.1	EST HUMAN	Homo sapiens testis 11 (HKS3) mRNA
10759	23043	37078	0.72	0.0E+00	BE589113.1	EST HUMAN	301642226F1 NH1_MGC_72 Homo sapiens cDNA clone IMAGE:367463.5
10762	23048	37031	0.39	0.0E+00	11659151.1	EST HUMAN	Homo sapiens lymphatic system fibroblast protein FL22501 (FL2250A) mRNA
10771	23053	37037	0.84	0.0E+00	A362650.1	EST HUMAN	Homo sapiens mRNA for actin cytoplasmic A36250, complete cds
10772	23055	37032	4.32	0.0E+00	A362650.1	EST HUMAN	Homo sapiens mRNA for actin cytoplasmic A36250, complete cds
10779	23065	37032	4.32	0.0E+00	A362650.1	EST HUMAN	Homo sapiens mRNA for actin cytoplasmic A36250, complete cds
10784	23070	37036	1.4	0.0E+00	A4701497.1	EST HUMAN	313905151 Soares_fetal liver, spleen, INR1.5 S1 Homo sapiens cDNA clone IMAGE:460777.3 similar to p0M14123, ccd1 RETROVIRUS-RELATED GAG POLYPROTEIN (HUMAN)
10789	23072	37100	0.66	0.0E+00	U22821.1	EST HUMAN	Human beta 1-fibrinogen-related mRNA, complete cds
10790	23073	37103	0.73	0.0E+00	U22821.1	EST HUMAN	Human beta 1-fibrinogen-related mRNA, complete cds
10798	23074	37104	4.73	0.0E+00	BF540331.1	EST HUMAN	602037045F1 NQ1_OGAP_Brd4 Homo sapiens cDNA clone IMAGE:1181630.5
10798	23074	37104	4.73	0.0E+00	BF540331.1	EST HUMAN	602037045F1 NQ1_OGAP_Brd4 Homo sapiens cDNA clone IMAGE:1181630.5
10813	23069	37126	0.9	0.0E+00	BE587149.1	EST HUMAN	601439713F1 NH1_MGC_72 Homo sapiens cDNA clone IMAGE:3924578.5
10813	23069	37127	0.9	0.0E+00	BE587149.1	EST HUMAN	601439713F1 NH1_MGC_72 Homo sapiens cDNA clone IMAGE:3924578.5
10822	23769	37183	0.73	0.0E+00	A6931818.1	EST HUMAN	wa38403.x1 NQ1_OGAP_Kid1 Homo sapiens cDNA clone IMAGE:2300188.3 similar to TR-Q81204
10872	23769	37183	0.73	0.0E+00	A6931818.1	EST HUMAN	wa38403.x1 NQ1_OGAP_Kid1 Homo sapiens cDNA clone IMAGE:2300188.3 similar to TR-Q81204
10884	23760	37184	0.73	0.0E+00	A6931818.1	EST HUMAN	wa38403.x1 NQ1_OGAP_Kid1 Homo sapiens cDNA clone IMAGE:2300188.3 similar to TR-Q81204
10884	23760	37184	0.73	0.0E+00	U30378.1	EST HUMAN	FE2344 Fetal brain, Striatum: Homo sapiens cDNA clone F823A4.3'end
10909	23761	37220	0.82	0.0E+00	AU122429.1	EST HUMAN	AU122429 MAMMAT1 Homo sapiens cDNA clone VAMMAT002368.5
10931	23819	37245	2.41	0.0E+00	BF456218.1	EST HUMAN	na616c12.x1 Soares_NSIF_F8_BW_OT_PA_31 Homo sapiens cDNA clone IMAGE:3268271.3
10932	23817		1.75	0.0E+00	AV654765.1	EST HUMAN	AV654765 GLC-Homo sapiens cDNA clone GLC02007.3
10950	23844	37291	3.78	0.0E+00	AW517960.1	EST HUMAN	wa74607.x1 NQ1_OGAP_Kid8 Homo sapiens cDNA clone IMAGE:2907401.3 similar to gb1M69066 MOESIN (HUMAN)
10954	23848	37295	5.05	0.0E+00	BE449213.1	EST HUMAN	301642217F1 NH1_MGC_72 Homo sapiens cDNA clone IMAGE:3664702.5
10970	23804	37281	0.7	0.0E+00	11438005.1	EST HUMAN	Homo sapiens hypothetical protein DCFZ2761P1010 (DCFZ2761P1010), mRNA
10980	23860	37311	0.61	0.0E+00	X06893.1	EST HUMAN	J-Lapins mRNA for NK receptor (183 Kd)
10987	23861	37312	2.07	0.0E+00	BE781742.1	EST HUMAN	301647143F1 NH1_MGC_57 Homo sapiens cDNA clone IMAGE:3870700.5
11016	23900	37337	2.27	0.0E+00	BE586720.1	EST HUMAN	RC2-3170642-130206-07-2403 B10662 Homo sapiens cDNA
11016	23900	37338	2.27	0.0E+00	BE586720.1	EST HUMAN	RC2-3170642-130206-07-2403 B10662 Homo sapiens cDNA
11021	23055	37344	0.64	0.0E+00	U70602.1	EST HUMAN	Human endoplasmic reticulum, LTR, US and gag gene
11027	23811	37383	0.76	0.0E+00	A685860.1	EST HUMAN	164647.x1 NQ1_OGAP_Kid8 Homo sapiens cDNA clone IMAGE:2244612.3

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID No.	Exon SEQ ID No.	ORF SEQ ID No.	Expression Signal	Max Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
11033	23017	37939	3.04	0.0E+00	BE743215.1	EST HUMAN	601573855.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11033	23017	37950	3.04	0.0E+00	BE743215.1	EST HUMAN	601573855.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11068	23020	37951	0.88	0.0E+00	BE677655.1	EST HUMAN	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11068	23020	37952	0.88	0.0E+00	BE677655.1	EST HUMAN	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11064	23038	37976	0.54	0.0E+00	H43806.1	EST HUMAN	701441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11072	23056	37982	2.27	0.0E+00	C97076.1	NT	U01441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11079	23059	37994	0.58	0.0E+00	BE172254.1	EST HUMAN	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11079	23059	37995	0.58	0.0E+00	BE172254.1	EST HUMAN	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11081	24013	37435	3.41	0.0E+00	AW161393.1	EST HUMAN	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11081	24013	37435	3.41	0.0E+00	AW161393.1	EST HUMAN	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11083	24013	37468	2.08	0.0E+00	AW161393.1	EST HUMAN	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11102	24033	37477	2.18	0.0E+00	AW161393.1	EST HUMAN	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11102	24033	37478	2.25	0.0E+00	11431124.1	EST HUMAN	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11104	24035	37480	1.94	0.0E+00	AW057824.1	EST HUMAN	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11113	24043	37488	1.83	0.0E+00	BE243270.1	EST HUMAN	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11114	24044	37489	3.23	0.0E+00	AW62239.1	EST HUMAN	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11114	24044	37489	3.23	0.0E+00	AW62239.1	EST HUMAN	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11124	24054	37500	4.29	0.0E+00	11545911	EST	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11124	24054	37501	4.29	0.0E+00	11545911	EST	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11140	24060	37515	1.08	0.0E+00	AW04706.1	EST HUMAN	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11144	24070	37520	3.87	0.0E+00	11426293	NT	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11144	24074	37521	8.6	0.0E+00	4504598	NT	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11145	24074	37522	8.3	0.0E+00	4504598	NT	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11145	24074	37523	3.40	0.0E+00	00616207.1	EST HUMAN	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11149	24079	37527	2.03	0.0E+00	BE82109.1	EST HUMAN	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11153	24082	37528	7.78	0.0E+00	BE01650.1	EST HUMAN	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11158	24084	37530	2.4	0.0E+00	8023690	NT	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11165	24094	37531	2.4	0.0E+00	8023690	NT	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5
11167	24095	37536	1.74	0.0E+00	U674408.1	NT	601441723.1 NR_10632.9 Homo sapiens cDNA clone IMAGE:2345198.5

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Table 4

Single Exon Probe Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	QBE SEQ ID NO:	Expression Signal	Most Similar (90%) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11161	24089	37547	1.74	0.0E+00	AB074908.1	EST_HUMAN	Homo sapiens mRNA for KIAA0700 protein, partial cds
11166	24097	37544	3.32	0.0E+00	BE030394.1	EST_HUMAN	g016423291 INT_NGCG_21 Homo sapiens cDNA clone IMAGE:587943.9
11172	10052	32177	1.88	0.0E+00	AA189995.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11192	24118	37605	3.77	0.0E+00	AA530890.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11193	24119	37605	5.68	0.0E+00	BE763495.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11200	24126	37572	16.88	0.0E+00	AA773292.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11201	24128	37673	16.88	0.0E+00	AA773292.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11214	24149	37692	20.51	0.0E+00	AA169551.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11220	24146	37697	1.6	0.0E+00	AJ158741.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11226	24151	37690	3.11	0.0E+00	AA593333.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11228	24161	37691	3.11	0.0E+00	AA593333.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11229	24151	37692	3.11	0.0E+00	AA593333.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11228	24154	37694	1.60	0.0E+00	Z24497.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11229	24155	37695	3.08	0.0E+00	F13060.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11255	24179	37628	3.12	0.0E+00	AA36994.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11259	24190	37629	4.38	0.0E+00	AA46120.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11260	24190	37630	4.38	0.0E+00	AA46120.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11261	24190	37630	4.38	0.0E+00	AA46120.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11269	24188	37632	1.73	0.0E+00	AB0714807.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11274	24198	37649	1.77	0.0E+00	BE298449.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11281	24200	37650	1.86	0.0E+00	AB071117.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11302	24221	37670	1.58	0.0E+00	BE762165.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11303	24222	37671	73.46	0.0E+00	BE762165.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11305	24224	37672	3.86	0.0E+00	AJ118396.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11309	24225	37673	1.7	0.0E+00	AA726039.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9
11311	24330	37676	6.79	0.0E+00	AJ146899.1	EST_HUMAN	249801171 Staphylococcus aureus 83200 Homo sapiens cDNA clone IMAGE:587943.9

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similarity (Top) HK BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
11311	24230	37677	5.79	0.0E+00	AI143606.1	EST HUMAN	g53033.1 Sulfate, sulfate, NHT Homo sapiens cDNA clone IMAGE:176272.3
11312	24231	37678	2.28	0.0E+00	AW287630.1	EST HUMAN	QV437024.1 G160-G35 S27022 Homo sapiens cDNA
11325	24244	37686	2.18	0.0E+00	AU116956.1	EST HUMAN	AUT16938 HEMBA1 Homo sapiens cDNA clone HEMBA100235.5
11329	24246	37688	3.97	0.0E+00	W14546.1	EST HUMAN	Homo sapiens brain, neocortex (N35) mRNA
11330	24250	37692	3.74	0.0E+00	W14546.1	EST HUMAN	Homo sapiens brain, neocortex (N35) mRNA
11331	24250	37692	3.74	0.0E+00	W14546.1	EST HUMAN	Homo sapiens brain, neocortex (N35) mRNA
11337	24259	37695	1.77	0.0E+00	BF346938.1	EST HUMAN	QV2410053-179400-191-200 LM0033 Homo sapiens cDNA
11339	24260	37697	26.65	0.0E+00	IE237106.1	EST HUMAN	60230701.F1 NCL CGAP_3164 Homo sapiens cDNA clone IMAGE:194970.5
11343	24262	37702	1.82	0.0E+00	AB202040.1	EST HUMAN	69114857.F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163310.5
11348	24263	37707	4.33	0.0E+00	U05238.1	NT	Homo sapiens mRNA for KNA1117 protein, partial cds
11375	24291	37735	65.09	0.0E+00	AA740782.1	EST HUMAN	Human protein kinase C subfamily BCK-1 (PKC- β) gene, exon 15-17
11382	24293	37744	3.05	0.0E+00	AF252303.1	NT	MSR1 negative element
11390	24312	37756	5.69	0.0E+00	U05238.1	EST HUMAN	Homo sapiens protein, lymphocyte activation molecule (SLAM) gene, exon 2
11403	24319	37758	2.44	0.0E+00	AA746375.1	EST HUMAN	QV6589 Homo sapiens heart cDNA (YNAKamara) Homo sapiens cDNA clone 3NH-C4817
11403	24319	37758	2.44	0.0E+00	AA746375.1	EST HUMAN	QV6589 Homo sapiens heart cDNA (YNAKamara) Homo sapiens cDNA clone 3NH-C4817
11411	24327	37757	1.88	0.0E+00	BF346938.1	EST HUMAN	QV2410053-179400-191-200 LM0033 Homo sapiens cDNA
11414	24330	37778	1.57	0.0E+00	BF346938.1	EST HUMAN	QV2410053-179400-191-200 LM0033 Homo sapiens cDNA
11415	24331	37779	5.95	0.0E+00	AL117693.1	EST HUMAN	QV2410053-179400-191-200 LM0033 Homo sapiens cDNA
11427	24343	37788	7.08	0.0E+00	AU116963.1	EST HUMAN	AUT16938 HEMBA1 Homo sapiens cDNA clone GKCCNC03.5
11440	24356	37804	1.98	0.0E+00	AU116963.1	EST HUMAN	AUT16938 HEMBA1 Homo sapiens cDNA clone GKCCNC03.5
11448	24364	37813	1.4	0.0E+00	BF346938.1	EST HUMAN	QV2410053-179400-191-200 LM0033 Homo sapiens cDNA
11474	24387	37837	2.7	0.0E+00	IE182800.1	EST HUMAN	QV2410053-179400-191-200 LM0033 Homo sapiens cDNA
11484	24397	37847	1.72	0.0E+00	AA740782.1	EST HUMAN	QV2410053-179400-191-200 LM0033 Homo sapiens cDNA
11488	24400	37890	3.69	0.0E+00	IE182800.1	EST HUMAN	QV2410053-179400-191-200 LM0033 Homo sapiens cDNA
11498	24407	37891	1.63	0.0E+00	AA740782.1	EST HUMAN	QV2410053-179400-191-200 LM0033 Homo sapiens cDNA
11498	24407	37891	1.63	0.0E+00	AA740782.1	EST HUMAN	QV2410053-179400-191-200 LM0033 Homo sapiens cDNA
11499	24413	37894	1.71	0.0E+00	BF346938.1	EST HUMAN	QV2410053-179400-191-200 LM0033 Homo sapiens cDNA
11524	24434	37902	1.62	0.0E+00	AU121877.1	EST HUMAN	AUT171877 MAMM1 Homo sapiens cDNA clone MAMM100731.5
11530	24436	37907	3.94	0.0E+00	BF346938.1	EST HUMAN	QV2410053-179400-191-200 LM0033 Homo sapiens cDNA
11538	24448	37910	1.68	0.0E+00	AA49546.1	EST HUMAN	g658511.1 Schlier membrane Homo sapiens cDNA clone IMAGE:192204.3

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expressi on Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11538	24448	37911	1.68	0.0E+00/AJ65946.1	EST_HUMAN	EST_HUMAN	cdg8g.11.1 Schlatter meningioma Homo sapiens cDNA clone IMAGE1962804.3
11539	24449	37965	3.1	0.0E+00/B200691.1	EST_HUMAN	EST_HUMAN	Homo sapiens neuromus III (N303X) mRNA
11574	24498	37665	3.1	0.0E+00/B200691.1	EST_HUMAN	EST_HUMAN	031870600.01 NH MG-13 Homo sapiens cDNA clone IMAGE1401483.3
11586	24494	37663	13.79	0.0E+00/AJ120734.1	EST_HUMAN	EST_HUMAN	U4H-B2; ang-5-01-01.1 rat NCI-GSP-3342-Homo sapiens cDNA clone IMAGE2724812.3
11586	24494	37664	13.79	0.0E+00/AJ120734.1	EST_HUMAN	EST_HUMAN	Homo sapiens mRNA for TM60717 protein, partial cds
11586	24497	37665	3.18	0.0E+00/AJ5018300.1	EST_HUMAN	EST_HUMAN	034407.01 NH MG-7 Homo sapiens cDNA clone IMAGE362337.9 similar to TR076622 076622 E1B
11586	24497	37665	3.18	0.0E+00/AJ5018300.1	EST_HUMAN	EST_HUMAN	034407.01 NH MG-7 Homo sapiens cDNA clone IMAGE362337.9 similar to TR076622 076622 E1B
11590	24499	37667	4.97	0.0E+00/BE200846.1	EST_HUMAN	EST_HUMAN	034407.01 NH MG-7 Homo sapiens cDNA clone IMAGE362337.9 similar to TR076622 076622 E1B
11590	24499	37668	4.97	0.0E+00/BE200846.1	EST_HUMAN	EST_HUMAN	034407.01 NH MG-7 Homo sapiens cDNA clone IMAGE362337.9 similar to TR076622 076622 E1B
11613	24563	37667	1.83	0.0E+00/1102471.1	EST_HUMAN	EST_HUMAN	034407.01 NH MG-7 Homo sapiens cDNA clone IMAGE362337.9 similar to TR076622 076622 E1B
11613	24563	37668	1.83	0.0E+00/1102471.1	EST_HUMAN	EST_HUMAN	034407.01 NH MG-7 Homo sapiens cDNA clone IMAGE362337.9 similar to TR076622 076622 E1B
11621	24528	37666	2.44	0.0E+00/BE140876.1	EST_HUMAN	EST_HUMAN	034407.01 NH MG-7 Homo sapiens cDNA clone IMAGE362337.9 similar to TR076622 076622 E1B
11621	24528	37667	2.44	0.0E+00/BE140876.1	EST_HUMAN	EST_HUMAN	034407.01 NH MG-7 Homo sapiens cDNA clone IMAGE362337.9 similar to TR076622 076622 E1B
11643	24546	39020	1.59	0.0E+00/AJ675469.1	EST_HUMAN	EST_HUMAN	034407.01 NH MG-7 Homo sapiens cDNA clone IMAGE362337.9 similar to TR076622 076622 E1B
11643	24546	39021	1.59	0.0E+00/AJ675469.1	EST_HUMAN	EST_HUMAN	034407.01 NH MG-7 Homo sapiens cDNA clone IMAGE362337.9 similar to TR076622 076622 E1B
11663	24569	38044	6.1	0.0E+00/BF050776.1	EST_HUMAN	EST_HUMAN	U4H-B4; ang-5-10-01.1 rat NCI-GSP-3348 Homo sapiens cDNA clone IMAGE305628.3
11663	24569	38045	6.1	0.0E+00/BF050776.1	EST_HUMAN	EST_HUMAN	U4H-B4; ang-5-10-01.1 rat NCI-GSP-3348 Homo sapiens cDNA clone IMAGE305628.3
11671	24575	39051	1.69	0.0E+00/BF195710.1	EST_HUMAN	EST_HUMAN	U4H37017 FLAET1 Homo sapiens cDNA clone PLACE1003381.9
11675	24579	39055	1.69	0.0E+00/BF195710.1	EST_HUMAN	EST_HUMAN	0317324569.01 NH MG-31 Homo sapiens cDNA clone IMAGE1471500.9
11675	24579	39056	1.63	0.0E+00/BF195710.1	EST_HUMAN	EST_HUMAN	0317324569.01 NH MG-31 Homo sapiens cDNA clone IMAGE1471500.9
11676	24580	39057	1.713	0.0E+00/BF195710.1	EST_HUMAN	EST_HUMAN	0317324569.01 NH MG-31 Homo sapiens cDNA clone IMAGE1471500.9
11676	24580	39057	1.713	0.0E+00/BF195710.1	EST_HUMAN	EST_HUMAN	0317324569.01 NH MG-31 Homo sapiens cDNA clone IMAGE1471500.9
11676	24580	39058	1.713	0.0E+00/BF195710.1	EST_HUMAN	EST_HUMAN	0317324569.01 NH MG-31 Homo sapiens cDNA clone IMAGE1471500.9
11686	24588	39071	2.21	0.0E+00/BF037367.1	EST_HUMAN	EST_HUMAN	0317324569.01 NH MG-31 Homo sapiens cDNA clone IMAGE3856207.5
11686	24588	39072	2.21	0.0E+00/BF037367.1	EST_HUMAN	EST_HUMAN	0317324569.01 NH MG-31 Homo sapiens cDNA clone IMAGE3856207.5
11700	24600	39078	2.21	0.0E+00/BF037367.1	EST_HUMAN	EST_HUMAN	0317324569.01 NH MG-31 Homo sapiens cDNA clone IMAGE4099710.5
11700	24600	39078	2.21	0.0E+00/BF037367.1	EST_HUMAN	EST_HUMAN	0317324569.01 NH MG-31 Homo sapiens cDNA clone IMAGE4099710.5
11704	24600	39091	3.42	0.0E+00/11430968.NT	EST_HUMAN	EST_HUMAN	Homo sapiens mRNA for KIAA1316 protein, partial cds
11704	24600	39132	3.42	0.0E+00/11430968.NT	EST_HUMAN	EST_HUMAN	Homo sapiens ribosomal subunit 2 (p130) (RPL2), mRNA
11721	24623	38103	6.03	0.0E+00/AJ228176.1	EST_HUMAN	EST_HUMAN	Homo sapiens ribosomal subunit 2 (p130) (RPL2), mRNA
11721	24623	38103	6.03	0.0E+00/AJ228176.1	EST_HUMAN	EST_HUMAN	Homo sapiens subunit yotic translation initiation factor 5A (EIF5A) mRNA
11730	24635	39113	29.52	0.0E+00/AB03903.1	EST_HUMAN	EST_HUMAN	030405.01 NH MG-3 Homo sapiens cDNA clone IMAGE284777.5
11733	24635	39133	29.52	0.0E+00/AB03903.1	EST_HUMAN	EST_HUMAN	Human gamma actin-like pseudogene, complete cds

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mean Similar (Top) HN BLAST E Value	Top HN Accession No.	Top HN Database Source	Top Hit Description
11876	29076	37412	1.93	0.0E+00	U551696.1	EST_HUMAN	86127035F1 NHL_MGC_36 Homo sapiens cDNA clone IMAGE:3811144 5'
11879	29079	37413	1.90	0.0E+00	U551696.1	EST_HUMAN	90127035F1 NHL_MGC_36 Homo sapiens cDNA clone IMAGE:3811144 5'
11882	29082	37420	1.57	0.0E+00	AF787420.1	EST_HUMAN	AV787420 Bst Homo sapiens cDNA clone B10P403 5'
11911	27458	39253	1.76	0.0E+00	U38991.1	NT	Homo sapiens polyoma kidney disease-associated protein (PKD1) gene, complete cds
11911	27458	39254	1.76	0.0E+00	U38991.1	NT	Homo sapiens polyoma kidney disease-associated protein (PKD1) gene, complete cds
11925	24770	39257	3.98	0.0E+00	AU18211.1	EST_HUMAN	AU18211 PUCH1 Homo sapiens cDNA clone P1C3E103677 5'
11944	24788	39284	29.97	0.0E+00	AU18211.1	EST_HUMAN	AU18211 PUCH1 Homo sapiens cDNA clone P1C3E103677 5'
11944	24788	39285	29.97	0.0E+00	AU18211.1	EST_HUMAN	AU18211 PUCH1 Homo sapiens cDNA clone P1C3E103677 5'
11972	24675	39306	7.56	0.0E+00	U207425.1	EST_HUMAN	U207425 Homo sapiens cDNA clone IMAGE:3456012 3'
11972	24675	39306	7.56	0.0E+00	U207425.1	EST_HUMAN	U207425 Homo sapiens cDNA clone IMAGE:3456012 3'
11972	24675	39306	7.56	0.0E+00	U207425.1	EST_HUMAN	U207425 Homo sapiens cDNA clone IMAGE:3456012 3'
11983	24628	39322	2.01	0.0E+00	AU11882	EST_HUMAN	AU11882 THYR01 Homo sapiens cDNA clone THYR01001388 5'
11983	24628	39323	2.01	0.0E+00	AU11882	EST_HUMAN	AU11882 THYR01 Homo sapiens cDNA clone THYR01001388 5'
11986	24629	39326	6	0.0E+00	AU1007022.1	EST_HUMAN	CE1040 ZINC_FINGER_C9H5 TYPE1
11990	29700	39330	2.7	0.0E+00	BF002333.1	EST_HUMAN	702281021 NCL_CGAP_C016 Homo sapiens cDNA clone IMAGE:3318562 3' similar to TRQ13488 Q18458
12010	24682	39332	2.60	0.0E+00	AF038776.1	EST_HUMAN	TRQ13488
12010	24682	39332	2.60	0.0E+00	AF038776.1	EST_HUMAN	TRQ13488
12010	24682	39335	2.60	0.0E+00	AF038776.1	EST_HUMAN	TRQ13488
12031	24673	39377	4.66	0.0E+00	U1455244	NT	MR4-S10118-251068-0.2-303 ST0118 Homo sapiens cDNA
12031	24673	39377	4.66	0.0E+00	U1455244	NT	MR4-S10118-251068-0.2-303 ST0118 Homo sapiens cDNA
12031	24673	39378	4.66	0.0E+00	U1455244	NT	MR4-S10118-251068-0.2-303 ST0118 Homo sapiens cDNA
12031	24673	39384	9.4	0.0E+00	U93535.1	EST_HUMAN	Homo sapiens KIA0247 gene product (KIA0247), mRNA
12038	24681	39396	5.52	0.0E+00	BE376254.1	EST_HUMAN	Homo sapiens KIA0247 gene product (KIA0247), mRNA
12038	24681	39397	5.52	0.0E+00	BE376254.1	EST_HUMAN	Homo sapiens KIA0247 gene product (KIA0247), mRNA
12046	24697	39392	6.95	0.0E+00	U12228.1	NT	Homo sapiens KIA0247 gene product (KIA0247), mRNA
12051	24692	39395	1.81	0.0E+00	AA488894.1	EST_HUMAN	Homo sapiens KIA0247 gene product (KIA0247), mRNA
12058	24690	39404	2.46	0.0E+00	BE747458.1	EST_HUMAN	Homo sapiens KIA0247 gene product (KIA0247), mRNA
12062	24693	39405	36.48	0.0E+00	BE747458.1	EST_HUMAN	Homo sapiens KIA0247 gene product (KIA0247), mRNA
12067	24698	39410	2.31	0.0E+00	4759827	NT	Homo sapiens KIA0247 gene product (KIA0247), mRNA
12067	24698	39411	2.31	0.0E+00	4759827	NT	Homo sapiens KIA0247 gene product (KIA0247), mRNA
12071	24692	39415	1.75	0.0E+00	AF095343.1	NT	Homo sapiens KIA0247 gene product (KIA0247), mRNA
12079	24616	39416	2.18	0.0E+00	U01476.1	EST_HUMAN	Homo sapiens KIA0247 gene product (KIA0247), mRNA

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Protein SEQ ID NO.	Eno. SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Annotation No.	Top Hit Database Source	Top Hit Descriptor
12376	24619	38420	2.18	0.0E+00 W01478.1	EST_HUMAN	EST_HUMAN	z6402.71 Sources fetal liver spleen N1E5 Homo sapiens cDNA clone IMAGE:281434 5' similar to
12380	24621	38423	2.65	0.0E+00 AF09893.1	EST_HUMAN	EST_HUMAN	SW NABA RAT P28458 SODIUM-LE ACID COTRANSPORTER;
12381	24622	38424	1.48	0.0E+00 BE14869.1	EST_HUMAN	EST_HUMAN	W07-29040317-NH MGC 21 Homo sapiens cDNA clone IMAGE:362544 5'
12382	24623	38425	1.52	0.0E+00 I1427345.NT	EST_HUMAN	EST_HUMAN	W07-104211-15090011-502 H120211 Homo sapiens cDNA
12383	24624	38426	1.62	0.0E+00 I1427345.NT	EST_HUMAN	EST_HUMAN	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
12384	24625	38427	1.52	0.0E+00 I1427345.NT	EST_HUMAN	EST_HUMAN	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
12385	24626	38428	1.62	0.0E+00 I1427345.NT	EST_HUMAN	EST_HUMAN	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
12386	24627	38429	1.52	0.0E+00 I1427345.NT	EST_HUMAN	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-40, and partial cds, alternatively spliced
12387	24628	38430	2.70	0.0E+00 AF223391.1	NT	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-40, and partial cds, alternatively spliced
12388	24629	38431	2.76	0.0E+00 AF223391.1	NT	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-40, and partial cds, alternatively spliced
12389	24630	38432	2.76	0.0E+00 AF223391.1	NT	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-40, and partial cds, alternatively spliced
12390	24631	38433	2.76	0.0E+00 AF223391.1	NT	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-40, and partial cds, alternatively spliced
12391	24632	38434	2.76	0.0E+00 AF223391.1	NT	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-40, and partial cds, alternatively spliced
12392	24633	38440	2.2	0.0E+00 AF223391.1	NT	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-40, and partial cds, alternatively spliced
12393	24634	38441	2.2	0.0E+00 AF223391.1	NT	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-40, and partial cds, alternatively spliced
12394	24635	38442	2.73	0.0E+00 BE03371.2	EST_HUMAN	EST_HUMAN	AT135001.NT28P17 Homo sapiens cDNA clone YF85403020 5'
12395	24636	38443	2.73	0.0E+00 BE03371.2	EST_HUMAN	EST_HUMAN	AT135001.NT28P17 Homo sapiens cDNA clone YF85403020 5'
12396	24637	38444	2.73	0.0E+00 BE03371.2	EST_HUMAN	EST_HUMAN	AT135001.NT28P17 Homo sapiens cDNA clone YF85403020 5'
12397	24638	38445	2.73	0.0E+00 BE03371.2	EST_HUMAN	EST_HUMAN	AT135001.NT28P17 Homo sapiens cDNA clone YF85403020 5'
12398	24639	38446	2.73	0.0E+00 BE03371.2	EST_HUMAN	EST_HUMAN	AT135001.NT28P17 Homo sapiens cDNA clone YF85403020 5'
12399	24640	38447	2.73	0.0E+00 BE03371.2	EST_HUMAN	EST_HUMAN	AT135001.NT28P17 Homo sapiens cDNA clone YF85403020 5'
12400	24641	38448	2.73	0.0E+00 BE03371.2	EST_HUMAN	EST_HUMAN	AT135001.NT28P17 Homo sapiens cDNA clone YF85403020 5'
12401	24642	38449	2.73	0.0E+00 BE03371.2	EST_HUMAN	EST_HUMAN	AT135001.NT28P17 Homo sapiens cDNA clone YF85403020 5'
12402	24643	38450	2.73	0.0E+00 BE03371.2	EST_HUMAN	EST_HUMAN	AT135001.NT28P17 Homo sapiens cDNA clone YF85403020 5'
12403	24644	38451	2.73	0.0E+00 BE03371.2	EST_HUMAN	EST_HUMAN	AT135001.NT28P17 Homo sapiens cDNA clone YF85403020 5'
12404	24645	38452	2.73	0.0E+00 BE03371.2	EST_HUMAN	EST_HUMAN	AT135001.NT28P17 Homo sapiens cDNA clone YF85403020 5'
12405	24646	38453	2.73	0.0E+00 BE03371.2	EST_HUMAN	EST_HUMAN	AT135001.NT28P17 Homo sapiens cDNA clone YF85403020 5'
12406	24647	38454	2.73	0.0E+00 BE03371.2	EST_HUMAN	EST_HUMAN	AT135001.NT28P17 Homo sapiens cDNA clone YF85403020 5'
12407	24648	38455	2.73	0.0E+00 BE03371.2	EST_HUMAN	EST_HUMAN	AT135001.NT28P17 Homo sapiens cDNA clone YF85403020 5'
12408	24649	38456	2.73	0.0E+00 BE03371.2	EST_HUMAN	EST_HUMAN	AT135001.NT28P17 Homo sapiens cDNA clone YF85403020 5'
12409	24650	38457	2.73	0.0E+00 BE03371.2	EST_HUMAN	EST_HUMAN	AT135001.NT28P17 Homo sapiens cDNA clone YF85403020 5'
12410	24651	38458	2.73	0.0E+00 BE03371.2	EST_HUMAN	EST_HUMAN	AT135001.NT28P17 Homo sapiens cDNA clone YF85403020 5'
12411	24652	38459	2.73	0.0E+00 BE03371.2	EST_HUMAN	EST_HUMAN	AT135001.NT28P17 Homo sapiens cDNA clone YF85403020 5'
12412	24653	38460	2.73	0.0E+00 BE03371.2	EST_HUMAN	EST_HUMAN	AT135001.NT28P17 Homo sapiens cDNA clone YF

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	Q9F SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12140	13021	28958	7.93	0.0E+00	4907500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
12149	29021		2.17	0.0E+00	4002557	NT	Homo sapiens nuclear factor of activated T-cells, cytochrome, calcineurin-dependent 2 (NFATC2) mRNA
12174	13038		3.25	0.0E+00	A003528.1	NT	Homo sapiens X-linked adrenergic endoneurial dysplasia protein gene (EDA), exon 2 and flanking repeat
12503	25713	31739	2.44	0.0E+00	TH50.60	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2) mRNA
12562	29764	31575	2.82	0.0E+00	AV150083.1	EST_HUMAN	hg31cds.v1 NC_024608 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
12563	29768		1.51	0.0E+00	L20463.1	EST_HUMAN	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
12564	29767		3.04	0.0E+00	A048757.1	NT	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
12565	29812		4.02	0.0E+00	5033447	NT	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
12566	29812		1.87	0.0E+00	A204914.1	EST_HUMAN	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
12719	23007		2.69	0.0E+00	A041346.1	EST_HUMAN	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
12721	23008		1.6	0.0E+00	BEA39762.1	EST_HUMAN	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
12760	14738	27706	4.48	0.0E+00	H00132.1	EST_HUMAN	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
12760	14738	27707	4.48	0.0E+00	H00132.1	EST_HUMAN	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
12771	25405		18.65	0.0E+00	D50556.1	NT	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
12781	25410	31793	4.86	0.0E+00	11415186	NT	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
12781	25410	31794	4.86	0.0E+00	11415186	NT	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
12784	25413		1.57	0.0E+00	A002686.1	NT	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
12827	25445		2.60	0.0E+00	A0054999.1	EST_HUMAN	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
12871	25473		1.74	0.0E+00	11503591	NT	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
12897	16403	25304	2.69	0.0E+00	4880312	NT	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
12903	16430	31393	1.86	0.0E+00	6800916	NT	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
12908	25462		2.45	0.0E+00	A0039900.1	NT	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
12945	25511	31773	1.84	0.0E+00	6889724	NT	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
12969	25564		3.31	0.0E+00	A1163246.2	NT	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
12976	13111	25518	1.56	0.0E+00	6800916	NT	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
13044	25579		3.08	0.0E+00	7657202	NT	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu
13080	25598		2.03	0.0E+00	A002388.1	NT	U03165.1 Homo sapiens cDNA clone IMAGE:2847234.3 similar to consense Alu

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) HA BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13097	28506		1.98	0.0E+00	X5747.1	NT	Human endogenous retrovirus p16.1 (ERV9)

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CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human adult liver comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 13,109 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 13,110 - 25,995.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

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average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.
9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.
10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.
11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.
12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.
13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human adult liver comprising a nucleotide sequence as set out in any of SEQ ID NOs. 1 - 13,109 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human adult liver.

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14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 13,110 - 25,995 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human adult liver which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 25,996 - 38,578, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human adult liver.

10

16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

15

17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

20

18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

25

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

30

20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

21. A single exon nucleic acid probe as claimed in any one

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of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample
5 derived from human adult liver, comprising:
 contacting the microarray of claim 12, with a first
 collection of detectably labeled nucleic acids,
 said first collection of nucleic acids derived
 from mRNA of human adult liver; and then
10 measuring the label detectably bound to each probe of
 said microarray.
23. A method of identifying exons in a eukaryotic genome,
comprising:
15 algorithmically predicting at least one exon from
 genomic sequence of said eukaryote; and then
 detecting specific hybridization of detectably labeled
 nucleic acids to a single exon probe,
 wherein said detectably labeled nucleic acids are derived
20 from mRNA from the adult liver of said eukaryote, said
 probe is a single exon probe having a fragment identical in
 sequence to, or complementary in sequence to, said
 predicted exon, said probe is included within a microarray
 according to claim 12, and said fragment is selectively
25 hybridizable at high stringency.
24. A method of assigning exons to a single gene,
comprising:
 identifying a plurality of exons from genomic
30 sequence according to the method of claim 23; and
 then
 measuring the expression of each of said exons in a
 plurality of tissues and/or cell types using
 hybridization to single exon microarrays having a
35 probe with said exon,

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wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

5 25. A nucleic acid sequence as set out in any of SEQ ID Nos: 1 - 25,995 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 - 25,995.

10

27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 25,996 - 38,578.

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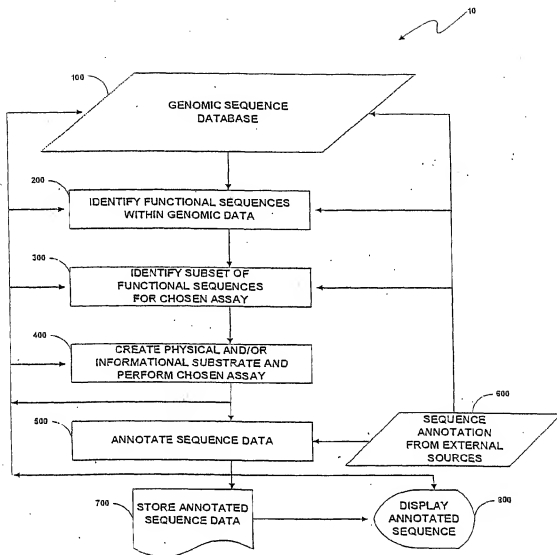


Fig. 1

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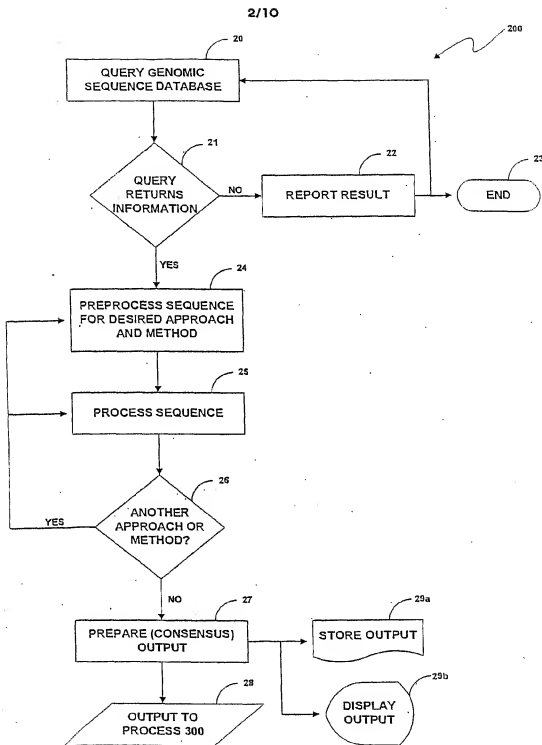


Fig. 2

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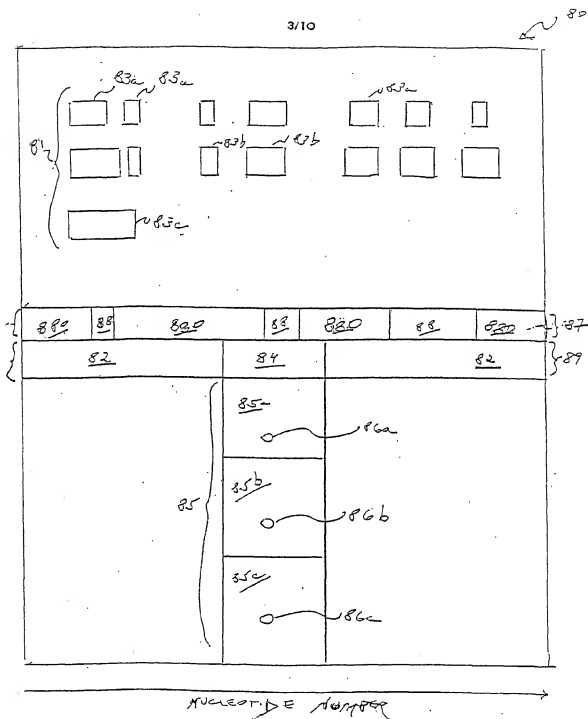


Fig. 3

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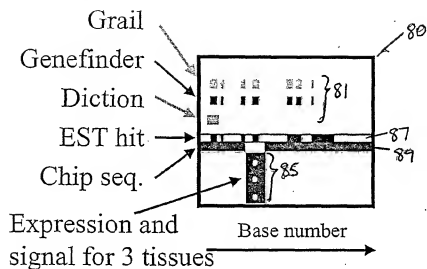


Fig. 4

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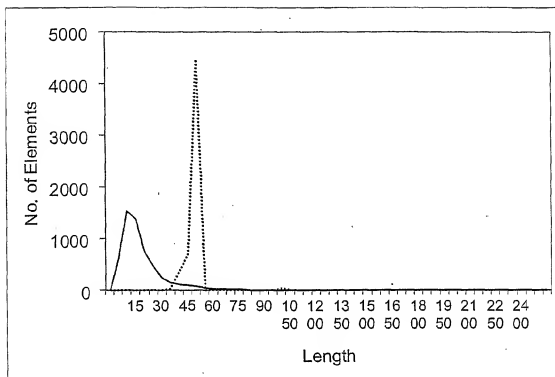


Fig. 5

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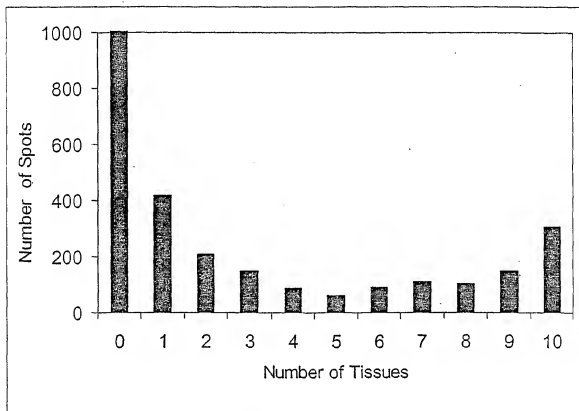


Fig. 6

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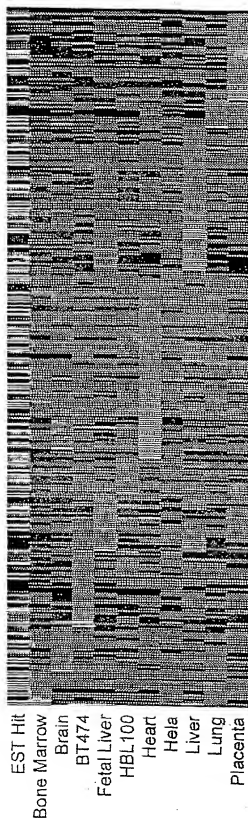


Fig. 7a

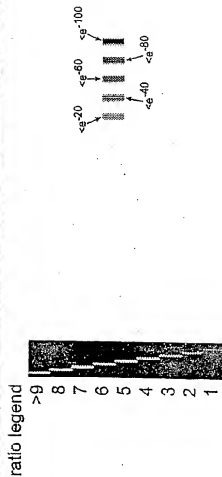


Fig. 7b

Fig. 7c

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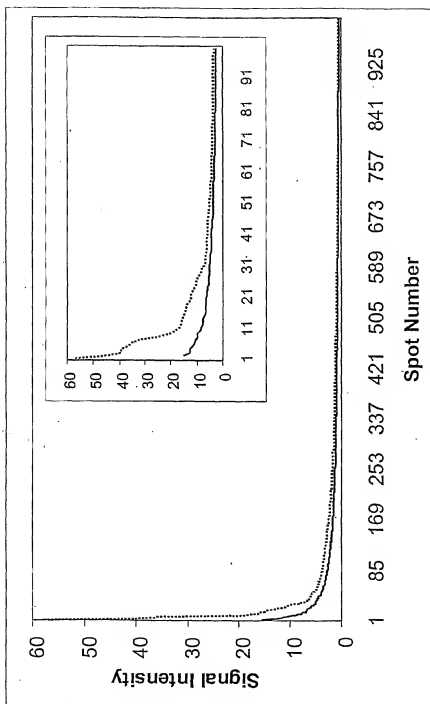


Fig. 8

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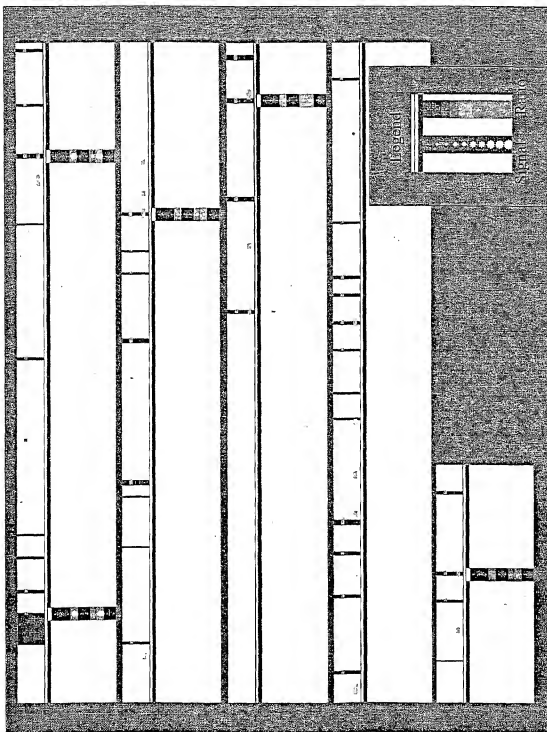


Fig. 9

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Fig. 10

